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Gearing Up: Animal Science and Beyond

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E.A. Akuru^{1#}, C. Nel¹, W.J. Steyn^{1,3} & C. Jansen van Rensburg^{1,2}

Comparison of GWAS methods reveals improved detection using Mixed Linear Models in sheep

B. Bhika Kooverjee^{1,2#}, M.D. MacNeil^{1,2,3} & P. Soma¹

Preliminary results: influence of pre-storage incubation treatments on hatching outcomes of ostrich eggs

Z. Brand^{1#} & B.R. Snyman¹

Evaluation of different inclusion levels of processed mopani worm meal with multienzymes on growth performance and nutrient digestibility of broilers

M.J. Chipa^{1#}, S.D. Kolobe¹, E. Malematj¹, M.B. Sekhonyana¹ & M. Mabelebele¹

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M. Ramuada¹, T.L. Tyasi¹, L. Gumede¹, P. Tebeila² & T. Chitura^{3#}

The effect of supplementation on reproduction and weight in extensively managed beef cattle in the eastern Kalahari bushveld

S. Diamond^{1,4#}, S.M. Grobler², M.M Scholtz^{2,3} & P.J. Fourie⁴

Effect of cereal-based diets on growth performance and nutrient digestibility of weaned Californian rabbits

N.P. Dlodlo^{1#}, Z.T. Rani¹, R. Gous¹ & T.L. Tyasi²

Effect of moringa leaf and seed extract blend on the growth performance and meat quality of broiler chickens

C.F. Egbu^{1#}, L.E. Motsei², A.O. Yusuf³ & C.J. Smit¹

The applicability of the temperature-humidity-index model as a heat stress indicator in South African dairy cattle

L. Erasmus^{1#}, E. van Marle-Köster¹ & D. Berry²

Effect of condensed tannin on the fibrolytic activity of microbial ecosystem from both wild and domestic browsers

N.N.P. Msimango¹ & F.N. Fon^{1#}

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M. Gomo^{1#}, L.F. Brito^{1,2}, A.O. Rocha² & C. Visser¹

Toxigenic *Clostridioides difficile* associated with food-producing animals and game in South Africa

M. Gouws^{1#}, P.E. Strydom² & D. Rip¹

Post-mortem pH and meat colour of four slow-growing chicken breeds reared intensively in South Africa

F.Y. Hlongwana^{1,2}, S.M. Mdletshe¹, P.L. Seema¹, M. Magoro¹, L. Shikweni¹, A. Basson¹, Z.T. Rani², C.N. Ncobela³ & E. Moholisa^{1#}

Haplotype-resolved de novo genome assembly using trio binning reveals patterns of genetic divergence in the Windsnyer indigenous pig

N.L. Hlongwane^{1#}, R.M. Smith², T.S. Tshilata¹, L.T. Nesengani¹, S. Mdyogolo¹, S.A Hadebe¹, A.H. Molotsi¹, T.M. Masebe² & N.O. Mapholi¹

Antibiogram fingerprinting of *Vibrio* species recovered from commercial fish specimens collected from key retailers in the Eastern Cape region of South Africa

A. Hobe^{1,2,3}, L. Msolo^{1,2}, A.I. Okoh^{1,2} & I.F. Jaja^{1,2,3}

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J.J. Joubert¹, E. Pieterse², H.A. O'Neill¹, M. Mphaphathi³, M. Erasmus⁴, E.D. Cason¹, J.D.V. van Wyngaardt⁵, A. Hugo¹ & O.B. Einkamerer^{1#}

Effect of dietary kenaf leaf meal on the hormonal profile, mating behaviour, and testicular histology of rabbit bucks

T.C. Kujoana^{1#}, M. Mabelebele¹ & N.A. Sebola¹

The influence of milk feeding strategy on the rumen development of Holstein heifer calves

H. Lambrechts^{1#}, J.A. Rice¹ & J.H.C. Van Zyl¹

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H. Lambrechts^{1#}, J.A. Rice¹ & J.H.C. Van Zyl¹

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S.F. Lashmar^{1#}

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M.R. Ledwaba^{1,2}, Z. Seekford³, T.Minela³, H.A. O'Neill², M.A. Thema¹, T.L. Mashilo^{2,4}, A. Maqhashu², G.C. Lamb³, K.G. Pohler³ & M.L. Mphaphathi^{1#}

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T.M. Joe^{1, 2#}, C. Nyamukondiwa^{2,3,4} & H. Machekano^{1,5}

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E. Madiba^{1#}, K. Marima¹, K. Dzama¹ & A. Molotsi^{1,2}

Spatiotemporal analysis of bovine tuberculosis incidence in cattle in South Africa

E. Maguta^{1#}, A. Michel² & I.F. Jaja¹

Generational trends on growth performance of stud Bonsmara beef cattle across agro-ecological zones of South Africa

C. Makaleng^{1#}, O. Tada¹ & T.L. Tyasi²

Protein source and lactic acid bacteria inoculation effects on fermentation dynamics, aerobic stability, and nutrient degradability of maize silage

I.M.M. Malebana^{1#}, B.D. Nkosi¹, T. Langa¹, M. Vuma², M.M. Ratsaka² & J.T. Tjelele³

Adaptive morpho-physiological responses of Boer, Kalahari Red, and indigenous goats across climatic seasons

C.F. Mashaba^{1#}, S.S. Molapo¹, K.N. Sibiya¹ & O. Tada¹

Baseline long-read sequencing metrics for the Bonsmara cattle breed

M.M. Mbedzi^{1,2#}, S.F. Lashmar¹, T. Klingström³, A.E. Lundberg³ & R. Erasmus¹

Effects of green betaine-coated nano-silver in large white grower pigs fed marula nut cake-containing diets

Y. Mbenga¹, D.M.N. Mthiyane^{1#}, C.M. Mnisi¹ & D.C. Onwudiwe²

Investigation of mutant traits in indigenous chickens and their production performance in Polokwane local municipality, Limpopo

S. Mhlabini^{1#}, T.L. Tyasi¹ & K.R. Nemutandani¹

Effects of grass silages on gut microbial ecology, fecal characteristics and production performance in finisher pigs

Y. Mjadu^{1#}, F.N. Fon¹ & F. Tshabuse²

Effect of breed and age on egg quality characteristics of South African indigenous chickens

P.S. Mokgapa^{1#}, K. Mokoena¹, J.T. Mugwabana¹ & T.L. Tyasi¹

Whole metagenome shotgun sequencing characterises seasonal dynamics of the faecal microbiome in Nguni cattle

J. Mokoena^{1,2#}, D.P. Malatji², T. Raphulu³ & T.M. Ramantswana¹

An integrated manual-digital recording system within a pilot community program for small-scale goat farmers in Kwazulu- Natal and Eastern Cape provinces of South Africa

N.K. Molete^{1#}, M. Segakoeng¹, S.L. Gcabashe¹, A. Mchunu², O. Bixa² & K. Hadebe¹

Effect of *bacillus*-based probiotic and butyric acid on growth performance, physiological status and welfare in broilers offered diet containing sorghum

R.D. Mukwevho^{1#} & U. Marume¹

Reproductive traits and live weight in merino rams divergently selected for and against number of lambs weaned per mating

S.W.P. Cloete^{1#}, C.L. Nel^{1,2} & J.J.E. Cloete³

Diurnal variation of rumen temperature in South African sheep breeds under mediterranean summer conditions

K. Mafunga^{1,4#}, C.L. Nel^{1,2}, S.K. Maloney³, K. Dzama¹ & S.W.P. Cloete¹

Effect of Kalahari melon (*Citrullus lanatus*) essential oil and butyric acid in grower pig diets on growth performance, meat quality and fatty acid profile

R.B. Nhara^{1,2#} & U. Marume¹

Effect of different varieties of rosemary (*Rosmarinus officinalis*) plant extracts on in vitro methane production of *Eragrostis curvula* hay

S.K. Nthinya^{1#}, A.M. Akanmu¹ & A. Hassen¹

Genomic regions under selection in Ayrshire cattle identified using integrated haplotype score

M.L. Papo^{1#}, S.F. Lashmar^{2#}, K.T. Ncube³, A.M. Magoro¹, M.C. Modiba¹ & B. Mtileni¹

Empowering smallholder sheep farmers using data-driven body weight prediction algorithms in Dorper sheep from two villages in Limpopo province, South Africa

A.M. Phaladi^{1#}, T.L. Tyasi¹ & O. Tada¹

Effect of replacing lucerne hay with *Serriphium plumosum* meal in diet on live weight gain, meat quality and sensory attributes of Nguni steers

M.E. Phoko^{1,3#}, T.J. Tjelele⁴, J.W. Nga'mbi⁴ & K. Munhuweyi²

Genomic characterisation of the South African Wagyu populations

T. Pieterse^{1,2#}, E. van Marle-Köster¹ & C. Visser¹

Genetic (co)variance components of faecal egg count and production traits in Elsenburg South African Mutton Merino and Dormer sheep

T. Rapudi^{1#}, C.L. Nel^{1,2}, S.W.P. Cloete¹ & K. Dzama¹

Evaluation of factors influencing the detection of selection signatures in populations selected for traits with different genetic architectures using simulated data

A. Retief^{1,2#}, L.F. Brito^{1,2} & C. Visser¹

Preliminary results on the influence of enzyme-treated insect meal on growth and gonad development of abalone (*Haliotis midae*)

K. Roodt¹, H. Lambrechts¹ & J.H.C. Van Zyl¹

Feather harvesting methods influence feather quality and yield in South African Black breeder ostriches (*Struthio camelus* var. *Domesticus*)

C.L. Sampson^{1#}, S.W.P. Cloete¹, M. Bonato², H. Lambrechts¹ & A. Engelbrecht³

The effect of Mopane worm (*Imbrasia belina* meal) and multienzyme inclusion on gut morphology, digesta pH, and growth performance of Ross 308 broiler chicks

B. Sekhonyana^{1#}, E. Malematja¹, M. Mabelebele¹ & J. Chipa¹

Nutritional and phenolic characterisation of Spineless Cactus (*Opuntia ficus-indica*) cladodes as a functional feed resource for slow-growing goats

C.M. Seloane^{1#}, T.G. Manyelo¹ & Z.M. Mdletshe¹

The effect of climatic factors on calving percentage of Bonsmara cows in the Eastern Kalahari Bushveld

M.M. Seshoka^{1,3#}, S.M. Grobler², M.M. Scholtz^{2,3}, L. Morey⁴, G. Pyoos² & F.W.C. Naser³

The effect of moisture content on the sensory properties of rabbit biltong

M.Z. Shangase¹, M.P. Sodella¹, M. Siwela², Z.T. Rani-Kamwendo^{1#}

The maternal heritability of ewes to reunite with their lambs during the neonatal period

L. Snyman^{1#}, C.L. Nel^{1,2}, S.W.P. Cloete¹ & K. Dzama¹

Temporal dynamics of ruminal metabolome, degradability, and fermentation in response to molasses-treated guinea grass–cowpea silage

A.P.G. Sossou^{1#} & M. Yayota^{1,2}

Effects of a novel *Bacillus subtilis*-based probiotic blend on jejunal histomorphology and phylogenetic composition of cecal microbiota in densely stocked broilers

Z. Mahlangu¹, C.M. Mnisi², V.O. Sumanu^{1,2#}, G. Moonsamy³, O.E. Fayemi², R. Jha^{2,4} & V. Mlambo¹

Gestational and early-life rainfall effects on lifetime reproductive output in two sheep breeds farmed under arid conditions

P.G. Theron^{1,2, #}, T.S. Brand², S.W.P. Cloete², M.A. Snyman³ & J.H.C van Zyl²

The genetic diversity and breed composition of South African Bosveld sheep

N.S. Zulu^{1#}, K.C. Lehloenyia¹, S. Gcabashe², M. Segakoeng², M. Nkadimeng³, F.V. Ramukhithi⁴ & K. Hadebe²

Poster presentation abstracts.....

Adaptive growth responses of indigenous goats to water restriction

O.F. Akinmoladun^{1,2#}, R. Mnyobisi² & Z. Mpetile²

Macadamia oil cake as an alternative feed ingredient in pork production

S.J. Corbett¹, E.A. Akuru^{1#}, W.J. Steyn^{1,3} & C. Jansen van Rensburg^{1,2}

The use of a multi- enzyme complex in grower pig diets containing maize distillers dried grains with solubles

H. Lemmer¹, E.A. Akuru^{1#}, W.J. Steyn^{1,2} & C. Jansen van Rensburg^{1,2}

Evaluation of the antioxidant and antimicrobial roles of underutilized medicinal leaves in fortified beef sausage

O.P. Aluko^{1#}, P.O. Fakolade¹, B.E. Olorede¹, O.M. Oke¹, G.O. Atoyebi¹ & J.O. Omiwole¹

Bone quality parameters, including medullary bone scraping, to establish reference benchmarks in cage- and floor-reared layer flocks

J.T. Ashford^{1,2#}, P. Plumstead², K.M. Venter^{1,2} & C. Jansen van Rensburg^{1,3}

Evaluation of the proximate composition, nutritional quality, and sensory attributes of different shaped *patsey* products from chevon

P.O. Fakolade¹, G.O. Atoyebi¹, O.P. Aluko¹, J.O. Omiwole¹, R.A. Moronfolu¹, A.A. Afeez¹, O.C. Ogunwumi¹ & T.H. Adedoyin¹

The use of a partially activated vitamin d₃ source at differing phytase doses to improve calcium and phosphorus digestibility in broilers

S.T. Bekker^{1,2#}, K.M. Venter^{1,2} & C. Jansen van Rensburg^{1,3}

Observational study of commercial sow behaviour in mid-gestation during summer and winter seasons in South Africa

D. Bryant^{1#}, E. van Marle-Köster¹ & J. Johnson²

Effects of dam parity and foal sex on birth, weaning and survival parameters of the Elsenburg Percheron horse stud

M. Burger^{1#}, C.E. Davids¹ & P.G. Theron^{1,2}

Concentration analysis of trace minerals of veterinary importance in cattle grazing in the Mpumalanga province

C.S. Buys^{1#}, E.C. Webb², C. Austin¹, S. Steenkamp-Jonker³ & L. Mphaphuli Nedzingahe⁴

Validation of survival EBVS for young merino sires using the LR-method

C.S. Carter^{1,2#}, C.L. Nel^{1,2}, S.W.P. Cloete²

Wound healing and weight gain in Bonsmara weaner calves following dehorning

M. Combrink^{1,2}, E. van Marle-Köster¹, C. Uys³ & R. Erasmus²

Economic implications of age at first calving in TMR Holstein herds

H.L. de Waal^{1#} & R.D. Kgari^{1,2}

Effects of dietary fossil shell flour supplementation on growth performance, serum biochemistry, and carcass characteristics of broiler chickens

C.S. Gajana^{1#}, O.O. Ikusika¹, O.F. Akinmoladun^{1,2} & C.T. Mpendulo³

The carbon footprint of Bonsmara cattle grazing natural rangeland

S.M. Grobler^{1#}, M Kidson², HT Pule¹ & M.M. Scholtz^{1,3}

Heritability estimates and genome-wide association study of coat colour and patterns in Nguni cattle

M. Hadebe^{1#}, S. Mdyogolo², C.B. Banga^{1,3} & N.O. Mapholi¹

Effect of different limestone sources and phytase doses on Ca and P digestibility in broilers

A. Herbst¹, C. Jansen Van Rensburg¹, K.M. Venter^{1,2}, P. Plumstead² & B.C. Hillen³

Effects of fermentation period and amino acid supplementation of pigeon pea seed-based diets on the performance, carcass traits, and blood characteristics of Ross 308 broiler chickens

A.E. Ibok¹, C.A. Mbajorgu¹ & E. Janse van Rensburg^{1#}

The effect of space allowance and marketing strategy on production performance of grower-finisher pigs

W.J. Steyn^{1,2}, J. Raath², E. A. Akuru¹ & C. Jansen van Rensburg^{1#}

Optimal dietary lysine concentration for pigs during summer and winter

I. Smith¹, W. J. Steyn^{1,2}, E. A. Akuru¹ & C. Jansen van Rensburg^{1#}

Hempseed oil supplementation: effects on meat production and quality in *Haemonchus contortus* infected lambs

S. Kantuchitani¹, F. Semwogerere^{1,2}, C. Marufu³ & C. Mapiye^{1#}

Oral use of probiotics for ostrich chicks

A. Engelbrecht^{1#}, M.R. Kekana¹ & S.W.P. Cloete²

Peripartum supplementation of *Moringa oleifera* leaf meal improves antioxidant status and reproductive recovery in transition dairy cows

T.W. Kekana^{1#}, U. Marume² & F.V. Nherera-Chokuda³

Detection of putative lethal haplotypes and their associated candidate genes in South African Brahman cattle

R.D Kgari^{1,2#}, K. Dzama² & M.L. Makgahlela^{1,3}

Effect of Kalahari melon (*Citrullus lanatus*) meal inclusion in lamb diets on growth performance and meat quality characteristics

K.S. Kgaswane¹, U. Marume^{1,2#}, G.M. Chelopo²

Influence of defatted winged termite (*Macrotermes natalensis*) meal inclusion on gut morphology and carcass characteristics of Ross 308 broiler chickens

S.D. Kolobe^{1#}, N.A. Sebola¹, J.W. Ng'ambi¹, E. Malematja¹ & M. Mabelebele¹

The effects of small contemporary groups and limited pedigree depth on estimation of variance components in South African beef cattle

H.N Kruger^{1#}, E. van Marle-Köster¹, Dr H.E Theron²

Effect of dried water hyacinth supplemented rations on feedlot steers

K-J Leeuw^{1#}, I.M.M Malebana¹, L.G. Makhanya¹ & N Cochrane²

The influence of habituation on temperament traits of Namaqua Afrikaner rams

P.T. Letsoalo^{1,2#}, W.J. Olivier¹, M.A. Snyman¹ & H. Lambrechts²

Genomic assessment of non-descript cattle in three districts of KwaZulu-Natal province, South Africa

E.S. Likanza^{1,2#}, B. Bhika Kooverjee², M.P. Roux-van der Merwe¹, J. Badenhorst¹ & P. Soma²

Evaluating two feeding programs for feedlot cattle: The potential use of supplementing *Lithothamnium glaciale*, a rumen buffer (Acid Buf), on top of an ionophore antibiotic within high-starch diets fed to finishing cattle

J.C. Lotriet¹, F.M. Hagg², P. Swiegers³, E. Pieterse⁴ & O.B. Einkamerer^{1#}

Effect of mastitis incidence on milk production and SCC in Swedish dairy herds

R.D. Lötter^{1#}, K. Marima¹, A.H. Molotsi^{1,2}, J.I. Ohlsson³, T. Klingström³, K. Dzama¹

Case-control genome-wide association analysis of dermatosparaxis in South African Drakensberger cattle

W. Mabuza^{1,2#}, K.S. Mafolo¹, E.D. Cason¹ & R. Erasmus²

Targeted supplementation with bioactive plants sustainably improves goat health and decreases antiparasitic drug use

H. Machekano^{1,2,3#}, J. Ventura-Cordero⁴, P.M. Airs⁴, L. C. Gwiriri^{5,10}, A. Cooke^{5,11}, J. Virgil¹, A. Safalaoh⁷, P.C. Nalivata⁷, M.R.F. Lee⁸, T. Takahashi^{5,6}, J. van Wyk⁹, E.R. Morgan⁴ & C. Nyamukondiwa^{1,12,13}

Evaluation of breeding practices and trait preferences of Bapedi sheep farmers in Sekhukhune district, Limpopo province, South Africa

K.F.M. Madia^{1,2#}, T.J. Mugwabana¹, P.J. Sebei², T. Raphulu², K. Mokoena¹ & T.L. Tyasi¹

Gut microbiota and transcriptome profiling analysis of indigenous chickens infested with *Ascaridia galli* parasite

N. Mishumo¹, S.R. Marvin¹, R.T. Madeleine², D.P. Malatji^{1#}

Comparative recovery and quality of *Bos indicus* cauda epididymal sperm influenced by retrieval technique and equilibration duration

T.L. Mashilo^{1,2,3#}, M.L. Mphaphathi², M. R. Ledwaba^{1,2}, M.M. Setati³ & A. Maqhashu¹

The effect of early weaning on performance, health parameters, and carcass traits of Bonsmara bull calves under feedlot conditions

K.P. Matli¹, T.L. Tyasi² & P.J. Fourie^{1#}

Preliminary study: genomic regions for immune response in South African non-descript cattle from Mpumalanga and KwaZulu Natal provinces

T. Matloa^{1,2#}, B. Bhika Kooverjee¹, D.P. Malatji² & P. Soma¹

Application of high-potency white-rot fungal strains to enhance the nutritional composition and *in vitro* ruminal degradability of grape pomace

K.P. Meso^{1,2#}, L.E. Motsei^{1,2}, V. Mlambo³, T.F. Buthane⁴

Functional and genomic characterization of *Pediococcus acidilactici* RTMP1 isolated from South African Cape Speckled goats

M.R. Modiba^{1,2#}, G. Makete¹, A.M. Ngxumeshe², E. Sihlangu², T.P. Mamphogoro¹

Differences in meat quality attributes between the *Bos indicus*, *Bos taurus*, and *Sanga* breeds

K. Modika^{1#}, A. Ramabulana¹ & K. Moloto¹

Complementary effects of probiotics and stimbiotics inclusion on growth performance and bone development in broiler chickens exposed to cyclic heat stress

R.M. Mokonyama^{1#}, U. Marume¹ & G. Moonsamy²

Effects of local plants on internal parasites in different goat breeds of Botswana

P. Lechani¹, P.I. Monau^{1,3#}, K. Ntesang⁴, D.M. Pfukenyi² & O.R. Madibela¹

The effect of dietary peach pomace meal on growth performance, blood parameters and meat quality of broiler chickens

T. Moroka^{1#}, K.P. Meso¹, L.E. Motsei^{1,2} & C.F. Egbu^{2,3}

Relationship between village chicken availability and dietary diversity along a rural-urban gradient

C. Mseleku¹, M.S.C. Ngidi¹, R. Slotow³ & M. Chimonyo^{2#}

Dietary effect of marula seed cake as soybean replacement on caecal microbial diversity and abundance in broiler chickens

M.S. Mthana^{1#}, D.M.N. Mthiyane² & V. Mlambo¹

Livestock theft and retrieval constraints: Perspectives of Bizana livestock farmers of Alfred Nzo district, Eastern Cape province

V.T. Mthombeni^{1#}

Comparing age at first calving between early and late born heifers among smallholder farmers in Mpumalanga province

N.J. Mulaudzi^{1#} & M.D. Motiang¹

The effect of Ralgro® implant on the growth performance and carcass traits of Nguni and Merino sheep in a feedlot system

D.Z. Ndlovu^{1#}, M. Khanyile², N.B. Nkabinde¹ & L. Khumalo³

Synergistic influence of controlled LN₂ vapour exposure and *Moringa oleifera* leaf extract on epididymal bull sperm cryosurvival and functional parameters

N.C. Negota¹, E. Bhebhe¹, T.L. Nedamable², & M.L. Mphaphathi^{3#}

Methanogenic potential of selected agro-industrial by-products under simulated ruminal conditions

S. Nell^{1#}, L. Steyn¹ & H.P.J. Smit^{2,3}

Effects of hempseed oil on haematological and parasitological responses in lambs challenged with *Haemonchus contortus*

S. Ngwini¹, L.N. Mahachi¹, F. Semwogerere^{1,2}, C. Marufu³ & C. Mapiye^{1#}

Effects of partial replacement of soybean meal with fermented water hyacinth on haematobiochemical indices, and gut microbiome in hy-line brown hens

J. Antonio¹, T. Mutibvu¹, J.J. Baloyi² & R.B. Nhara^{1,2*}

Nutritive values and *in vitro* protein degradation of oil cakes from *Tylosema esculentum* (morama) and *Schinziophyton rautanenii* (mongongo) as feed supplements for ruminants

B.D. Nkosi^{1#}, T. Nkukwana², I. Sebolai³ & O.R. Madibela³

Assessment of identity disequilibrium and inbreeding variation in Gauteng and Mpumalanga provinces of South Africa

D. Nonyane^{1#}, B. Bhika Kooverjee¹ & P. Soma¹

The relationship between staple strength, fibre diameter and coefficient of variation of fibre diameter in a dual-purpose sheep breed

W.J. Olivier^{1,2#} & M. van Heerden¹

Effect of fruit fortification on vitamin and mineral composition of yoghurt

J.O. Omiwole^{1#}, P.O. Fakolade¹, O.P. Aluko¹, O.C. Ogunwumi¹ & G.O. Atoyebi¹

Growth performance and prevalence of gastrointestinal nematodes in weaned goat kids foraging in grassland and forestland vegetation type

L. Qokweni^{1#}, M. Chimonyo² & N. Faku³

Biosecurity measures and their impact on health performance -on small-scale broiler farms in Limpopo province

T.F. Ramukhithi^{1,2#}, T. Raphulu¹, T.J. Mpofu², K.A. Nephawe², P.J. Sebei¹, K. Munhuweyi³, F.V. Ramukhithi¹ & B. Mtileni²

Flock composition, production and reproductive performance of indigenous village chickens of the Limpopo province

T.C. Rasekgoalo^{1#}, P.J. Sebei¹, K. Hadebe² & T. Raphulu¹

Whole-plant nutrient and tannin characterization of Bambara groundnut (*Vigna subterranea*) as a climate smart feed resource for sustainable livestock production

L. Ratseke^{1#}, L. Leboho¹, S. Jiyana¹ & B. Gunya¹

Impact of anti-tick vaccination on cattle and pasture tick loads in an extensive beef system

J.M. Rust^{1#}, K. Goosen², D.J. Goosen², I. Rautenbach², T. Rust¹, N. Nyangiwe³ & Y Mkabile¹

The effect of climate patterns on prenatal reproductive performance and pre-weaning kid losses of Boer goats at the Adelaide Research Center, Eastern Cape, South Africa

T. Rust^{1#}, J.M. Rust¹ & C. Trethewey²

Shifts in the distributional ranges of *Rhipicephalus (boophilus)* ticks in South Africa: Displacement of the native tick, *Rhipicephalus decoloratus* by the invasive cattle tick, *Rhipicephalus microplus* in communal areas of the Eastern Cape

T. Sako^{1#}, M. Yawa², M. Tawana¹, N. Koza¹, N. Nyangiwe¹ & S. Mbizeni¹

Daily manure production impact on anaerobic biogas digester design for small-scale pig farmers in Gauteng

P.M. Sebothoma^{1#}, P. Magama², K. Mphofu³, & E. Maseema⁴

The impact of temperature and humidity on aflatoxigenic *Aspergillus* species in broiler feeds

K.G. Setsetse^{1#}, S.A. Akinola², L. Ngoma¹ & M. Mwanza¹

Dynamic systems interactions shaping indigenous chicken productivity in South Africa

A.N. Sithole^{1#}, S.A. Gumede¹ & T.P. Mpanza¹

Chemical composition of *Vachellia erioloba* pods silage treated with bacterial inoculant, molasses and Nano-ZnO for use as an antibiotic alternative in indigenous chickens

H.P. Sitshinga^{1#}, Z.I. Twala¹ & D.M.N. Mthiyane²

Impact of varying levels of ascorbic acid on quality attributes and shelf life of beef and pork during simulated retail display

T.L. Chitima¹ & T. Stempa^{1#}

Field evaluation of monitoring tools for dairy fly burden assessment

L. Theart^{1#} & L.H. Maartens¹

The effect of *Berchemia discolor* (Muni tree) leaf meal on gastrointestinal nematode infections of South African non-descript goats

T. Hypatia^{1#}, G. Manyelo¹ & B. Gunya¹

The effect of canola oil on intrinsic methane production and the performance of feedlot lambs

K. van Blerk^{1#}, J.H.C. Van Zyl¹ & C.W. Cruywagen¹

The effect of canola oil on *in vitro* ruminal gas production kinetics

K. van Blerk^{1#}, J.H.C. Van Zyl¹ & C.W. Cruywagen¹

Quantifying the relationship between fleece colour and objective and subjective wool characteristics

W.J. Olivier^{1,2#}, A.C. van Graan³ & C.C. Reeners

Repeatability and between-animal correlation between rumen and rectal temperature in South African sheep recorded during summer

F.P. Zonke^{1#}, C.L. Nel^{1,2}, K. Mafunga^{1,4}, S.W.P. Cloete¹ & S.K. Maloney³

Programme

Day 1: 7 July 2026			
07:30	Registration		
08:30	Theme introduction and housekeeping - LOC		
08:40	Prof Carina Visser - President, SASAS		
09:00	Prof Subusiso Moyo - DVC Research, Innovation and Postgraduate Studies, SU		
09:30	Dr Mogale Sebopetsa - Head of Department, WCDA		
10:00	Prof Kennedy Dzama - Honorary President		
10:30	Tea break + Poster viewing		
11:00	KNA 1: Dr Munyaradzi Saruchera - The importance of professional wellbeing of South African Animal Scientists		
11:30	KNA 2: Prof Mizeck Chagunda - Innovative genomic solution to define genotypes for disease resistance, adaptation resilience and enteric methane emissions		
12:15	KNA 3: Prof Casper Nyamukondiwa - Driving innovations to manage and adapt to climate impacts in Africa		
13:00	Lunch break		
14:00	Climate smart agriculture Chairperson: Dr W. Olivier (Pacific)	Molecular technologies Chairperson: Dr A. Molotsi (Adriatic 1)	Monogastric nutrition Chairperson: Prof C. J van Rensburg (Adriatic 2)
14:05	Gestational and early-life rainfall effects on lifetime reproductive output in two sheep breeds farmed under arid conditions. Theron, P.G.	Inqaba Biotechnical Industries (Pty) Ltd	Detoxifying cotton seed. Prof Polycarpe Kayodé
14:30	The applicability of the THI model as a heat stress indicator in South African dairy cattle. Erasmus, L.	Haplotype-resolved <i>de novo</i> genome assembly using trio binning reveals patterns of genetic divergence in the Windsnyer indigenous pig. Hlongwane, N.	Processed mopani worm meal supplemented with multienzymes as an alternative protein source in Ross 308 broilers. Chipa, M.J.
14:45	Diurnal variation of rumen temperature in South African sheep breeds under mediterranean summer conditions. Nel, C.L.	Baseline long-read sequencing metrics for the Bonsmara cattle breed. Mbedzi, M.	Effect of moringa leaf and seed extract blend on the growth performance and meat quality of broiler chickens. Egbu, C.F.
15:00	Generational trends on growth performance of stud Bonsmara beef cattle across agro-ecological zones of South Africa. Makaleng, C.	Genomic regions under selection in Ayrshire cattle identified using integrated haplotype score. Papo, M.	Effects of a novel <i>Bacillus subtilis</i> -based probiotic blend on jejunal histomorphology and phylogenetic composition of caecal microbiota in densely stocked broilers. Sumanu, V.O.
15:15	Adaptive morphophysiological responses of Boer, Kalahari Red, and indigenous goats across climatic seasons. Mashaba, C.F.	Whole metagenome shotgun sequencing reveals seasonal shifts in the faecal microbiome of Nguni cattle. Mokoena, J.	The effect of mopane worm (<i>Imbrasia belinal</i>) meal and multienzyme inclusion on gut morphology, digesta pH, and growth performance of Ross 308 broiler chicks. Sekhonyana, B.
15:30	Effect of different varieties of Rosemary (<i>Rosmarinus officinalis</i>) plant extracts on <i>in vitro</i> methane production of <i>Eragrostis curvula</i> hay. Nthinya, S.	Genomic characterisation of the South African Wagyu populations. Pieterse, T.	Effect of <i>bacillus</i> -based probiotic and butyric acid on growth protein utility, physiological status and welfare in broilers offered diet containing sorghum. Mukwevho, R.D.
15:45	The effect of climatic factors on calving percentage of Bonsmara cows in the eastern Kalahari bushveld. Seshoka, M.M.	Comparative analysis of functional SNP variation and biological pathways in Dorper, White Dorper, Pedi and Zulu sheep breeds. Madiba, E.	Preliminary results on the influence of enzyme-treated insect meal on growth and gonad development of abalone (<i>Haliotis midae</i>). Roodt, K.
16:00	Tea break + Poster viewing		
16:30	Panel Discussion - Foot and Mouth Disease: Turning the Tide on a Persistent Threat		

17:30	Student quiz		
19:00	Welcome cocktail event – Atrium, Lagoon Beach Hotel		
Day 2: 8 July 2026			
07:30	Registration		
08:00	KNA 4: Dr Lindy Rose - Invisible Fungi: Emerging Insights for Feed Safety and Quality		
08:45	KNA 5: Prof Pieter Swanepoel - The potential of crop-livestock integration and conservation agriculture as interventions for resilient agricultural production systems		
09:30	Panel Discussion - Breaking Silos: Rethinking Collaboration Between Veterinarians and Animal Scientists		
10:30	Tea break + Poster viewing		
11:00	Breeding and genetics Chairperson: Prof L. Makgahlela (Pacific)	Ruminant nutrition Chairperson: Dr B. van Zyl (Adriatic 1)	Animal physiology Chairperson: M. Mulaudzi (Adriatic 2)
11:05	Evaluation of factors influencing the detection of selection signatures in populations selected for traits with different genetic architectures using simulated data. Retief, A.	The influence of pre-weaning feeding strategy on abomasum function, growth and wellbeing of Holstein heifer calves. Lambrechts, H.	Influence of pre-storage incubation treatments on hatchability of ostrich eggs. Brand, Z.
11:30	Comparison of GWAS methods reveals improved detection using mixed linear models in sheep. Bhika Kooverjee, B.	The effect of supplementation on reproduction and weight in extensively managed beef cattle in the eastern Kalahari bushveld. Diamond, S.	Point prevalence of subclinical mastitis in a smallholder dairy cattle herd. Chitura, T.
11:45	Reproductive traits and live weight in Merino rams divergently selected for and against number of lambs weaned per mating. Nel, C.	Evaluation of plant- and insect-based indigenous supplements for sustainable goat health. Machekano, H.	Feather harvesting methods influence feather quality and yield In South African Black Breeder Ostriches (<i>Struthio camelus var. Domesticus</i>). Sampson, C.L.
12:00	Estimation of genetic parameters and genetic trends for growth and reproductive traits in Mashona cattle of Zimbabwe. Visser, C.	The effect of wheat germ-, canola- and fish oil on the ruminal bacterial composition, semen- and wool quality of Dohne merino rams. Joubert, J.J.	Spatiotemporal analysis of bovine tuberculosis incidence in cattle in South Africa. Maguta, E.
12:15	Additive genetic diversity retention in the contemporary South African Shorthorn population. Lashmar, S.F.	Protein source and lactic acid bacteria inoculation effects on fermentation dynamics, aerobic stability, and nutrient degradability of maize silage. Malebana, I.M.M.	Effect of dietary kenaf leaf meal on the hormonal profile, mating behaviour, and testicular histology of rabbit bucks. Kujoana, T.C.
12:30	Genetic (co)variance components of faecal egg count and production traits in Elsenburg South African Mutton Merino and Dormer sheep. Rapudi, T.	Effect of condensed tannin on the fibrolytic activity of microbial ecosystem from both wild and domestic browsers. Fon, F.N.	Differential impacts of polyvinylpyrrolidone and hyaluronic acid as sperm handling media on functional quality traits of bull sperm. Ledwaba, M.
12:45	The maternal heritability of ewes to reunite with their lambs during the neonatal period. Snyman, L.	Temporal dynamics of ruminal metabolome, degradability, and fermentation in response to molasses-treated guinea grass–cowpea silage. Sossou, A.P.G.	The influence of milk feeding strategy on the rumen development of Holstein heifer calves. Lambrechts, H.
13:00	Lunch break		
14:00	AGM		
19:00	Gala evening – Two Oceans Aquarium		

Day 3: 9 July 2026			
07:30	Registration		
08:00	KNA 6: Prof Stephanie Midgley - Agriculture under climate pressure: Potential risks and future scenarios		
08:45	KNA 7: Dr Bruno Ieda Cappellozza - Harnessing microbial solutions to support dairy herd health, performance and productivity		
09:30	Panel Discussion - Where Science Meets Practice: Unlocking Industry–Academia Synergy		
10:30	Tea break + Poster viewing		
11:00	Product science Chairperson: Prof C. Mapiye (Pacific)	Emerging farming practices Chairperson: Dr K. Hadebe (Adriatic 1)	Monogastric nutrition Chairperson: Dr E. Akuru (Adriatic 2)
11:05	Will meat still be on our plates in 2050? Hoffman, L.	The genetic diversity and breed composition of South African Bosveld sheep. Zulu, N.	Optimizing kilograms of pork per square metre: New perspectives on stocking density in modern pig production. Steyn, W.J.
11:30	Post-mortem pH and meat colour of four culled slow-growing chicken breeds reared intensively in South Africa. Hlongwana, F.Y.	Investigation of qualitative mutant traits and their influence on body measurement traits and egg-laying performance of indigenous chickens in Polokwane local municipality, Limpopo province, South Africa. Mhlabini, S.	Effects of grass silages on gut microbial ecology, fecal characteristics and production performance in finisher pigs. Mjadu, Y
11:45	Effect of replacing lucerne hay with <i>Serriphium plumosum</i> meal on live weight gain, meat quality and sensory attributes of Nguni steers. Phoko, M.	Effect of breed and age on egg quality characteristics of South African indigenous chickens. Mokgapa, P.	Effects of green betaine-coated nano-silver in Large White grower pigs fed marula nut cake-containing diets. Mbenga, Y.
12:00	The effect of moisture content on the sensory properties of rabbit biltong. Shangase, M.	An integrated manual-digital recording system within a pilot community program for small-scale goat farmers in KwaZulu Natal and Eastern Cape Provinces of South Africa. Moletse, N.	Effect of Kalahari melon (<i>Citrullus lanatus</i>) essential oil and butyric acid in grower pig diets on growth performance, meat quality and fatty acid profile. Nhara, R.B.
12:15	Toxigenic <i>Clostridioides difficile</i> associated with food-producing animals and game in South Africa. Gouws, M.	Empowering smallholder sheep farmers using data-driven body weight prediction algorithms in dorper sheep from two villages in Limpopo Province, South Africa. Phaladi, A.M.	Effect of cereal-based diets on growth performance and nutrient digestibility of weaned Californian rabbits. Dlodlo, N.
12:30	Antibiogram fingerprinting of <i>Vibrio</i> species recovered from commercial fish specimens collected from key retailers in the Eastern Cape region of South Africa. Jaja, I.F.	Nutritional and phenolic characterisation of Spineless cactus cladodes (<i>Opuntia ficus-indica</i>) as a functional feed resource for slow-growing goats. Seloane, C.M.	Piglet birth weight predicts grow-finish performance despite dietary lysine adjustment. Steyn, W.J.
12:45	Final remarks and closing of congress		
13:00	Lunch and Departure		

Reviewers

Name	Organisation
• Dr Anel Engelbrecht	Western Cape Department of Agriculture
• Dr Cornelius Nel	Western Cape Department of Agriculture
• Dr Doctor Mthiyane	North-West University
• Dr Eunice Amaka Akuru	University of Pretoria
• Dr Farouk Semwogerere	Stellenbosch University
• Dr Fortune Thabethe	University of Zululand
• Dr Helet Lambrechts	Stellenbosch University
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• Prof Linky Makgahlela	University of the Free State
• Prof Obert Tada	University of Limpopo
• Prof Schalk Cloete	Stellenbosch University
• Prof Tlou Grace Manyelo	University of Limpopo

Keynote Speakers



Dr. Bruno Ieda Cappellozza



Bruno Ieda Cappellozza - Ph.D.-trained animal scientist and global technical leader with extensive experience in ruminant nutrition, product development, and applied research for beef and dairy systems. Currently serving as Global Technical Product Manager at Novonosis, leading international projects across innovation, scientific validation, and commercialization of feed additives and microbial solutions. Author of 110+ peer-reviewed publications and co-inventor on multiple patents, with strong expertise in animal physiology, microbiome-based technologies, and production efficiency.



Dr. Lindy Joy Rose



Dr. Lindy Joy Rose is a Senior Lecturer in the Department of Plant Pathology at Stellenbosch University, with over 15 years of experience in plant pathology, mycotoxin research, and crop disease management. She holds a PhD in Plant Pathology and has established herself as a leading researcher in the fields of Fusarium diseases, mycotoxin contamination, and sustainable plant health.



Prof. Mizeck Chagunda



Mizeck Chagunda, is a full professor (holding a chair) in Tropical Livestock Genetics at the University of Edinburgh, and Director of the Centre for Tropical Livestock Genetics and Health based at the Roslin Institute, Easter Bush Campus, The University of Edinburgh. Prior, Professor Chagunda was Chair of Animal Breeding and Husbandry in the Tropics and Subtropics at the University of Hohenheim, Germany. During part of that time, he was Director of Institute of Agricultural Sciences in the Tropics (Hans-Ruthenberg-Institute). The Hans-Ruthenberg-Institute has 10 departments each headed by a professor with focus on tropical agricultural research and higher education.



Prof. Munya Saruchera



Professor Munya Saruchera is the Director of the Africa Centre for Inclusive Health Management in the Faculty of Economic and Management Sciences at Stellenbosch University. He is a transdisciplinary researcher straddling public and development management. He currently teaches and supervises postgraduate students and supervises postdoc research fellows, and is an Ashoka, SUNRISE and African institute of Public Health Fellow. He is a Professional Associate with the Anti-Corruption Centre for Education and Research (ACCERUS) at Stellenbosch University's School of Public Leadership, an Associate of the School for Climate Studies and presenter of the Sociology of Sustainable Agriculture master's module in the Faculty of Agri Sciences at Stellenbosch University.



Prof. Pieter Swanepoel



Prof. Pieter A. Swanepoel is the Head of the Department of Agronomy at Stellenbosch University and an Associate Professor specializing in sustainable agricultural systems, conservation agriculture, and crop-livestock integration. With a PhD in Soil and Grassland Science and more than 68 peer-reviewed publications, his research focuses on improving soil health, resource-use efficiency, and climate resilience in agricultural production systems. Prof. Swanepoel is widely recognized for his leadership in agronomic research, industry collaboration, and postgraduate supervision, and currently serves on several national and international agricultural research and advisory bodies.



Prof. Stephanie Midgley



Prof. Stephanie Midgley holds an MSc(Agric) in Horticultural Science from Stellenbosch University, and a PhD in Botany from the University of Cape Town. She has 35 years' experience in research and policy on climate change and its impacts on plants, agriculture and natural resources. Stephanie is currently the Specialist Scientist for Climate Change at the Western Cape Department of Agriculture and is also an Extraordinary Associate Professor in the AgriSciences Faculty at Stellenbosch University. Stephanie engages with a wide range of audiences, from scientists and politicians to farmers and rural youth, and continues to supervise Masters and Doctoral students.



Prof. Casper Nyamukondiwa



Prof. Casper Nyamukondiwa is an Associate Professor of Entomology and a prominent member of the Senate at the Botswana International University of Science and Technology (BIUST). Specializing in insect physiological ecology and climate change, he heads a Research Lab focused on sustainable pest management and biopesticide development.

Harnessing the Power of Genomics: Innovative Solutions for Disease Resistance, Adaptation Resilience, and Mitigating Enteric Methane Emissions

Mizeck Chagunda

Centre for Tropical Livestock Genetics and Health (CTLGH), Roslin Institute, University of Edinburgh, Easter Bush Campus, Midlothian, EH25 9RG, UK

Abstract:

The increasing global challenges such as climate change, biodiversity loss, increase disease and parasite occurrence and increase resistance antibiotics, exert increased burden on sustainable and resilient food systems. This necessitates the development of innovative genomic solutions to enhance disease resistance, adaptation resilience, and reduce enteric methane emissions in livestock. Recent advances in genomics and gene editing technologies have created unprecedented opportunities to dissect the complex genetic architecture underlying these traits. These are technologies such as high-density single nucleotide polymorphism (SNP) genotypes, gene-editing, genomic breeding value estimation, and genomic selection. These technologies are making it possible to identify, select, and disseminate elite breeding animals with high accuracy at a younger age. This would mitigate the impact of the global challenge to productivity, fertility and reproductive, disease resistance, longevity, and productive lifetime, thermotolerance, feed efficiency, and adaptation. The said genomic technologies have the ability to be bundled and stacked among themselves or with other technologies. This creates an intersection, leading to the development of new breeding strategies that can accelerate genetic gain in livestock populations. With examples from different livestock species, this current presentation highlights the potential applications of the intersection to improve disease resistance and improving animal health; enhanced productivity; increased feed efficiency; and better animal welfare. Overall, harnessing the power of the intersection between innovative genomic solutions has the potential to transform the livestock industry, improving efficiency, productivity, and sustainability while also promoting animal health and welfare, and identifying appropriate animals for specific production environments.

THE WESTERN CAPE DEPARTMENT OF AGRICULTURE AT A GLANCE



The Western Cape Department of Agriculture provides a wide range of development, research and support services to the agricultural community in the Western Cape.

The department's administrative headquarters is situated on the historic Elsenburg farm, near Stellenbosch, while new and commercial farmers are accommodated at research farms, ASD training centres, extension offices and state veterinary offices.

The agricultural sector not only stimulates economic growth in the province, it also plays a major role in creating sustainable job opportunities.

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Oral presentation abstracts

Piglet birth weight predicts grow-finish performance despite dietary lysine adjustment

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Low-birthweight (LBW) piglets are predisposed to intrauterine growth restriction, impaired muscle accretion, reduced daily gain, and poor litter and carcass uniformity. In conventional all-in-all-out systems, dietary phase changes are based on age or feed allocation, rather than individual body weight and physiological requirements, potentially under- or oversupplying nutrients to LBW pigs. Understanding how birth weight and nutritional interventions influence grow-finish performance is therefore essential. This study evaluated the effect of piglet birth weight on grow-finish performance and the response of LBW pigs to graded dietary standard ileal digestible (SID) lysine levels compared to high-birthweight (HBW) pigs. The study was approved by the Animal Ethics Committee of the University of Pretoria, South Africa (Approval No: EC078-17). Prior to trial commencement, piglets' birth weight (BW) ranges were established at a commercial piggery. Piglets were classified at birth as LBW (0.9–1.2 kg) or HBW (1.7–2.0 kg) and marked accordingly. At 70 days of age, a total of 144 piglets (72 LBW; 72 HBW; equal sexes) from 20 second-parity litters were moved to the experimental farm of the University of Pretoria. The pigs were allocated to a 3 × 2 × 2 factorial arrangement (lysine level × birth weight × sex) with four replicate pens (three pigs/pen) over a 77-day grow-finish period. Diets were isocaloric maize-soybean meal-based and formulated to contain control, +10%, or -10% SID lysine. Growth performance was recorded weekly, and carcass traits were measured at slaughter age of 147 days. Data were analysed using PROC GLM (SAS). Birth weight influenced ($P < 0.05$) body weight and average daily gain, with HBW pigs producing heavier ($P < 0.05$) carcasses and greater backfat thickness. Finisher HBW pigs increased ($P < 0.05$) feed intake when fed the low-lysine diet, while LBW pigs had decreased ($P < 0.05$) feed intake and enhanced feed conversion ratio, with no negative impact on growth rate. While birth weight or dietary SID lysine level did not influence ($P < 0.05$) lean meat percentage, sex effects on carcass traits were observed mainly under low-lysine conditions, with females producing heavier carcasses and greater backfat thickness. Male and female pigs differ in carcass composition due to hormonal differences, such as androgen levels, which affects energy metabolism and tissue deposition. At low inclusion levels, dietary SID lysine becomes a limiting factor to protein deposition in boars, and excess energy is diverted towards fat deposition and increased backfat thickness. Hence, different dietary SID lysine:NE levels may be more cost-effective and beneficial for growth performance in finishing boars and gilts. Piglet birth weight significantly influenced growth performance and carcass characteristics throughout the grow-finish period, with HBW pigs outperforming LBW pigs up to slaughter. Pigs showed a limited response to SID Lys level within birth weight groups. Overall, these findings confirm piglet birth weight as a robust predictor of finishing performance and highlight the importance of early-life nutritional and management interventions to improve outcomes in low-birth-weight pigs.

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Comparison of GWAS methods reveals improved detection using Mixed Linear Models in sheep

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Genome-wide association studies (GWAS) have become the standard approach for identifying genomic regions or specifics associated with disease in livestock. However, methods for conducting GWAS studies are not all equivalent, particularly when population stratification and relatedness may inflate false-positive signals. Data used herein originated from a study of wet carcass syndrome (WCS) which is a meat quality defect in South African sheep with a suspected genetic component. To compare two GWAS approaches—single-marker association using Fisher's exact test and mixed linear model association (MLMA)—to identify genomic regions associated with wet carcass syndrome (WCS) in a South African sheep population. Ethical clearance was obtained from the Agricultural Research Council Ethics Committee (APIEC 23/07). Genotypes from the Ovine 50K SNP BeadChip were available for 164 WCS-affected (cases) and 82 unaffected (controls) animals. Quality control was conducted in PLINK v1.9, excluding SNPs with call rate <95%, minor allele frequency <0.01, deviation from Hardy–Weinberg equilibrium in controls ($p < 1 \times 10^{-4}$), and individuals with >10% missing genotypes. Following filtering, 42 183 SNPs and 219 animals (146 cases and 73 controls) were retained. GWAS was performed using Fisher's exact test in PLINK and MLMA in GCTA, with Bonferroni-corrected thresholds applied separately for autosomes and the X chromosome. Manhattan and quantile-quantile (Q-Q) plots were created to visualize the GWAS results with R packages 'qqman' and 'ggplot2'. Previously conducted principal component analysis provided preliminary indications of population structure by clustering afflicted and unaffected animals primarily in separate groups. When conducting the GWAS analysis, the Q-Q plots for the Fisher's exact test showed general upward deviation of observed p-values from the null expectation, indicating inflation of test statistics across the distribution. This single-marker association analysis revealed 13 and 90 SNPs at genome-wide and suggestive threshold levels, respectively. The sex-specific analysis showed 22 SNPs in males while 114 SNPs in females. However, the pattern of the Q-Q plots is consistent with the presence of population structure and relatedness not accounted for by single-marker tests. In contrast, the MLMA analysis revealed only 6 SNPs on the autosomes at the suggestive significance level, with Q-Q plots being indicative of correction for the population structure. Compared to Fisher's exact test, MLMA analysis that incorporated the genomic relationship matrix improved control of population structure and relatedness, reducing genomic inflation and false-positive associations while retaining biologically meaningful signals. Overall, compared to the single-marker analysis MLMA reduced false positive indications of associations by controlling population structure, while detecting relevant candidate loci. These findings demonstrate that mixed linear models are a cautionary tale in conducting GWAS analyses to ensure reliable results and provide a framework for future genetic studies.

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Preliminary results: influence of pre-storage incubation treatments on hatching outcomes of ostrich eggs

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Optimal storage temperature for ostrich eggs is 17–20°C for up to six days. In practice, however, storage conditions vary widely (15–30°C), leading to embryos at different developmental stages when incubation begins. Infrequent egg collection, especially when eggs remain in warm nests before storage, may contribute to increased late embryonic mortality. Avian blastoderms can temporarily arrest development after oviposition (diapause), which likely occurs in ostriches. This is supported by hatchability rates of up to 80% under natural conditions, where females may lay eggs over more than 20 days before incubation starts, yet still achieve synchronous hatching. This study evaluated the effect of pre-storage incubation (PRESI) on hatchability of ostrich eggs and determined the response time of eggs to temperature changes. Data were collected from 1,752 eggs produced by a commercial pair-bred South African Black ostrich flock at the Oudtshoorn Research Farm, South Africa, during the 2023 and 2024 breeding seasons. The fresh eggs were collected twice daily (08:00 and 16:00) from the paddocks. After disinfection, eggs were randomly assigned daily to five treatment groups. Treatment 1 (control) eggs were stored for 2–6 days at 18°C and 75% relative humidity (RH). Treatments 2–5 were pre-incubated at 36°C and 24% RH for 2, 4, 6, or 8 hours, respectively, before placement in setters on day 7 of storage. Temperature sensors monitored eggshell, incubator, and storage temperatures throughout the trial. The experiment was repeated three times per breeding season (winter, spring, summer) across two consecutive years to evaluate seasonal and annual effects. Data were analysed using linear mixed-effects models. PRESI treatment was fitted as a fixed effect, while year, season, sire, and dam were random effects. Variables included hatchability (infertile eggs, early embryonic mortality [EEM], late embryonic mortality [LEM], and chicks (hatched), moisture loss at 21 (ML21) and 35 (ML35) days, day-old chick weight (CWT), and pipping time (PT). Ethical approval was granted by the Western Cape Department of Agriculture's Departmental Ethical Committee for Research on Animals (Ref No.: R10/2022). Preliminary results showed limited effects of PRESI on production parameters. Early (0.050–0.073) and late (0.114–0.132) embryonic mortality did not differ among treatments ($P \geq 0.49$). Infertility was higher in Treatment 5 (8 h PRESI; 0.059 ± 0.030 ; $P \leq 0.010$) compared with the control (0.027), while Treatments 2–4 did not differ from the control. Hatchability was similar for Treatments 1–4 ($0.549\text{--}0.596$; $P \geq 0.40$) but lower in Treatment 5 (0.440 ± 0.066 ; $P \leq 0.045$). PRESI had no effect on ML21 ($8.72\text{--}9.05 \pm 0.40$) or ML35 ($13.8\text{--}14.1 \pm 0.48$), chick weight at hatching ($823\text{--}840$ g; $P = 0.249$), or pipping time ($41.67\text{--}41.82$ h; $P = 0.751$). Overall, only the 8-hour PRESI treatment negatively affected fertility and hatch probability. Eggshell temperature data indicated that eggs required approximately 5 hours to reach incubator temperature and about 16 hours to cool back to storage temperature after pre-heating. Ostrich eggs demonstrate inherent thermal buffering capacity, limiting the practical benefits of short-term PRESI. However, prolonged pre-incubation (8 hours) appears detrimental, reducing fertility and overall hatch probability.

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Evaluation of different inclusion levels of processed mopani worm meal with multienzymes on growth performance and nutrient digestibility of broilers

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Broiler production is one of the fastest-growing livestock sectors globally, largely driven by population growth and increasing demand for chicken meat. The rising cost of high-quality feed remains a major constraint to sustainable broiler production. Soybean meal (SBM), the primary protein source in poultry diets, requires extensive land resources for cultivation, contributing to increased production costs and environmental pressure. Mopani worms (*Imbrasia belina*) are rich in protein and present a promising alternative protein source for broiler diets. However, their utilisation is limited by the presence of chitin, a non-starch polysaccharide that is poorly digested by poultry and may negatively affect nutrient utilisation and growth performance. To determine the optimal inclusion level of processed Mopani worm meal with a multienzyme supplement on day-old Ross 308 broiler growth performance and digestibility. It was hypothesised that supplementation of MWM with multienzymes would improve nutrient digestibility and enhance growth performance. All experimental procedures were approved by the University of South Africa Animal Research Ethics Committee (Ref: 2023/CAES_AREC/2157). A total of 300 unsexed day-old Ross 308 broiler chicks were randomly allocated to five dietary treatments in a completely randomised design. Each treatment was replicated five times, with 12 birds per replicate. Broilers received isonitrogenous and isoenergetic diets supplemented with multienzymes at 0.5%. Five dietary treatments with varying inclusion levels (12–18%) of processed mopani worm meal, with or without multienzyme supplementation. Body weight was recorded at hatch and weekly thereafter. Titanium dioxide was included during the last three days as a digestibility marker. Starter, grower, and finisher diets were provided sequentially at two-week intervals. At the end of each feeding phase, two birds per replicate were randomly selected for slaughter, and ileal digesta were collected to determine nutrient digestibility. Growth performance and digestibility data were analysed using the General Linear Model (GLM), and treatment means were separated using Duncan's multiple range test at $P < 0.05$. Broilers fed T1 showed higher ($P < 0.05$) feed intake (FI). Birds receiving T4 recorded higher ($P < 0.05$) body weight gain (BWG) and improved nutrient digestibility. The Feed conversion ratio (FCR) and mortality (MR) rate were higher ($P < 0.05$) in T1 during the starter and grower phases. Birds fed T5 had higher ($P < 0.05$) FI at the finisher phase. BWG for T3 and T4 was similar ($P > 0.05$). T4 achieved significantly higher ($P < 0.05$) nutrient digestibility. T1 maintained poorer FCR performance at the finisher phase. Overall, results indicate that the interaction between multienzymes and MWM improved nutrient utilisation and growth efficiency. Processed mopani worm meal at 16% supplemented with 0.5% multienzymes significantly improved growth performance, nutrient digestibility, and feed conversion efficiency while reducing feed intake. Therefore, the inclusion of MWM at 16% with multienzyme supplementation is recommended as an effective alternative feed ingredient in broiler nutrition.

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Point prevalence of subclinical mastitis in a smallholder dairy cattle herd located in greater Tzaneen local municipality

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Mastitis is highly ranked among the economically significant diseases of dairy cattle. The disease is widely reported to reduce milk yield and quality and increase production costs. This study explored the prevalence of subclinical mastitis in the dairy herd by identifying bacterial pathogens from quarter milk samples and evaluating their antibiotic susceptibility. The study was carried out at a smallholder dairy cattle farm that is located in the Greater Tzaneen Local Municipality, Limpopo Province, South Africa with coordinates 23.8361° S, 30.1357°. A single group observation design was adopted to enable a pilot assessment of the occurrence and risk factors for subclinical mastitis in the dairy herd. The study population comprised of dairy cattle that were grazed on natural pastures throughout the year with minimal supplementary feeding. From this population group, all the milking cows (twenty-five) with different parities (from 2 to 5), and at different stages of lactation were sampled for the California Mastitis Test. The cows were being milked twice a day using the hand milking procedure. Milk samples (100) were collected once from all the quarters of the selected cows during the summer season (January 2025) after ethical clearance was granted by the hosting institution's animal care and use committee under license number AREC/12/2024: PG. The milk samples were further subjected to somatic cell count and microbial culture tests to detect cow-level and quarter-level subclinical mastitis. Bacterial pathogens that were isolated were subjected to antimicrobial susceptibility testing, which was performed according to the Clinical Laboratory Standards Institute (CLSI) guidelines. Furthermore, an attempt was made to identify the potential risk factors (cow age, stage of lactation, parity and previous history of mastitis) for subclinical mastitis in the herd. The data were presented using descriptive statistics, and chi-square tests were used to assess differences in subclinical mastitis prevalence among risk factor groups ($P < 0.05$). The average prevalence of subclinical mastitis in the herd was 32%, and 21% at the quarter and cow levels, respectively. The predominantly isolated pathogens were *Staphylococcus aureus* and isolates from the Streptococcus group. *Staphylococcus aureus* exhibited a 44% resistance rate to the nine antibiotics tested across the three bacterial isolates, corresponding to a Mar index of 0.3. The highest resistance was observed against Penicillin, Ampicillin, Cloxacillin, and Oxacillin. Age, parity, and stage of lactation were not significantly associated with the prevalence of subclinical mastitis ($p > 0.05$). The 95% confidence intervals for the prevalence proportions in each category also overlapped, indicating no meaningful differences between groups. These findings highlight the importance of early detection of subclinical mastitis through regular screening of milking cows and the need for improved control strategies. Antimicrobial stewardship and enhanced management practices that reduce the reliance on synthetic antibiotics are key to sustainable dairy production systems. This study revealed an occurrence of subclinical mastitis in the dairy herd. Poor hygiene practices that are linked to hand milking, a previous history of mastitis, and not adhering to the recommended udder health management practices were identified as potential contributors. Antimicrobial resistance of the test isolates to penicillin G, ampicillin, and the combination of cloxacillin/oxacillin poses a potential public health risk to the consumers of milk and related products from the study area. Key recommendations include routine monitoring with SCC and CMT for early detection, improved hygiene practices, and selective antimicrobial use based on bacterial susceptibility testing.

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The effect of supplementation on reproduction and weight in extensively managed beef cattle in the eastern Kalahari bushveld

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A cow's lifetime productivity is influenced not only by breed and age at first calving, but also by feeding conditions and appropriate supplementation. Cow fertility is the main component influencing total herd efficiency. Cow size, survival rate of calves, calf weaning weight and cow productive lifetime are also traits of economic importance that influences herd efficiency. Lick supplementation for extensive beef production's main focus is to supplement nutritional shortages of the rangeland and to promote intake and digestibility of the low-quality grazing rather than to substitute the grazing partially with supplements. In the study area during spring and early summer, the most limited nutrients in the rangeland are mostly trace elements and phosphate. The most limited nutrient in autumn and winter is protein when the grass is dry, with a lack of Vitamin A necessary for reproduction. The objective of the study was to determine the effect of two different lick supplementation strategies between weaning and first conception on the subsequent calving percentage and cow and calf weights, as well as calving percentage and weight over the second and third calving seasons. In the study, 24 Bonsmara heifers were divided into two groups of 12 animals each after weaning at the Koopmansfontein Research Station in the Eastern Kalahari bushveld of South Africa. The two heifer groups received the same mineral lick (60 g/kg Phosphorus; 120 g/kg Calcium) during summer (October – March). During winter months (April – September), the one group received a protein rich winter lick (400 g/kg protein) while the second group received a production lick which consisted of the same winter lick supplemented with yellow maize in a ratio of 2:1. Summer lick intake differed between 100 – 200 g/day, while winter lick intake differed between 400-600 g/day. Production lick intake was approximately 1000-1300 g/day. The heifers were bred naturally from the age of 24 months during a three-month summer breeding season (December – February). Calving percentage and conception rates of the group which received production lick in the winter before the first breeding season were 92%, 50% and 42% for the first, second and third calving seasons. This was much higher than the calving percentage of 82%, 45% and 18% for the group which received only winter lick. Although heifers' average weight did not differ at the commencement of the first breeding season at 24 months of age (289 kg), cow weight at calving and calf 205 day corrected weaning weight were higher over the three consecutive calving seasons for the heifers receiving production lick during winter before the first mating. These results indicate that it may be worthwhile for farmers to provide good nutrition and supplementation before the first breeding season for the incentive of a better calving percentage and higher calf weaning weights up to the third calving season.

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Effect of cereal-based diets on growth performance and nutrient digestibility of weaned Californian rabbits

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Contrasting the use of nutritious ingredients in rabbit's diets such as maize, wheat and barley could give more insight on how these materials can be used to enhance rabbit's performance. This will be an important strategy to increase choice of ingredients for feed formulators or nutritionists and will give an ability to prioritize cheap sources of protein and energy, which will give quality feed that will not compromise production quality of rabbits. This study aims to evaluate the effect of cereal-based diets on growth performance and nutrient digestibility of weaned Californian rabbits. The permission to conduct this study was approved by university of KwaZulu-Natal animal research ethics committee with protocol reference number: AREC/00004193/2022. A total of thirty weaned Californian rabbits were randomly assigned to individual pens and fed maize (280g/kg), wheat (280g/kg) and oats (280g/kg) diets. For weight gain and feed intake, from weaning age, experimental animals had unrestricted access to fresh feed and water for eight weeks. The feed intake and weight gain were recorded weekly. The feeders were refilled once each day in the afternoon, and the rabbits were watched twice daily in the morning and the afternoon. For digestibility, excreta were collected from the trapping netting wire with hands covered with clinical gloves at 09h00 daily after 24h from the commencement of the digestibility trial. They were inserted into plastic zipper bags and stored into the cooler box and transported to the ridge in the laboratory. Faeces collected daily from each treatment group were pooled and stored in a fridge at 4°C immediately after collection. Collected samples were then dried at 80°C for 24h. Data were statistically examined utilizing the general statistical package (Genstat 20th edition, VSN international 2023), with means being assessed for the analysis of variance (ANOVA) through One-way ANOVA. Tukey's multiple range test was employed for multiple mean comparisons and differences were pronounced significant at $P \leq 0.05$. Rabbits fed oats-based diet had significantly ($P < 0.05$) lower final body weight (2787) than the maize (3168) group. Rabbits fed maize and wheat-based diets had significantly higher ($P < 0.05$) average daily feed intake (160, 148) and average daily weight gain (36.1, 36.8) respectively. Nutrient digestibility results showed significant differences ($P < 0.05$) in crude protein and Ash digestibility. Oats-based diet had higher crude protein digestibility values (74.5) followed by wheat and maize-based diets (63.3 and 50.8) respectively. Maize-based diet showed higher Ash digestibility value (82.9) than wheat and oats-based diets (54.3 and 61.2) respectively. Faecal of rabbits on oats-based diet had significantly ($P < 0.05$) lower moisture (52.2) than the maize group (60.3). The increase gain in weight of the rabbits fed maize diets are associated with nutritional benefits from maize such as ferulic acid. These compounds are good in minimising oxidative stress, hence increasing a conducive bowel capacity for proper metabolism, which further increases efficacy in protein metabolism and enhance conversion of metabolizable energy to live or carcass weight. Wheat and maize are also reported to have several prebiotic factors that supports feed intake, hence supporting increased feed intake. Results obtained from the current study show that formulated cereal-based diets are having potential to improve growth performance of weaned Californian rabbits. Nutrient digestibility of these diets is optimal. It was concluded wheat and maize-based diets can be used by feed manufactures with the benefit of increased choice of ingredients to formulate rabbits' diets as they have greater potential to enhance growth performance.

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Effect of moringa leaf and seed extract blend on the growth performance and meat quality of broiler chickens

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The widespread use of antibiotic growth promoters (AGPs) in poultry production has contributed significantly to antimicrobial resistance (AMR) emergence, which is a growing public health threat globally and in South Africa. Prolonged sub-therapeutic antibiotic use in poultry production predisposes humans to resistant bacterial strains that can be transmitted through the food chain, direct contact, or the environment. Furthermore, antibiotic residues detected in poultry products pose direct risks to consumer health. These concerns have intensified interest in safe, effective, and natural feed additives that can sustain or improve production performance without the associated AMR and food safety risks. *Moringa oleifera* leaf and seed extracts are rich in polyphenols with demonstrated antioxidant, antimicrobial, and growth-promoting properties, making them candidates worth investigating as a natural alternative to AGPs. This study evaluated the effect of incremental levels of a moringa leaf and seed extract blend (ME) administered via drinking water on the growth performance and meat quality of Cobb 500 broiler chickens. Ethical approval [NWU-02002-20-A5] for this study was obtained from the North-West University Animal Production Research Ethics Committee. A total of 250 one-day-old Cobb 500 broiler chicks were randomly allocated to five treatments with five replicates of 10 birds. Treatments comprised a negative control (NC; water only), a positive control (PC; 5 g multi-strain probiotic [5×10^8 CFU/g]/L of drinking water), ME60 (30 mL moringa leaf extract + 30 mL moringa seed extract/L of drinking water), ME90 (45 mL moringa leaf extract + 45 mL moringa seed extract/L of drinking water), and ME120 (60 mL moringa leaf extract + 60 mL moringa seed extract/L of drinking water). Growth performance was recorded over 42 days, while meat quality parameters were assessed after slaughter. Data was subjected to ANOVA using the general linear model procedure (PROC GLM) of SAS. Birds reared on the ME120 had the highest body weight gain and the best feed conversion ratio (1933 g/bird; 1.69) compared to NC (1819 g/bird; 1.91) ($p < 0.05$), suggesting that the bioactive compounds in ME enhanced nutrient utilisation efficiency. The pH, colour, drip loss, cooking loss, water holding capacity, and shear force of chicken breasts did not vary ($p > 0.05$), indicating that ME did not compromise the meat's structural integrity. Moreover, ME significantly improved proximate meat composition ($p < 0.05$): crude protein content was higher in ME-treated groups (24.48–24.54%) than NC (22.75%) and PC (19.71%), while crude fat content was reduced (0.65–0.66% vs. 2.09% in PC). This likely reflects the role of ME's polyphenols in modulating lipid metabolism and promoting lean muscle deposition, which has important implications for meat nutritional quality. Moringa leaf and seed extract blend administered via drinking water improved feed efficiency and produced leaner meat with higher crude protein content compared to the controls. Hence, moringa leaf and seed extract blend is a promising natural growth promoter with the potential to reduce reliance on AGPs, thereby contributing to AMR mitigation and improved food safety in the South African poultry industry. Although FCR values exceeded commercial benchmarks due to experimental conditions, the improvement in ME120 over the negative control confirms a treatment effect and supports the trial's conclusions.

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The applicability of the temperature-humidity-index model as a heat stress indicator in South African dairy cattle

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The traditional method for assessing heat stress in dairy cattle relies on the Temperature-Humidity Index (THI), which combines air temperature and relative humidity into a single indicative value. The THI is preferred because of its convenience, simplicity, and broad applicability to both intensive and extensive systems. However, despite its popularity, the THI has notable limitations. It was originally developed for human use and later adapted for livestock. The THI threshold, commonly cited as 72 and above, was estimated by researchers in 2000 and has not been updated to reflect recent climate challenges. The aim of this study was to evaluate the applicability of the THI model as a heat stress indicator on Total Mixed Ration (TMR) based South African dairy farms. Data from four dairy farms located in Louis Trichardt (Limpopo, Holstein cows), Rayton (Gauteng, Holstein cows), Swellendam (Western Cape, Jersey cows) and Kluitjieskraal (Western Cape, Jersey cows) were analysed. Test-day milk yield records were combined with daily weather data. Linear mixed-effects models were utilised to assess the relationship between milk yield and two versions of the THI model: THlave (based on average daily conditions) and THlmax (representing peak daily heat load). Other weather predictors were also examined to compare the performance of the THI models. Farm and cow were included as random effects, and model performance was evaluated using information criteria (AIC/BIC). Data spanning the 2014 to 2025 period were included to account for inter-annual climatic variability. As breed was confounded with farm, breed effects were not analysed separately but are implicitly reflected within farm-level responses. Ethical approval was obtained from the University of Pretoria (NAS244/2024). Dominant weather predictors varied across farms. However, THlave showed the lowest AIC and BIC values for both Farms B and C, indicating that the combined temperature-humidity load captured biologically meaningful variation in milk yield within these systems. In contrast, both Farms A and D were better explained by non-THI predictors, reinforcing that heat-stress drivers are context-dependent rather than uniform across production environments. Comparisons between the two THI versions showed that THlave consistently produced lower AIC and BIC values than THlmax, indicating that sustained daily heat exposure explained more variation in milk yield than short-term peak conditions. This highlights the importance of cumulative thermal load and limited recovery periods in driving production responses. The distributional patterns of THI values revealed repeated exceedance of commonly cited stress thresholds during warmer periods, particularly on Farms B, C and D. Overall, these results highlight the progressive nature of heat stress and emphasise the importance of selecting weather predictors that accurately reflect the key climatic limitations of each system. Across farms and climatic regions, THI was only the strongest predictor for two of the four farms. Heat stress dynamics are specific to each system and environment and are not always captured by the THI model. The results emphasise the importance of selecting appropriate environmental parameters when quantifying heat stress.

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Effect of condensed tannin on the fibrolytic activity of microbial ecosystem from both wild and domestic browsers

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Harsh climate conditions and severe winters often led to ruminant losses among smallholder farmers either by sale for cheap or death caused by starvation. These ruminants tend to rely mostly on drought tolerant trees and shrubs which are often higher in condensed tannins limiting nutrient harvest, hence the need to browse wild herbivores for potential evolved fibrolytic microbes that can be used to improve fermentation in domestic goats. Such studies align with Africa Agenda 2063 and SDG2030 that speaks to Africa resource transformation and improved livestock productivity, and zero hunger, respectively. Therefore, screening different microbial ecosystems for tannin tolerant microbes with fibrolytic potential is very important. This study investigated the effect of condensed tannin on the fibrolytic activity of microbial ecosystem from domestic goat (G), wild life [giraffe (GR), kudu (K), impala (IM)] and consortia [A1 (G+IM), A2 (G+K), A3 (G+GR), A4 (GR+IM), A5 (GR+K), A6 (IM+K), A7 (G+GR+IM), A8 (G+GR+K), A9 (G+IM+K), A10 (GR+K+IM), A11 (G+GR+K+IM)]. Fresh faecal samples (50g) were collected from domestic (G) and game animals (GR, K and IM) and mixed with homogenization buffer (50ml) for crude protein extraction. Crude protein enzyme was precipitated with 60% ammonium sulphate followed by dialysis, and assayed for endocellulase, exocellulase and xylanase activities by incubating with carboxymethyl cellulose, microcrystalline cellulose and xylan, respectively, at varying tannin concentrations [control (feed without adjustment 5.34 %), 8 and 10%]. *In vitro* degradability was measured by incubating strained faecal inoculum with salivary buffer containing 1g of *Vachellia sieberiana* adjusted to the different concentrations of condensed tannin. Degradability parameters including measured included, Apparent degradability (APD), True digestibility (TD), Neutral detergent fiber digestibility (NDFd), Acid detergent fiber digestibility (ADFd) and Microbial yield (MY) were measured. Ethics certificate number: UZREC 171 | I 0-030 PGD 20 | 8/279. The results showed that 8 and 10% condensed tannin reduced ($P<0.05$) the specific activities of endocellulase, exocellulase and xylanase in all microbial ecosystems. In all enzyme assays, endocellulase activity was the most active ($P<0.05$) compared to that of exocellulase and xylanase. Enzymes from wildlife animals and consortia exhibited higher fibrolytic activity than goat (Ghiasi et al., 2024). Impala and kudu showed the highest enzymatic activity for individual system and A9, A10 and A11 for consortia. *In vitro* digestibility of *Vachellia* generally decreased ($P<0.05$) at 8 and 10% condensed tannin when compared to the control for all individual systems and consortia. Wildlife animals, generally, fermented more *Vachellia* than goat at 8% tannin and consortia, hence in agreement with Li et al. (2022). Apparent digestibility (APD), true degradability (TD), neutral detergent fiber degradability (NDFd) and acid detergent fiber degradability (ADFd) were highest in Kudo and impala as well as A8, 10 and 11. This study showed that microbes especially from the wild systems might have evolved with relatively high tolerance of tannin without losing their ability to ferment high fibre, hence can be used to improve domestic browsers forage utilization.

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Estimation of genetic parameters and trends for growth and reproductive traits in Mashona cattle of Zimbabwe

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Mashona cattle have experienced climatic changes, which contributed to recurrent droughts, disease outbreaks, and altered herd structures since the mid-1990. These changes, together with several decades of selection, may have shifted genetic parameter estimates from pre-1990s values. Earlier studies on this breed were based on small sample sizes, mainly from research stations, which excluded reproductive traits and later growth traits such as final weight and mature cow weight, limiting understanding of long-term genetic responses under current production conditions. Although selection for weaning weight is widely practiced in this population, the genetic relationships between growth and reproductive traits have not been fully quantified. To estimate genetic parameters and trends for growth and reproductive traits in Mashona cattle, accounting for direct and maternal genetic effects. The study (NAS287/2024) used pedigree and performance records of 15,020 Mashona cattle born between 1960 and 2025 to analyze birth weight (BW), weaning weight (WW), yearling weight (YW), final weight (FW), mature cow weight (MW), pre-and-post-weaning average daily gain (ADG), age at first calving (AFC), and inter-calving period (ICP), with records ranging from 1,010 for MW to 7,034 for WW. Variance components and estimated breeding values (EBV) were obtained with BLUPF90+ software. Heritability's were estimated using univariate animal models, and genetic correlations using bivariate models, with maternal effects fitted only for BW and WW. Fixed effects included contemporary group (herd-year-season), sex, and age at measurement. Annual genetic trends were evaluated by regressing EBVs on birth year. Growth trait means were 27.07 ± 3.80 kg (BW), 162.14 ± 35.25 (WW), 191.42 ± 37.59 (YW), 256.69 ± 54.76 (FW), and 363.53 ± 50.13 kg (MW), while reproductive traits averaged 1073.18 ± 152.19 days (AFC) and 496.11 ± 113.04 days (ICP). Direct heritability's for growth traits were low to moderate, ranging from 0.19 ± 0.05 to 0.39 ± 0.03 for early growth and 0.20 ± 0.03 to 0.37 ± 0.08 for post-weaning weights. Maternal heritability estimates were low for BW (0.13 ± 0.03) and moderate for WW (0.25 ± 0.02). ADG heritability's ranged from negligible post-weaning to moderate (0.35 ± 0.11) pre-weaning, while heritability's for reproductive traits were low (AFC = 0.04 ± 0.03 ; ICP = 0.12 ± 0.04). Strong positive genetic correlations occurred among growth traits (0.66-0.98), with generally weak and negative correlations with reproductive traits. Selection on WW improved BW, YW and FW, but negatively affected ADG_WW_YW. Genetic trends were positive for WW and YW, while maternal WW declined as direct WW increased ($P < 0.001$). Results suggest selection for early growth has been effective, but balanced strategies are needed to prevent unintended responses in later growth and reproduction. Selection improved WW and YW, but the low heritability of reproductive traits, weak correlations between growth and reproductive performance, and low EBV accuracy limit genetic progress in these traits. Therefore, incorporating genomic selection and prioritizing maternal effects could improve fertility and support Mashona cows as a maternal line in crossbreeding.

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Toxigenic *Clostridioides difficile* associated with food-producing animals and game in South Africa

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Clostridioides difficile, an emerging zoonotic pathogen, was previously only limited to hospital environments. However, a rise in community-acquired *C. difficile* infections (CA-CDIs) may suggest that the pathogen could be linked to food-producing and game (wildlife) animals. To determine whether *C. difficile* can be associated with food-producing and game animals in South Africa. Faecal samples (N=109) were collected from food-producing animals (pigs (n=20), free-range poultry (n=19), dairy cattle (n=21), small ruminants (n=20)), game (*Damaliscus pygargus phillipsi*) (n=20) and game birds (*Numida meleagris*; guinea fowl) (n=9) across 10 different farms, or animal production systems, in the Western Cape. Faecal samples were collected opportunistically either through identifying fresh faecal matter within animal housing or grazing areas or taken directly from the small intestine of animals that have been hunted for private use. *C. difficile* was isolated by adding 90 mL of maximum recovery diluent to 10 g of each sample, and thoroughly mixed. A dilution series of up to 10⁻³ was performed, plated onto *C. difficile* moxalactam norfloxacin (CDMN) agar with 5% defibrinated horse blood, and incubated at 37°C for 48 hours under anaerobic conditions (Whitley A20 Anaerobic Workstation). To account for *C. difficile* spores, an adapted protocol by Marcos *et al.* (2022) was followed. Presumptive positive colonies were identified based on morphology and confirmed by PCR targeting the *tpi*-gene. To determine toxin profiles of isolates, a multiplex PCR was performed based on the protocol from Persson *et al.* (2008, 2011). The study received ethical approval from Stellenbosch University Research Ethics Committee for Animal Care and Use (ACU-2023-29610) and Biological and Environmental Safety Committee (BES-2023-28480). *C. difficile* was detected in 43.1% of samples, of which pig (80%), dairy cattle (52.4%) and poultry (36.8%) had the highest prevalence of the pathogen. It was also detected in game (30%) and one isolate was obtained from guinea fowl. This is the first study to isolate *C. difficile* from the agricultural-food sector in South Africa, as well as from guinea fowl globally. The majority of the isolates (83%) were toxigenic (i.e., ability to cause disease). Isolates carrying both toxin genes (*tcdA*⁺ and *tcdB*⁺) as well as both binary toxin genes (*cdtAB*⁺) were mainly associated with pig and dairy cattle. Such toxin profiles can cause severe, recurrent infections and is often associated with hypervirulent strains, posing a threat to individuals in close contact with these animals and further has the potential to burden South African healthcare settings as it may contribute to CA-CDIs. Toxigenic *C. difficile* was present in animal production systems in South Africa and is strongly associated with dairy cattle and pigs.

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Post-mortem pH and meat colour of four slow-growing chicken breeds reared intensively in South Africa

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Post-mortem pH value influences the major meat quality attributes such as appearance, texture, juiciness and overall acceptability. The acceptance of meat at the point of purchase largely depends on its colour; which varies with the rate of muscle pH decline. A rapid or slow drop in post-mortem muscle pH results in pale or dark meat, respectively, which is often undesirable. However, the ultimate pH of chicken breast remains inconclusive, as reported values vary across studies, with ideal meat pH being considered to be 5.7 – 6.1. This variability reflects the influence of interacting factors, including pre-slaughter management practices, sex, genotype, age and diet. Older slow-growing birds are regularly culled due to reduced reproductive efficiency. Despite their availability, meat from culled birds remain underutilised in the formal poultry value chain in South Africa, which could be due to limited information on meat quality attributes. Hence, investigation of pH and colour from slow-growing culled chickens are critical for improving meat quality for consumer acceptance. To evaluate post-mortem breast meat pH and colour traits of four slow-growing chicken breeds reared under an intensive production system, at culling. Ethical clearance (approval number: APIEC2022/10) was obtained from Agricultural Research Council (ARC) Animal Ethics Committee. A total of eighty birds (10 female; 10 male) from each breed (Black Australorp, Potchefstroom Koekoek, New Hampshire and Venda) were raised intensively and fed ad libitum standard commercial diet at ARC Poultry Breeding Unit. At 24 months, chickens with an average live weight of 2.7 kg were slaughtered at mobile abattoir according to standard South African chicken slaughter protocols (electrical stunning, neck cutting, efficient bleeding, scalding, dressing, washing and chilling carcasses). The pH analysis was carried out with a penetration electrode at three different time intervals (15min, 30min and 24hrs) in the chicken breast, using a calibrated pH meter. After 24hrs, chilled carcasses were portioned and primal cuts deboned manually. Colour traits (L^* , a^* , b^* , chroma and hue angle) were determined from deboned breast meat using a Minolta colorimeter. Data was subjected to analysis of variance and Fisher's least significant difference was used to separate the means at $P < 0.05$. Both breed and sex did not affect ($P > 0.05$) the initial pH of breast muscles but influenced the rate of pH fall over time. At 30 min post-mortem, Black Australorp males had the lowest pH value (faster pH fall) compared to other breeds, and significantly lower than Potchefstroom Koekoek. At 24 hours post-mortem, the breast meat pH values in females were significantly lower than those recorded in males, except for the Black Australorp. The lower ultimate pH observed in female breast meat suggests a more rapid post-mortem glycolysis resulting in a faster decline in muscle pH, resulting in pale meat colour, reflected by the higher L^* (lightness) values in female breasts ($P < 0.0001$) compared to male breasts with no significant difference for the New Hampshire. However, all L^* scores were below the range that is considered normal ($56 \leq L^* \leq 62$) for poultry breast meat in both sexes. Across all breeds, male chicken breasts had higher a^* (redness) values than female chickens ($P < 0.0001$) reflecting a slower pH decline, which may result from increased muscle activity. The findings emphasise the strong sex influence on meat colour traits, with males producing breast meat of deeper red hues and females tending towards paler meat colour, varying across breeds, which may influence consumer perception and formal market preference. Hence, improving management strategies from farm production to processing may increase utilisation of culled slow-growing chickens.

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Haplotype-resolved de novo genome assembly using trio binning reveals patterns of genetic divergence in the Windsnyer indigenous pig

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The Windsnyer pig (*Sus scrofa domesticus*) a pig breed widely used in South Africa and preserved at the Agricultural Research Council and private stud farmers. It is known for its hardiness, efficient utilisation of low-quality feed and can survive intermittent feed shortages. However, heterozygosity in diploid genomes complicates the assembly process which may cause the two chromosome copies to mistakenly merge thereby masking genetic and structural variations thus preventing the detection of structural differences between parental chromosomes. Trio binning resolves this problem as it separate reads according to their parent. Comprehensive analysis of within-individual genomic differences becomes possible. Examining the genome of the indigenous Windsnyer pig offers valuable insights of the unique genetic variation that can support their conservation as a genetic resource. The aim of this study was to use trio binning genome assembly to investigate nucleotide diversity, genome-wide divergence and identify low and high divergence regions with associated genes. Ethical approval was granted by the University of South Africa's Animal Research Ethics Committee (AREC-100818-024) and the Department of Agriculture Land Reform and Rural Development (DALRRD) under section 20 of the Animal Diseases Act 1984 (Act 35 of 84) (12/11/1/1/23 (6508 AC). High molecular weight DNA from a boar, sow and female progeny was sequenced using PacBio HiFi technology, complemented by Omni-C library for chromosome-scale scaffolding. The Vertebrate Genome Project pipeline processed reads, using trio binning for haplotype-resolved assembly, removing duplicates and chromatin-based scaffolding. Minimapp2 aligned parental haplotype, followed by SAMtools, BCFtools and BEDtools for processing alignment and estimating variant divergence against *Sus scrofa* 11.1 (GCA_000003025.6) as a reference. Although haplotype comparison was the primary focus, the *Sus scrofa* 11.1 reference genome was used for variant calling to provide a standardised functional annotation and biological interpretation. Nucleotide diversity (π) across sliding windows (50 kb with 25 steps) was calculated using BCFtools to identify regions of significantly low and high divergence. Parental haplotype comparison identified 3,780,322 single nucleotide polymorphisms (SNPs) with 2.249 transition/transversion (Ts/Tv) ratio. Mean nucleotide divergence was $\pi=0.0021$ (2,1 SNPs per kb). The substantial number of SNPs, consistent Ts/Tv ratio (2.0-2.3) and moderate divergence showed good variant quality and expected heterozygosity. Divergence patterns showed 44% low-divergence and 7% high-divergence regions indicating conserved segments and divergence hotspots. Chromosome 4 harboured a major low-divergence block (h1tg00004l:13,5 Mb) overlapping 549 genes linked to fertility (*RSPO2*, *ZFPM2*, *ODF1*), growth (*AZIN1*, *ANGPT1*, *CTHRC1*) and adaptation (*OXR1*, *UBR5*, *YWHAZ*). Chromosome 1 contained a high-divergence block (h1tg000028: 0,125 Mb) with 110 genes such as *IPCEF1* (growth and heat tolerance), *FOXB1* (feeding) and *APH1B* (growth). These findings demonstrate clear divergence between parental haplotypes, detecting regions of conservation and high variability that may contribute to the Windsnyer adaptation to harsh environments and low-input production system. The genomic map generated provides a foundation for future breeding decisions and conservation efforts to preserve and protect indigenous pig breeds in South Africa.

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Antibiogram fingerprinting of *Vibrio* species recovered from commercial fish specimens collected from key retailers in the Eastern Cape region of South Africa

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Antimicrobial resistance (AMR) is a major global public health threat that compromises the effective treatment of infectious diseases. *Vibrio* species are naturally occurring aquatic pathogens increasingly associated with seafood contamination and the dissemination of antimicrobial resistance determinants. This study investigated the antimicrobial resistance patterns and associated resistance genes of *Vibrio* species isolated from fresh-frozen commercial fish obtained from major retail outlets in the Eastern Cape Province, South Africa. Fresh-frozen fish samples were collected from retail outlets across the study region. Presumptive *Vibrio* isolates were recovered using standard microbiological procedures and confirmed using polymerase chain reaction (PCR). Confirmed isolates were subjected to antimicrobial susceptibility testing using the disk diffusion method against clinically relevant antibiotics. The Multiple Antibiotic Resistance Index (MARI) was calculated to assess exposure to high-risk contamination sources. Resistance genes, including β -lactamase (*bla*TEM), plasmid-mediated colistin resistance (*mcr-1* to *mcr-5*), and tetracycline resistance (*tet*) genes, were detected using PCR. Ethical approval for the study was obtained from the University of Fort Hare Research Ethics Committee (Approval No. JAJ011SHOB01/23/A). A total of 190 presumptive isolates were recovered, of which 92 were molecularly confirmed as *Vibrio* species and subjected to antimicrobial susceptibility testing. Multidrug resistance was observed among the isolates, with high resistance rates to erythromycin (79%), nitrofurantoin (40.2%), colistin (34.8%), and ampicillin (31.5%). Moderate resistance was recorded against cefotaxime and oxytetracycline (17.4% each), azithromycin and ceftazidime (15.2% each), while lower resistance levels were observed for trimethoprim (5.4%), ciprofloxacin (3.3%), and imipenem (4%). MARI values ranged from 0.25 to 0.50, exceeding the threshold of 0.2 and indicating exposure to environments with frequent antibiotic use. Among resistance determinants, the *bla*TEM gene was detected in 12% of resistant isolates, plasmid-mediated colistin resistance genes (*mcr-1* to *mcr-5*) were identified in 30.8%, and tetracycline resistance genes were detected in 17.4% of resistant isolates. The presence of multidrug-resistant *Vibrio* species carrying clinically significant resistance genes in commercially sold fish in the Eastern Cape Province underscores serious food safety concerns.

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The effect of wheat germ-, canola- and fish oil on the ruminal bacterial composition, semen- and wool quality of Dohne Merino rams

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Dietary lipid supplementation has been proposed as a strategy to enhance male reproductive performance in livestock. Omega-3 fatty acids (e.g. fish oil) may improve sperm membrane fluidity and motility, while omega-6 fatty acids (e.g. wheat germ oil) are involved in steroid hormone synthesis. Unsaturated fatty acids can also alter ruminal microbial populations and fermentation patterns, potentially affecting nutrient availability and, indirectly, reproductive performance. This study evaluated the effects of supplementing oils differing in fatty acid profiles (n-3, n-6 and n-9) on semen quality, wool traits and ruminal bacterial composition of Dohne Merino rams, to assess whether such supplementation provides measurable reproductive or microbial benefits under practical feeding conditions. All procedures were approved by the Interfaculty Animal Research Ethics Committee of the University of the Free State (UFS-AED2025/0018). Fifty (50) Merino rams on average 11 months of age, weighing 55±5 kg (mean±SD) was randomly assigned to four dietary treatments (n=12/13 rams per treatment, n=1 ram per replicate). All animals were fed a maintenance diet. Each ram was dosed 15 mL twice a week (30 mL in total) according to each allotted treatment: water (CON: control), wheat germ oil (WGO: n-6), canola oil (CO: n-9) or fish oil (FO: n-3). The study lasted for a total of 48 days, excluding a 12-day adaptation period (total of 60 days). Semen was collected from each ram using an electro-ejaculator on days 2, 14 and 60. A fleece wool sample was collected from each ram on days 13 and 59 of the study and analysed for fibre diameter, staple length, and fibre consistency. All animals were slaughtered at the end of the feeding period, carcass characteristics recorded and rumen samples analysed for volatile fatty acid and microbial composition. Data was subjected to analysis of variance and significance declared at the 5% probability level ($P \leq 0.05$). Bacterial amplicon sequence data were processed and analysed in R (v4.3.2), differential abundance testing was performed using ANCOM-BC2 (ANCOMBC package vX.X.X) and within-sample (alpha) diversity was estimated from the rarefied ASV table using the phyloseq R package. There were no significant differences between the groups for any of the tested parameters. The absence of treatment effects may be attributed to the relatively low dosage and dosing frequency of oil supplementation, and the use of young, healthy rams maintained on an adequate basal diet, which may have limited the scope for measurable improvement. These findings question the practical value of routine oil supplementation in similar production systems and highlight the importance of evaluating such strategies under conditions of greater nutritional or physiological challenge. Future studies should investigate higher inclusion levels and animals with compromised reproductive performance.

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Effect of dietary kenaf leaf meal on the hormonal profile, mating behaviour, and testicular histology of rabbit bucks

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Leaf meals have been regarded as potential alternative feed to soyabean meal (SBM) that can enhance the health and reproductive efficiency of farm animals, including rabbit bucks. To determine the effect of kenaf leaf meal (KLM) supplementation on the hormonal status, mating behaviour, and testicular histopathology of New Zealand white rabbits (NZWR) bucks. Four experimental diets were created by partially replacing soyabean meal (SMB) in rabbit grower diet with ground air-dried KLM (ML): KLM_{0%} - rabbit grower diet without KLM as substitute, KLM_{2.5%} - rabbits grower diet with 2.5% KLM as substitute, KLM_{5.0%} - rabbit grower diet with 5.0% as a substitute and KLM_{7.5%} - rabbit grower diet with 7.5% as a substitute. Sixteen (16) rabbit bucks were fed a commercial rabbit grower diet for one week, the experimental diets were then offered until week 11 of the experiments. At week 10, blood samples were obtained for hormonal analysis and mating behaviour known as sexual desire of the rabbit bucks was assessed using a stopwatch recording their reaction time, they take to mount a sexually mature teaser doe in their individual cages and was recorded over four days. The rabbits were then slain after the 11th week (the completion of the feeding trial) and a pair of testes were harvested, weighed, and histologically examined. Hormonal, mating behaviour and testicular weights' data were analysed using SAS version 9.4, 2010. Significance difference was considered at $p < 0.05$ and means separated using Duncan's multiple-range test. These methods were reviewed and approved by the University of South Africa - College of Agriculture and Environmental Science - Animal Research Ethics Committee (2022/CAES_AREC/147). The incremental levels of KLM significantly influenced ($p < 0.05$) the oestrogen and testosterone hormones, with higher concentrations in KLM_{5%} and lower in KLM₀, KLM_{2.5} and KLM_{7.5%}. There was no diet effect ($p > 0.05$) on mating behaviour, whereas there was a significant influence ($p < 0.05$) of experimental diets on testicular weights. Diet KLM₀ and KLM_{2.5%} resulted in lower testicular weights than KLM₅ and KLM_{7.5%}. The rabbit bucks fed KLM_{7.5%} had increased generative changes of seminiferous tubules, Sertoli cells, tunica albuginea, the interstitial spaces between tubules containing interstitial cell of Leydig, epididymis, spermatozoa and spermatogonia. The enhanced reproductive hormones, higher testicular weights and histological development may be due to the higher concentration of protein, amino acids and phenolic compounds available in kenaf leaves that stimulates the release of reproductive hormones and reduce the effects of oxidative stress. It can be concluded that incorporating KLM up to 5% into commercial rabbit diet in place of soyabean meal, increased reproductive hormones, histological development, and higher testicular weights. Hence, further studies are encouraged to test effect the incorporation of KLM beyond 5% on the mating behaviour NZWR bucks.

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The influence of milk feeding strategy on the rumen development of Holstein heifer calves

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The potential synergistic effect of increased volumes of milk replacer (MR) and calf starter (CS) feeds with a crude protein (CP) content higher than 23% in a step-down weaning program, have not been extensively studied; and recent studies reported conflicting results on any potential benefit in terms of calf growth and gastrointestinal function. It is imperative that a feeding strategy is developed that can establish the nexus of ensuring sufficient nutrient intake to ensure rumen papillae development during the pre-weaning period to ensure post-weaning performance, especially in heifer calves destined to be incorporated in dairy herds. To investigate whether increasing the CP content of a CS feed to 260g/kg DM, will stimulate rumen papillae development and mitigate the negative influence that has been reported with high MR volumes fed. Ethical approval was obtained from the Research Ethics Committee: Animal Care and Use of Stellenbosch University (SU-ACU-2021-18719). Forty-eight Holstein Friesian heifer calves were used in the study, originated from the same production system, and were housed in a custom-designed calf house. Calves were randomly allocated to treatment groups, which consisted of a combination of a liquid diet (feeding rates of 4 L MR/day, 6 L MR/day or 9 L MR/day, respectively) and calf starter pellet diet formulated to contain either 210 g CP/day or 260 g CP/day. Rumen wall thickness and -development was measured using non-invasive diagnostic imaging in Weeks 4, 5, 6, 7, and 8; and BHBA levels were determined for 6 calves from each treatment group during Week 6 and 8 of the trial. No interaction was found between the respective treatment diets, feed intake, rumen wall thickness or BHBA levels. In Week 2, the average weekly CS feed intake was higher in the calves receiving 9 L MR/day (H), when compared to calves that received 6 L MR/day (M) and 4 L MR/day (L). From Week 3 to 6, the calves in the 4 L MR/day treatment group had a higher CS feed intake than the calves in the 9 L MR/day group, while CS feed intake in the 6 L MR/day group was intermediate. Similar CS feed intakes were reported in Week 7 for all treatment groups, while in Week 8 there was a tendency for calves in the 9 L MR/day and 6 L MR/day treatment groups to have a higher CS feed intake than the 4 L MR/day group. Rumen wall thickness was not influenced by the MR volume fed for most weeks; with Week 7 being the exception, where the calves from the 9 L-fed group had a thicker rumen wall. The MR volume fed or CS feed crude protein content did not influence the BHBA levels measured. Calves that receive the 9 L MR diet, tended to have greater calf starter feed intake post-weaning, when compared to calves receiving the 4 L MR diet. This suggests a beneficial effect on the development of the capacity of the rumen. Rumen wall thickness was not influenced by treatment, and an absence of feeding approach in BHBA levels support this observation.

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The influence of pre-weaning feeding strategy on abomasum function, growth, and wellbeing of Holstein heifer calves

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In pre-weaning calves, which are removed from their mother very soon after birth, colostrum- and milk replacer (MR) feeding strategy can have significant effects on the pre-weaning and post-weaning health and performance of the calf. Calf feeding strategy is reported to affect GIT functionality, with the feeding of more than 6L MR/day suggested to overload the ability of the calf's GIT to digest the milk, resulting in scours in young calves. Very few studies have investigated the influence of feeding strategy on GIT function, and how this may influence pre-weaning abomasum clotting, growth and wellbeing of Holstein heifer calves. To determine the influence of pre-weaning feeding strategy on abomasum clotting and emptying rate during the first three days after birth, and growth and wellbeing of Holstein heifer calves. Ethical approval was obtained from the Research Ethics Committee: Animal Care and Use of Stellenbosch University (SU-ACU-2021-18719). Forty-eight Holstein Friesian heifer calves were used in the study, originated from the same production system, and were housed in a custom-designed calf house. Calves were randomly allocated to treatment groups, which consisted of a combination of a liquid diet (feeding rates of 4 L MR/day, 6 L MR/day or 9 L MR/day, respectively) and calf starter (CS) pellet diet formulated to contain either 210 g crude protein (CP)/day or 260 g CP/day. Diagnostic imaging was used to evaluate abomasum clotting and -emptying rate, 1h, 2h, 3h, and 4h after ingestion of respectively colostrum- and transition milk. The neutrophil:lymphocyte ratio (N:L) and beta-hydroxybutyric acid (BHBA) levels were determined on days 8, 22, 57 and 71 days of the trial. Calf live weight (LW) was measured at birth, and weekly thereafter. Hip height (HH), wither height (WH) and heart girth (HG) was measured from week 1 and weekly thereafter. The MR volume fed did not exceed the abomasum's ability to process the volume fed. A tendency was observed for total serum protein to increase with an increase in milk clot size, which is indicative of successful transfer of passive immunity. The calves did not differ in terms of N:L ratio and BHBA levels, which indicate that the 9L MR volume that was fed, did not overpower the GIT's ability to process the larger volume of milk. The crude protein content of the CS feed did not have any beneficial effect of stimulating GIT development and function. An elevation in BHBA levels was observed with an increase in calf age (Day 8: 0.14 ± 0.03 vs Day 71: 0.39 ± 0.02 ; $P < 0.05$), indicating that the treatment diets were successfully metabolized and utilized. Calves fed the 9 L MR/day were significantly heavier compared to the 4 L MR/day calves, with the calves that received 6 L MR/day achieving an intermediate live weight. The average daily gain was significantly higher for the calves receiving the 6 L MR/day and 9 L MR/day, when compared to the calves receiving 4 L MR/day. The feed conversion ratio was similarly better for both the 6 L MR/day and 9 L MR /day groups, when compared to the calves receiving 4 L MR/day. The respective groups did not differ in terms of CS intake. Wither height differed significantly between the calves that received 9 L MR/day and 4 L MR/day, respectively. Hip height was the highest for the calves that were fed 6 L MR/day and the 9 L MR/day, when compared to the calves receiving 4 L MR/day. When considering the influence of diet CP level, the calves receiving the 260 g CP/day, had a higher total cumulative intake, higher ADG, and higher hip height, when compared to the calves that received the 210 g CP/day. The feeding strategy of 9 L MR/day and 260g CP/day resulted in a higher live weight from two weeks after birth, increased average daily gain and improved feed conversion ratio due to a higher total dry matter intake. Abomasal clotting ability and -emptying rate were not compromised with the high milk volume fed, which was evident in successful immunoglobulin transfer. The higher milk volume fed did also not result in inflammation in the abomasum or small intestine indicating that the physiological capacity of the abomasum or small intestine to accommodate and process the MR and CS feed, were not exceeded.

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Additive genetic diversity retention in the contemporary South African shorthorn population

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The South African (SA) Shorthorn has experienced a sustained decline in popularity since the 1990s, resulting in a reduced national footprint and a significant population bottleneck. Despite its foundational genetic contribution to over 50 composite breeds globally, the number of active breeders had fallen to a critical low of 13 by February 2026. Small, declining populations are highly vulnerable to genetic drift; therefore, an objective assessment of the breed's current genetic status is essential to devise optimal management and improvement strategies. To quantify the additive genetic diversity retained in the contemporary SA Shorthorn population and clarify its population genetics history through pedigree-based relationship analysis. Ethical approval was granted by the Agricultural Research Council-Animal Production (AECAP 25/03). Pedigree records for 35 444 animals born between 1925 and 2024 were provided by the Shorthorn Cattle Breeders' Society of South Africa. Genetic variation is partially managed through a grading-up Appendix system, which allows for the screening and registration of producer-level animals that meet mandatory phenotypic and performance standards (e.g., minimum weaning indices). A contemporary reference population was defined as animals born ≥ 2015 ($n=2\ 510$). Pedigree depth was evaluated using equivalent complete generations (CGE) and the pedigree completeness index (PCI). The *optiSel* package in *R* was used to construct the additive relationship matrix (*A*), and estimate mean co-ancestry ($\bar{f}$), from which additive genetic diversity (*GD*) was derived ($GD = 1 - \bar{f}$). Individual inbreeding (F_{PED}) and the rate of inbreeding (ΔF) were used to derive the effective population size (Ne_F). The reference population ($n=2\ 510$) showed a mean pedigree depth of CGE = 5.62 with a PCI of 0.684. While the PCI indicates moderate to high genealogical information, the presence of animals with $F_{PED} = 0$ (41.1% of the cohort) likely reflects some missing parental data within the historical record. The mean F_{PED} was 0.020 ± 0.039 . Mean co-ancestry was $\bar{f} = 0.0156$, indicating that 98.4% of founder genetic diversity is retained ($GD = 0.984$). However, because $F_{PED} > \bar{f}$, non-random mating or population structure is suggested. The estimated ΔF of 0.36% per generation corresponds to a Ne_F of 139, yet the Ne_F was only 32, reflecting a significant increase in relatedness within the current population compared to historical expectations. While a high proportion of founder diversity remains represented, the low Ne_F indicates an urgent need for intervention. To mitigate further loss of diversity, the implementation of automated mating tools like MateSel is recommended to manage the trade-off between genetic gain and the maintenance of the breed's remaining additive genetic variance.

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Differential impacts of polyvinylpyrrolidone and hyaluronic acid as sperm handling media on functional quality traits of bull sperm

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For cattle *in vitro* production methods, polyvinylpyrrolidone (PVP) has long been a required chemical for sperm immobilisation during intracytoplasmic sperm injection (ICSI). However, when injected into the oocyte's cytoplasm, this molecule has been demonstrated to be toxic, which could affect fertilization and sperm head de-condensation. Hyaluronic acid (HA) has been proposed as a chemical alternative for the selection of high-quality sperm in order to obtain better acrosome integrity and sperm viability results. This study evaluated sperm motility, viability, and acrosome integrity of bull semen exposed to PVP and HA treatments. We hypothesized that HA exposure would improve the motility, viability, and acrosome integrity of bull sperm. The study was carried out in strict accordance with the recommendations in the guide for the care and use of animals under the guidelines of the Agricultural Research Council, Animal Production Animal Ethics Committee (APIEC 23/03) and under Section 20 of the Animal Diseases Act, 1984 (Act No 35 of 1984): with reference 12/11/1/1/15 (5017NT). Frozen-thawed semen from five sexually mature bulls of known fertility was allocated to 3 experimental treatments consisting of no pre-treatment (Control); 7% PVP or 0.5% HA, followed by a 10 minutes co-incubation for all treatments at 37°C. Following co-incubation, sperm motility was analyzed using a portable computer assisted sperm analysis system (AndroScope). Sperm viability and acrosome integrity were assessed using fluorescence microscopy markers for fluorescence diacetate (FDA), peanut agglutinin (PNA), and propidium iodide (PI) staining. Sperm exposed to HA treatment recorded lower total motile sperm ($48.8 \pm 6.9\%$) compared to PVP ($55.2 \pm 7.5\%$) and control ($54.6 \pm 4.2\%$; $P < 0.05$). The progressive motile sperm was lower following HA treatment ($42.2 \pm 6.7\%$) compared to control ($47.7 \pm 5.1\%$; $P < 0.05$). Sperm exposed to HA ($92.2 \pm 3.6\%$) had a higher percentage of live sperm compared to control ($88.2 \pm 6.4\%$) and PVP ($87.8 \pm 2.9\%$) treatment ($P < 0.05$). Semen exposed to control ($38.7 \pm 10.0\%$) and HA ($40 \pm 11.5\%$) treatments had higher percentage of live sperm with intact acrosome compared to PVP ($24.4 \pm 11.3\%$; $P < 0.05$). In summary, the use of HA on bull semen reduced the percentage of motile sperm following cleanup; however, the proportion of viable and DNA-intact sperm was increased compared to control and PVP. The use of HA on bull semen yielded higher percentages of viable and DNA intact sperm. Therefore, a continuation study should be done to investigate the effect of HA as a sperm selection procedure on increasing fertilization and blastocyst formation following ART and ICSI procedure

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Evaluation of plant- and insect-based indigenous supplements for sustainable goat health

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The rapid growth of the global human population is intensifying pressure on livestock production systems to meet animal protein demands. Small ruminants, particularly goats, have a significant economic and environmental impact in sub-Saharan Africa. However, gastrointestinal nematode (GIN) infestations and infections remain a major constraint on goat productivity in smallholder systems. The challenge is further intensified by climate change and declining forage quality in communal grazing lands. Conventional control relies heavily on synthetic anthelmintics, which are costly, increasingly ineffective due to resistance, and associated with environmental contamination from chemical residues in animal products and ecosystems. Thus, this has driven increasing interest in sustainable parasite control strategies within smallholder livestock production systems. This study evaluated the efficacy of insect-derived protein and indigenous plant supplements as potential nutraceuticals through a targeted selective treatment (TST). Specifically, we assessed whether dietary inclusion of insect protein, *Hermetia illucens* larvae (BSF), and ethnoveterinary plant *Dichrostachys cinerea* pods with or without diatomaceous earth (DE) could improve goat health and reduce GIN worm burden. The study was ethically approved by the Animal Ethics Research Committee of Botswana International University of Science & Technology (Ref. AREC-201). A farmer-led participatory field experiment was conducted with twelve smallholder farmers in the Central District of Botswana. Sixty free-ranging goats were screened for gastrointestinal nematodes (GINs) using the Five-Point Check and Targeted Selective Treatment criteria. Each farmer managed 10 goats assigned to a specific treatment to prevent contamination. Treatments consisted of: T1: 80% BSFL+ 20% goat feed; T2: 85% T1 + 15% DE; T3: 100% pods; T4: 85% pods + 15% DE; T5: negative control (no treatment); and a positive control (chemical dewormer). Goats received the assigned feed for 7 days per month over 3 months and were monitored for an additional 3 months. Health indicators included monthly FAMACHA scores, body condition scores, and eggs per gram (EPG) using the modified McMaster technique. Preliminary findings showed significant differences in animal health indicators among treatment groups ($p < 0.05$). FAMACHA scores differed significantly among treatments, with pods-supplemented goats showing improved anaemia status ($p < 0.01$). Parasite egg counts for *Strongyles* spp., *Strongyloides* spp., and *Coccidia* spp. were significantly lower in BSF and pods-supplemented groups than in controls ($p < 0.05$). Body condition scores improved significantly in pods plus diatomaceous earth-supplemented goats ($p < 0.05$). Overall, supplemented groups showed improved health indicators, demonstrating that indigenous nutritional interventions can serve as sustainable, low-cost alternatives to synthetic anthelmintics, contributing to improved GIN control and productivity in smallholder goat production systems.

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Comparative analysis of functional SNP variation and biological pathways in Dorper, White Dorper, Pedi, and Zulu sheep breeds

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Genetic diversity is fundamental to sustainable livestock production, enabling resilience to climate change, emerging diseases, and fluctuating feed resources. Comparative genomics leverages whole-genome sequencing (WGS) to evaluate intra- and inter-breed variation, facilitating the identification of genes underlying adaptation and economically important traits. In sheep, these approaches strengthen breeding strategies and support conservation of indigenous genetic resources. This study aimed to compare Single Nucleotide Polymorphism (SNP) variation and identify enriched biological pathways associated with moderate and high-impact variants in Dorper, White Dorper, Pedi, and Zulu sheep breeds. Whole-genome assemblies of four sheep breeds (Dorper, White Dorper, Pedi, and Zulu) along with the Rambouillet reference genome (GCA_016772045.2) were obtained from the National Center for Biotechnology Information (NCBI). Each assembly represents a single individual per breed and was used as a representative genome for comparative analysis. Sequence reads were aligned to the Rambouillet reference using Minimap2 v2.28 and processed with SAMtools, with sorting, indexing, and duplicate marking performed using SAMtools sort v2.0.8, SAMtools index v2.0.8, and SAMtools markdup v2.2.0, respectively. Variant calling was performed using BCFtools v1.22 (mpileup, call, view, and filter functions). Functional annotation of variants was carried out with SnpEff v5.2, and moderate- to high-impact variants were filtered and extracted using SnpSift v4.3. The resulting gene lists were then sorted and deduplicated before KEGG 2026 pathway enrichment analysis via Enrichr, with statistical significance determined by adjusted p-values (false discovery rate, FDR < 0.05). A total of 188,466 (Dorper), 263,891 (White Dorper), 108,000 (Pedi), and 9,263,135 (Zulu) variants were identified. The substantially higher variant count observed in the Zulu genome is likely influenced by both biological divergence and technical factors, including differences in sequencing platforms, depths, and assembly strategies across the sourced datasets. Zulu exhibited the highest variant density (1 per 30 bp), followed by White Dorper (1 per 105 bp), Dorper (1 per 1,478 bp), and Pedi (1 per 2,579 bp). Across all genomes, moderate-impact variants ranged from 0.113% to 0.176%, while high-impact variants were rare (0.002%–0.006%). Missense variants comprised ~32%–34% of the coding variants, while ~65%–68% were silent variants, indicating that most coding variation is likely silent. Gene-level analysis revealed 310 (Dorper), 381 (White Dorper), 215 (Pedi), and 996 (Zulu) genes harboring functional SNPs. Although KEGG enrichment did not yield statistically significant pathways after FDR correction (adjusted p > 0.05), consistent trends in metabolic, endocrine, and immune-related functions were observed. These patterns suggest potential biological relevance to adaptation and productivity. However, these results are interpreted cautiously and considered exploratory given the lack of statistical significance and the use of single representative genomes. This study provides a comparative overview of SNP variation across four sheep genomes, highlighting differences in variant distribution and functional categories. While the findings suggest potential adaptive biological processes, conclusions are limited by methodological variation and the use of single individuals per breed. Future studies incorporating multiple samples per breed and standardized analytical pipelines are recommended to validate these observations and strengthen population-level inferences.

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Spatiotemporal analysis of bovine tuberculosis incidence in cattle in South Africa

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Bovine tuberculosis (BTB), caused by *Mycobacterium bovis*, is a notifiable disease in South Africa with implications for livestock health, trade, and zoonotic risk. The disease persists endemically, particularly at wildlife-livestock interfaces and in communal farming systems, where surveillance gaps and inadequate biosecurity complicate control efforts. To determine the spatiotemporal patterns of BTB incidence in cattle for the entire South Africa from 1993 to 2024. A retrospective analysis was conducted using 32 years of BTB surveillance data (1993–2024) obtained from the South African Department of Agriculture, Land Reform and Rural Development. Before the study was conducted, ethical clearance (JAJ011SMAG01) was obtained from the University of Fort Hare Inter-Faculty Human Research Ethics Committee. Temporal trends were assessed through descriptive statistics and linear trend graphs. Spatial patterns were visualised using QGIS (v3.42) to map the incidence of the disease bovine tuberculosis across the 52 metros and district municipalities in South Africa. spatial autocorrelation was quantified using Global Moran's I index in GeoDa software across eight time periods. A total of 5,645 BTB cases and 252 outbreaks were recorded over 32 years across South Africa. Notable peaks occurred in 1997 (660 cases) and a significant surge in 2004 (1,806 cases). A linear trend graph ($y = -9.83x + 19,914$) confirmed an overall downward trajectory. The Eastern Cape (2,140 cases), KwaZulu-Natal (1,015), and Mpumalanga (930) were persistent hotspots, while September (1,188 cases) and July (877 cases) were peak reporting months. GIS mapping revealed shifting spatial patterns: concentrated hotspots in the 1990s transitioned to more dispersed, lower-intensity distributions by 2017–2024. Global Moran's I indicated significant spatial dispersion in 2009–2012 ($I = -0.081$; $p = 0.008$) and 2021–2024 ($I = -0.037$; $p = 0.042$), suggesting spatial fragmentation of the disease. BTB-related mortality was negligible throughout the study period, reflecting the chronic, subclinical nature of the disease, while sporadic culling events (858 animals in 2004; 1,245 in 2009) indicate reactive rather than proactive herd management. BTB in South Africa is declining overall but persists in spatially fragmented hotspots possibly driven by wildlife-livestock interfaces, cattle movement, and communal farming practices. Effective long-term control requires targeted district-level surveillance, movement traceability systems, and a One Health approach that integrates wildlife and livestock health management beyond conventional test-and-slaughter strategies.

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Generational trends on growth performance of stud Bonsmara beef cattle across agro-ecological zones of South Africa

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Sustained genetic improvement in beef cattle requires continued selection response while maintaining genetic diversity under heterogeneous production environments. In South Africa, Bonsmara cattle are extensively utilised across diverse agro-ecological zones (AEZ), yet limited information exists on how generational dynamics and pedigree structure interact with environmental variation to influence long-term growth performance. This study aimed to (i) characterise pedigree structure and population genetic parameters (ii), quantify phenotypic and generational trends in growth traits across AEZ, and (iii) evaluate the influence of AEZ and systematic environmental factors on growth performance. The study was ethically cleared by the University of Limpopo – Animal Research Ethics Committee, with reference AREC/45/2025: PG. A total of 606,079 performance records (1975-2023) were obtained from the South African Stud Book. Traits analysed included birth weight (BW), weaning weight (WW), yearling weight (YW), 18-month weight (18MW), and 24-month weight (24MW). Pedigree structure attributes and generational parameters were computed using ENDOG (v4.1). Linear models included fixed effects of AEZ, generation, sex, season of birth, and year of birth. Least-squares means were compared and temporal trends evaluated across years and generations. Pedigree depth was substantial (mean complete generation equivalents = 6.8; maximum = 11.4), with >99% parent identification in the first generation and >80% through the fifth. Founder diversity metrics were $f_e = 265$, $f_a = 178$, and $f_g = 152$, indicating moderate historical bottlenecks but maintained genetic diversity. Pedigree analysis indicated a mean generation interval of 6.55 years. Effective population size (N_e) ranged from 420-480. Mean inbreeding (F) was 4.5% (maximum 18.7%), with a rate of inbreeding (ΔF) of 0.28% per generation. Agro-ecological zone significantly affected all growth traits ($P < 0.01$). Mean BW was highest in humid zones (40.23 ± 1.86 kg), while WW peaked in temperate regions (177.62 ± 6.18 kg). Progressive generational improvement was evident for later growth traits, including YW (217.08 ± 0.26 kg), 18MW (268.35 ± 0.52 kg), and 24MW (342.07 ± 0.74 kg) in dry sub-humid region. Autumn-born calves consistently outperformed other seasonal cohorts ($P < 0.01$). Long-term phenotypic trends showed increasing growth from the late 1970s to early 2000s, with peak WW in 1998 (150.69 ± 1.57 kg) and peak YW (231.30 ± 0.59 kg), 18MW (276.79 ± 1.13 kg), and 24MW (352.72 ± 1.41 kg) in 2001, followed by subsequent fluctuations, including reduced WW in 2018 (123.82 ± 1.71 kg). This demonstrate the genetic progress over generation however, ongoing evaluation on environment is needed to monitor the resilience of the breed at different climatic conditions. Growth performance in stud Bonsmara cattle has improved across generations, although significant spatial and temporal variation persists. The population exhibits moderate generation intervals, controlled inbreeding, and adequate genetic diversity to sustain long-term selection. Integrating pedigree monitoring with environment-specific breeding strategies is essential to optimise resilience and productivity in extensive beef production systems.

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Protein source and lactic acid bacteria inoculation effects on fermentation dynamics, aerobic stability, and nutrient degradability of maize silage

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Maize is widely used for silage due to its high fermentable carbohydrate content and reliable biomass yield; however, its low crude protein (CP) necessitates supplementation. Soybean meal (SBM) remains the conventional CP source but is constrained by cost, import tariffs, and human-livestock competition. Marula oilcake (MOC), an agro-industrial by-product, offers a potential alternative to SBM. Nevertheless, its residual oil may negatively affect fermentation, fibre degradability, and aerobic stability. Application of microbial inoculants might improve the silage fermentation indices and stability. To evaluate the effects of replacing SBM with MOC in maize silage, with or without lactic acid bacteria (LAB) inoculants, on fermentation characteristics, nutritive value, aerobic stability, and *in vitro* degradability. Ethical approval: ARC-AP (APIEC 26/08). Maize was split into two batches: one mixed with SBM, the other with MOC at equal inclusion (10% fresh weight) levels. Each batch received three treatments: heterofermentative LAB (Lalsil), homofermentative LAB (Sil-All), or distilled water (control). For six treatments (2 protein sources × 3 inoculants), each was ensiled in triplicate jars for fermentation analysis, plus triplicate jars sampled on days 3, 7, and 14 for pH, totalling 72 experimental units. Fermentation characteristics, nutrient composition, aerobic stability, and *in vitro* degradability were evaluated. The MOC showed high dry matter (DM), ether extract (EE), gross energy (GE), and acid detergent lignin (ADL), whereas SBM had high CP, ash, and *in vitro* organic matter digestibility (IVOMD). Acid detergent fibre (ADF) and neutral detergent fibre (NDF) were similar ($p > 0.05$). The SBM control showed significantly high ($p < 0.05$) lactic acid, ammonium nitrogen, CP, IVOMD, propionic acid, and early gas production, indicating efficient fermentation. The SBM + Lalsil maintained low pH, and early organic matter (OM), CP, and GE degradability. The SBM + Sil-All achieved high ($p < 0.05$) OM, NDF, and ADF degradability and acetic acid production. The MOC control showed low ($p < 0.05$) pH, butyric acid, and 48h gas production, but high fibre and GE, indicating slow fermentation but improved stability. The MOC + Lalsil had high ($p < 0.05$) DM, CP degradability, propionic acid, and peak gas production at 12h, and low carbon dioxide and yeasts and moulds. The MOC + Sil-All showed high ($p < 0.05$) GE and water-soluble carbohydrates with peak GE degradation at 12 h, but low NDF degradability and reduced gas production. Replacing SBM with MOC in maize silage enhances energy density and aerobic stability. The SBM + Lalsil optimises protein utilisation, while SBM + Sil-All improves degradability and fermentation efficiency. Thus, while MOC can replace SBM at equal inclusion levels, inoculant choice must complement the protein source to optimise the fermentation indices. Further research should assess different LAB inoculant inclusion rates, include a maize-only control, and evaluate protein sources under iso-nitrogenous conditions for more accurate comparisons.

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Adaptive morpho-physiological responses of Boer, Kalahari Red, and indigenous goats across climatic seasons

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Goat production plays a pivotal role in rural livelihoods, food security, and climate-resilient livestock systems in South Africa. Goats are particularly valued for their adaptability to harsh environments, efficient reproduction, and capacity to perform under low-input production systems. However, breed-specific differences in acclimation to seasonal climatic stressors remain inadequately quantified under semi-intensive conditions. This study evaluated seasonal adaptive responses in physiological, behavioral, and morphological traits of Boer, Kalahari Red, and Indigenous goats reared under semi-intensive management in Limpopo Province, South Africa, with emphasis on breed, age, and animal-class differences in production acclimation to contrasting thermal environments. Ethical approval was obtained from the University of Limpopo Animal Research Ethics Committee (AREC/24/2024:4H). A longitudinal observational study was conducted on 84 goats (kids, weaners, castrates, lactating does, non-lactating does, young bucks, and mature bucks), with 28 animals per breed and 4 animals per class within each breed, monitored across summer and winter seasons for one year. Of these, 28 goats were from Ga-Dikgale village and 56 from the UL experimental farm. Behavioral indicators (grazing, resting, shade-seeking, drinking) were recorded through timed direct visual observation using a stopwatch. Physiological parameters (respiratory rate, heart rate, skin temperature) were measured via flank movement observation, pulse oximeter, and infrared thermometer, respectively. Morphological traits (hair length, coat glossiness, wither height) were measured using a measuring tape, glossmeter, and standard height measurement procedures. The thermal environment was characterized using the Temperature-Humidity Index (THI). Data were analysed using Minitab 18.1 (2017), applying General Linear Models with breed, season, and physiological class as fixed effects, and age, live weight, body condition score, THI, and wither height as covariates. Significant breed differences ($p < 0.05$) were observed across adaptive traits. Indigenous goats showed greater heat tolerance, with longer grazing time (± 7.6 h/day) and lower shade-seeking behavior (± 3.24 h/day) compared to Boer goats (± 5.6 h/day grazing; ± 3.27 h/day shade) ($p < 0.05$), due to genetic adaptation enabling sustained activity under heat stress, while Kalahari Red goats were intermediate. Seasonal effects were pronounced ($p < 0.05$), with summer increasing drinking frequency, respiratory rate ($+5$ breaths/min), heart rate ($+12$ bpm), and skin temperature (± 37.45), while reducing resting time from ± 5.7 to ± 2.4 h/day ($p < 0.01$), reflecting evaporative cooling and increased water turnover to maintain thermal balance. Morphological traits varied with season, with hair length increasing in winter (± 3.7 – 3.83 cm) for insulation, and higher coat glossiness in summer enhancing solar reflectance and heat dissipation. Animal class influenced responses, with kids, weaners, and lactating does showing higher physiological reactivity due to elevated metabolic demands. Indigenous goats showed superior heat stress adaptation, maintaining longer grazing and less shade-seeking than Boer and Kalahari Red goats, reflecting genetic resilience. Seasonal variation significantly affected traits, with summer increasing thermoregulation and water demand, and winter promoting longer hair for insulation. Age and physiological status also influenced responses, with kids, weaners, and lactating does showing higher reactivity.

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Baseline long-read sequencing metrics for the Bonsmara cattle breed

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The Bonsmara composite is the most populous beef breed in South Africa (SA) and is a commercially important cattle genetic resource in the national beef industry. Although the breed has received marked genomics-based research attention, studies have mainly focused on single nucleotide polymorphism (SNP) level applications, while larger structural variations (SVs, e.g., insertions, deletions, copy number variations, and duplications), and their potential influence on phenotypic diversity and adaptation remain underexplored. Long-read sequencing technologies such as Pacific Biosciences (PacBio) and Oxford Nanopore have proven to be optimal platforms for detecting complex SVs and capturing full-length transcripts and isoforms, thereby overcoming the limitations of short-read sequencing. The availability of this data type will therefore allow for more comprehensive SV profiling in the SA Bonsmara breed and facilitate higher-resolution genomic characterization of this important national genetic resource. To generate and evaluate baseline PacBio high-fidelity (HiFi) long-read sequencing metrics for the SA Bonsmara breed and to assess the suitability of the generated data for future high-resolution genomic analyses, particularly SV discovery. Ethical approval was obtained from the Agricultural Research Council (APIEC 23/09). Genomic data from eight purebred SA Bonsmara (n=8) cattle were sequenced using Pacific Biosciences (PacBio) technology. HiFi reads, read lengths, yields, and polymerase read bases were generated, and several baseline metrics, including per-sample genome coverage, full genome coverage per animal, and physical coverage, were subsequently calculated. Per-sample genome coverage was calculated by dividing the HiFi yield by the bovine reference genome (ARS-UCD1.2) (2.7×10^9 base pairs; bp). The full genome coverage per animal was calculated by dividing the total HiFi yield by the bovine reference genome (ARS-UCD1.2), while the physical molecule coverage was calculated by dividing polymerase read bases by the bovine reference genome (ARS-UCD1.2). These metrics were used to assess sequencing depth, data completeness, and the overall robustness of the dataset for downstream SV detection. The average read quality was 97.1%, while the number of HiFi reads ranged from 1 521 791 to 5 074 249, with HiFi read lengths ranging from 10 kilobases (kb) to 29 kb. The total yield per animal ranged from 23 gigabases (Gb) to 75 Gb, with an average yield of 38 Gb across samples. The mean polymerase read length was 154.73 kb, while polymerase read bases ranged from 611 Gb to 1 395 Gb. Per-sample genome coverage ranged from 8.7× to 27.8×, while physical molecule coverage ranged from ~227× to ~517×, indicating sufficient sequencing depth and data robustness for reliable structural variant detection and downstream genomic analyses. Long-read sequencing technologies produce high-quality genomic data, which will significantly improve the detection of SVs in the SA Bonsmara breed and provide an important foundation for future genomic and functional studies aimed at improving beef production traits.

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Effects of green betaine-coated nano-silver in large white grower pigs fed marula nut cake-containing diets

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The exorbitant costs of soybean meal (SBM) and maize as major protein and energy sources, respectively, have prompted the search for cheaper alternative energy-protein sources such as marula (*Sclerocarya birrea caffra*) nut cake (MNC) for pig diets in Sub-Saharan Africa. MNC is rich in proteins (47% CP), energy (21-23 MJ/kg), and bioactive compounds, with considerable amounts of residual oil (16 – 39.4%) predominated by oleic acid (72% to 85%). Notwithstanding, complete dietary replacement of SBM with MNC is associated with adverse effects due to MNC endowment with performance-compromising antinutritional factors, necessitating a strategy such as green betaine-coated nano-silver (GBC-AgNPs) to resolve the problem. This study investigated the effects of dietary incorporation of green GBC-AgNPs on growth performance, haemato-biochemical indices, visceral organs, carcass traits, and meat physicochemical quality of Large White grower pigs fed MNC-containing diets. The study was ethically approved by the NWU-Animal Production Research Ethics Committee (NWU-00806-23-A5). Fabricated using the aqueous leaf extract of *Asparagus transvaalensis* as reducing and stabilizing agent, GBC-AgNPs were characterized, validated, and included in the pig diets. Twenty-eight (28) 9-week old Large White grower pigs were randomly allotted to 4 iso-energetic-nitrogenous diets (n = 7) with 0% MNC (Control), 100% MNC, 100% with green Ag-NPs (5mg/kg), and 100% MNC with GBC-AgNPs (5mg/kg) in a completely randomized design. They were *ad libitum* fed the diets in an electronic PPT system that automatically measured feed intake (FI), body weight gain (BWG), and feed conversion efficiency (FCE) for 60 days. On day 61, blood was collected for haemato-biochemical analysis, and the animals were then slaughtered, and samples of visceral organs and *Longissimus dorsi* muscle were harvested for analysis. Whilst the diet had no effect ($P > 0.05$) on BWG and FBW, dietary nanoparticles, particularly the GBC-AgNPs, decreased FI ($P < 0.01$) as they increased FCE ($P < 0.05$) of pigs. Also, whilst the diet had no effect on most carcass parameters and visceral organs ($P > 0.05$), dietary GBC-AgNPs decreased the rib length ($P < 0.05$) as they increased the weights of the foreleg ($P < 0.05$) and shoulder ($P < 0.05$). Further, both 100% MNC and GBC-AgNPs decreased the weights of the heart ($P < 0.05$), liver ($P < 0.05$), small intestines ($P = 0.001$), and rectum ($P = 0.01$). Regarding meat quality, the diet had no effect on all parameters ($P > 0.05$), except for the GBC-AgNP-induced decrease in meat temperature at 45 min post-slaughter ($P < 0.05$). Moreover, whilst the diet had no effects on most haemato-biochemical parameters ($P > 0.05$), both 100% MNC and GBC-AgNPs decreased white blood cells ($P < 0.05$), lymphocytes ($P < 0.01$) and monocytes ($P < 0.05$) as green Ag-NPs decreased and GBC-AgNPs increased serum creatine ($P < 0.05$). Dietary MNC, with or without the green synthesized nanomaterials, had no detrimental effects on most growth performance, carcass traits, meat quality, and haemo-biochemical parameters; however, incorporation of GBC-AgNPs improved FCE, reduced FI, and modulated some carcass and haematological parameters. Therefore, both 100% MNC and GBC-AgNPs (5 mg/kg diet) have potential functional roles in enhancing production efficiency in pigs.

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Investigation of mutant traits in indigenous chickens and their production performance in Polokwane local municipality, Limpopo

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Indigenous chickens are considered valuable gene reservoirs, particularly of genes that have adaptive features in tropical conditions. The climate has been observed as an obvious constraint to poultry production in the tropics, leading to reduced performance. Indigenous chickens possess unique genetic mutations that may enhance adaptability and productivity under low-input tropical conditions. Among these populations, qualitative mutant traits may offer advantages in growth performance and thermotolerance. To explore the prevalence of phenotypic mutant traits and their association with production performance among indigenous chickens in Polokwane Local Municipality. Ethical approvals; AREC/60/2024: PG and TREC/302/25: PG. A total of 300 indigenous chickens were purposively selected from 15 villages using a cross-sectional study design. Mutant traits were identified through direct visual observation based on established morphological descriptors and classified into discrete groups; Naked neck (reduced feathering on the neck), ptilopody (feathered shanks and toes), Fibromelanosis (dark pigmentation of the skin and connective tissues), crest feathered (presence of a feathered cap on the head), polydactyl (more than four toes), and fayoumi (extremely long feet). Statistical Package for Social Science (IBM SPSS, 2023) version 29.0 was used for analysis. Phenotypic trait frequencies were determined as proportions of the total population. Allele frequencies were estimated using Hardy-Weinberg equilibrium equation, and observed frequencies were compared to expected Mendelian ratios (0.75 and 0.25) using chi-square test. Additionally, analysis of variance (ANOVA) was used to determine the effect of the mutant traits on body measurement traits and egg-laying performance. Six mutant traits were identified in indigenous chickens of Polokwane Local Municipality; naked neck, ptilopody, fibromelanosis, crest feathered, polydactyl, and fayoumi. Naked neck was the only trait recognized, and most prevalent mutant trait (32%) and named by local farmers. Allele frequencies ranged from 0.04 to 0.23, and gene (naked neck (0.23), ptilopody (0.21), fibromelanosis (0.05), crest feathered (0.08), polydactyl (0.04), and fayoumi (0.09)) distributions differed significantly from expected Mendelian ratios ($p < 0.05$), suggesting possible influences of non-random mating, genetic drift, or small flock sizes. Mutant traits significantly affected several growth traits ($p < 0.05$). In females, naked neck polydactyl, crest feathered, and naked neck chickens had the heavier body weight, superior keel length, and performed better in toe length, respectively, while in males, the naked neck males recorded the superior body weight and body length, while fayoumi-ptilopody males had long shank and toe lengths. Naked neck birds generally showed superior growth performance. However, mutant traits had no significant effect on egg production traits ($p > 0.05$). These findings suggest that certain mutant traits, especially Naked neck, may enhance growth and adaptability under smallholder conditions. Future breeding programs should integrate these traits to enhance adaptability and productivity, while further studies using genomic tools are recommended for comprehensive trait validation.

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Effects of grass silages on gut microbial ecology, fecal characteristics and production performance in finisher pigs

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Grass silages are increasingly explored as alternative fiber sources in pig diets due to their potential to enhance gut health, improve nutrient utilization and support sustainable production systems. Forages such as Napier grass and Brachiaria are rich in structural carbohydrates that may modulate microbial fermentation within the large intestine, thereby influencing gut microbial balance, fecal characteristics and growth performance in finisher pigs. To evaluate the effects of Napier grass and Brachiaria silages on gut microbial ecology, fecal characteristics, fecal gas emissions and production performance in finisher pigs. A 30-day controlled feeding trial was conducted using 30 finisher boar pigs individually housed and randomly allocated to three dietary treatments (n = 10 per treatment): C group (control; compound feed only), N group (compound feed + Napier grass silage), and B group (compound feed + Brachiaria silage). All pigs were fed ad libitum with free access to clean drinking water throughout the experimental period. The chemical composition of the experimental diets was analysed prior to feeding to ensure nutritional adequacy. Growth performance parameters, including average daily gain and feed conversion ratio, were recorded. Samples from the cecum, colon and rectum were collected for microbial analysis and colon pH determination. Fecal samples were evaluated for microbial populations, fecal colour and gas emissions. Meat quality traits were assessed post-slaughter to determine dietary effects on carcass characteristics. Data were analysed using the Statistical Package for the Social Sciences (SPSS) and subjected to analysis of variance (ANOVA). Results were expressed as mean $\pm$ SEM, and differences were considered significant at $p < 0.05$. Ethical approval was obtained from the University of Zululand Research Ethics Committee. Dietary inclusion of Napier and Brachiaria silages significantly influenced gut microbial populations within the large intestine ($p < 0.05$), with pronounced effects observed in the cecum and colon compared to the control group. Silage-supplemented groups showed increased abundance of beneficial microbial populations and reduced fecal gas emissions ($p < 0.05$), suggesting improved fermentation efficiency. Colon pH differed among treatments, indicating dietary modulation of hindgut fermentation. Feed conversion ratio improved significantly ($p < 0.05$) in the N and B groups compared to the control, while average daily gain showed numerical improvements. Fecal colour and consistency reflected enhanced fiber fermentation, and meat quality traits were not adversely affected by silage supplementation. Supplementation of finisher pig diets with Napier or Brachiaria silages beneficially modulated large intestinal microbial ecology, improved feed efficiency and reduced fecal gas emissions without compromising meat quality. Grass silages therefore represent a promising sustainable feeding strategy for improving gut health and production performance in finisher pigs.

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Effect of breed and age on egg quality characteristics of South African indigenous chickens

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Indigenous chickens are essential to rural livelihoods in Africa, providing meat and eggs for household nutrition and food security. However, despite the contribution of indigenous chickens to the livelihoods of rural farmers and resilience to harsh environmental conditions, their production remains low and the indigenous chicken breed with superior egg quality remains unknown. This study evaluated the influence of breed and age on egg quality characteristics of Potchefstroom Koekoek and Boschveld chicken breeds. Ethical approval with project number AREC/57/2024:PG was granted by the University of Limpopo Animal Research Ethics Committee (ULAREC) before the commencement of the study. The chickens were hatched at the University of Limpopo Experimental Farm and then reared in an intensive management program in a restricted environment on deep litter from day one to the point of lay. A total of one hundred indigenous chickens ($n = 100$) were randomly selected at the same time ($n = 50$ Potchefstroom Koekoek, $n = 50$ Boschveld). A total of 800 eggs (400 eggs per breed) were then randomly collected at 28, 32, 36, and 40 weeks of age. An electronic weighing scale was used to measure egg weight (EW), shell weight (SW) and yolk weight (YW), while a digital vernier calliper measured egg width (EWD) and egg length (EL). Internal egg quality characteristics assessed included yolk ratio (YR), albumen weight (AW), albumen ratio (AR), yolk/albumen (Y/A), and egg volume (EV). External egg quality characteristics evaluated included egg shape index (ESI), shell ratio (SR), shell surface area (SSA), and unit surface shell weight (USSW). A two-way Analysis of variance (ANOVA) was used to achieve the objectives of the study. The findings revealed that the egg quality traits, including the EW (46.28 ± 0.33), SW (5.90 ± 0.03), EL (49.76 ± 0.32), EWD (36.55 ± 0.31), SSA (70.59 ± 0.39), ESI (73.16 ± 0.28), SR (12.86 ± 0.06), USSW (0.08 ± 0.00), YW (14.27 ± 0.12), EV (2747595.44 ± 63732.14), Y/A (55.76 ± 0.51), YR (30.95 ± 0.18), AW (26.10 ± 0.23), were higher in the Boschveld chicken, except the AR (56.60 ± 0.15), which was higher in the Potchefstroom Koekoek chicken breed. Age had a highly significant effect on all the studied egg quality characteristics ($P < 0.01$). The interaction effect of breed and age on egg quality characteristics also revealed a highly significant effect on all studied egg quality characteristics ($P < 0.01$). The findings suggest that the Boschveld chicken breed showed better egg quality characteristics, compared to the Potchefstroom Koekoek chicken breed. The study also found that the Boschveld and Potchefstroom Koekoek chicken breeds have better egg quality characteristics at 40 weeks of age, which indicates that the egg quality characteristics improve as the chickens mature. Breed and age significantly influence the egg quality characteristics and may be effectively used to improve egg quality. These findings provide a basis for improving the productivity and utilisation of South African indigenous chicken breeds through effective management and breeding practices.

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Whole metagenome shotgun sequencing characterises seasonal dynamics of the faecal microbiome in Nguni cattle

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Indigenous breeds such as the Nguni are largely underrepresented in gut microbiome research despite their economic and cultural significance across sub-Saharan Africa. Gastrointestinal microbial communities drive fibre fermentation, nutrient utilisation, and host health in veld-grazing ruminants, yet seasonal shifts in forage quality alter community dynamics considerably. Faecal samples were used as a validated non-invasive proxy for gut microbiota, and this study provides the first baseline characterisation of the faecal microbiome in a well-defined purebred Nguni herd. This study aimed to characterise the faecal microbial community of purebred Nguni cattle at Mara Research Station across wet and dry seasons using whole metagenome shotgun sequencing (WMS), and to assess seasonal dynamics in diversity and community composition. A total of 60 faecal samples (30 per season) were collected from pure Nguni cattle at Mara Research Station, Limpopo. DNA was extracted from each sample using ZymoBIOMICS DNA Miniprep kit. Raw sequencing data generated on the MGI DNBSEQ-G400 platform were quality-assessed using FastQC, followed by adapter trimming and low-quality read removal with Trimmomatic. Taxonomic classification was performed using Kraken2, with community composition visualised using Kaiju. Alpha diversity was assessed using paired Wilcoxon signed-rank tests ($n = 26$ pairs), and beta diversity was assessed using Bray-Curtis and Jaccard PERMANOVA. Ethical approval was obtained from UNISA CAES_AREC (Ref. 2024/CAES_AREC/6214) and the Section 20 permit from Department of Agriculture (Ref. 12/11/1/1(a) 6877PC). Species richness was significantly higher in the dry season than in the wet season across multiple alpha diversity metrics (observed species richness, $p = 0.002$; Chao1 richness estimate, $p = 0.0083$; and Fisher Alpha, $p = 0.0019$). Shannon diversity ($p = 0.80$) and Simpson evenness ($p = 0.19$) did not differ significantly between seasons, indicating that while more species were detected in the dry season, the relative dominance structure of the community was conserved. Beta diversity analysis confirmed a statistically significant, but modest seasonal differentiation in community composition (Bray-Curtis PERMANOVA: $R^2 = 0.087$, $F = 5.338$, $p = 0.002$; Jaccard PERMANOVA: $p = 0.001$), with season explaining 8.7% of community variation and homogeneous within-group dispersions confirmed (Betadisper: $p = 0.906$). The community was dominated by Firmicutes and Bacteroidetes across both seasons, with consistent detection of methanogenic archaea including *Methanobrevibacter ruminantium*, *M. millerae*, *M. olleyae*, and *Methanobrevibacter* sp. YE315 across seasons, underscoring the role of hydrogenotrophic methanogenesis in hindgut fermentation. *Akkermansia glycaniphila* and *Ruminococcus flavefaciens* were detected across both seasons, indicating ongoing contributions to gut barrier integrity and fibre degradation. Overall, these results suggest a resilient core microbiome that is maintained across season, with seasonal variation changes in species richness rather than an overall shift in community structure. Overall, the findings demonstrate a resilient core microbiome that supports fermentation, and nutrient utilization despite significant seasonal shifts in species richness and community composition. This baseline metagenomics dataset supports breed-specific management strategies programmes for Nguni cattle.

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An integrated manual-digital recording system within a pilot community program for small-scale goat farmers in Kwazulu- Natal and Eastern Cape provinces of South Africa

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Community level genetic improvement programs for low-input indigenous goat farming systems are limited by a lack of a recording system to determine pedigree, breed purity, and animal performance. The lack of traceable animal records constitutes a critical bottleneck in the indigenous goat value chain, restricting both genetic improvement and market access. The collaborative initiative between the Agricultural Research Council, Biotechnology Platform and the Kaonafatso Ya Dikgomo recording scheme, initiated two Community Based Breeding Program (CBBP) sites in KwaZulu-Natal and the Eastern Cape in 2023. The CBBP was designed to support smallholder farmers to improve production through sustainable breeding and management practices, as well as to promote *in situ* conservation of locally adapted goat populations. The aim of the study was to establish a harmonized and high-integrity field-to-storage baseline data pipeline that ensures validated, consistent and traceable animal records to foster evidence-based breeding decisions. This study obtained ethical approval from the Onderstepoort Veterinary Institute Animal Ethics committee of the ARC (Reference: AE22.15). Data was collected at centralized handling sites in Mantlani and Ncera villages (Buffalo City District) in the Eastern Cape and Ophande and Ezinkunini villages (uMkhanyakude District) in KwaZulu-Natal over three consecutive years, drawing from 195 semi-structured questionnaires in both provinces (n=150) in EC and (n=45) in KZN, indicating constraints in effective breeding practices. Each animal was EID tagged, assessed for breed type, dominant colour, sex, age using dentition and manually recorded along with farmer details in record books. A total of 4 238 animals were tagged and recorded (KZN=2 285; EC=1 953). A digital handheld EID reader was utilized to subsequently capture tag numbers. A total number of 251 beneficiaries participated across both sites (n=111) in KZN and (n=140) in the EC, respectively. Descriptive summary statistics were done in RStudio. Majority of farmers (60%) were above 60 years of age. At least 42.1% had primary-level education, and all were literate. On average, farmers had 15.5 ± 14.58 years of extensive farming experience on communal land. The average goat herd sizes were 13.95 ± 19.33 in Buffalo City with Cape Lobear dominating with an average proportion of 64.6%, and 20.59 ± 20.09 in uMkhanyakude district with the Nguni breed predominating with 79.5%. In EC, white was the dominant coat colour, with does comprising 77.5% of the studied population. In KZN, black and white combinations were common, with 75.3% does. Across both provinces, the age range was ≥ 1 to 5 years. The hybrid record-keeping system yielded a synergy gain of 10.37%. The age profile and educational background of farmers supported their capacity to manage manual record books and their receptiveness to visual-based digital training. Although flock sizes were small, these herds reflected genetic value, characterized by Indigenous Veld Goat (IVG) ecotypes. A population structure dominated by breeding-age does, signals potential for herd expansion. Furthermore, the adoption of an integrated recording system enhanced overall data completeness, strengthening the broader implementation and impact within the CBBPs.

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Effect of *Bacillus*-based probiotic and butyric acid on growth performance, physiological status and welfare in broilers offered diet containing sorghum

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The competition between human and broilers for maize has sparked interest in alternative feed ingredients like sorghum, albeit its use is limited by anti-nutritional effects and low protein digestibility. Nutritional techniques that use natural feed additives, particularly *Bacillus*-based probiotics and butyric acid have emerged as viable means to improve gut health, nutrient utilization and bird resistance. Thus, dietary supplementation of probiotics and butyric acid can improve growth performance, physiological health and welfare in broilers fed sorghum-based diets. The study was conducted to assess the effectiveness of the incorporation of *Bacillus*-based probiotic and butyric acid on growth protein utility physiological status and welfare in broilers fed diet containing sorghum. A total of 400-day-old Cobb 500 chicks were randomly assigned to five dietary treatment groups, with eight replicates per group (10 birds per replicate). The dietary treatments were formulated as follows: T1: a control diet (Commercial broiler diet), T2: SG-25% Sorghum, T3: SP-25% Sorghum + 0.05% Probiotics, T4: SBA-25% Sorghum + 0.03% Butyric Acid and T5: SPBA-25% Sorghum + 0.05% Probiotics + 0.03% Butyric acid. Experimental diets were offered in the grower (day 14–day 28) and finisher (day 29–day 42) phases. Data were collected and analysed using one-way ANOVA in a CRD with SAS (2010). Study protocols were approved by the NWU-ANIMPROD REC (Ethic no: NWU-00817-23-A5). Dietary treatment affected FCR, ADFI and ADG significantly ($P < 0.0001$) in the two (2) phases. The highest FCR was observed in the SBA group in the finisher phase while the lowest was obtained in the control group. Furthermore the FCR in both the growing and finishing phases was lower in birds in the control group (grower phase: 1.51 ± 0.06 ; finisher phase: 1.66 ± 0.06). Birds that were fed SG had the lowest ADG in both phases. The average daily gain was highest ($P < 0.0001$) in birds offered the control diet and birds in the finisher phase while the lowest was in those fed the SG diet. The dietary treatments showed no significant difference in RBC counts. However, a significant difference ($P < 0.05$) was distinguished in HGB, NEU, LYM, MONO, EOS, BASO, PLT, MPV and WBC cell counts. Broilers fed SBA diet had the highest standing persistency in the current study, followed by those provided with a diet containing SPBA. Broilers fed SG had the weakest bones. Furthermore, the tibia length decreases when birds are fed SG diets compared to the control diets. The results of the study show that *Bacillus*-based probiotic and butyric acid can work effectively in improving growth, physiological and welfare in birds offered sorghum-based diet individually. The inclusion of butyric acid on its own did have positive effects on all parameters measured. To that end, to optimize broilers performance *Bacillus*-based probiotics and butyric acid may not be used in synergy, however, it is suggested that they may be effective individually.

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Reproductive traits and live weight in merino rams divergently selected for and against number of lambs weaned per mating

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Overall reproductive output, expressed as number of lambs weaned per mating (NLW), is a trait of economic importance in South African sheep. Past research focused on the behaviour, genetics and systematic aspects of ewe reproduction. Yet, rams are also instrumental in successful reproduction. Local research on the genetics of male reproductive traits is limited, though. The aim was to compare latencies and counts for mating behaviour, testis size and live weight between rams from Merino lines selected divergently for NLW for more than three decades. This study used the Elsenburg Merino flock in the Western Cape (DAEC: R12/57). A line selected for NLW (H-Line) and a line selected against NLW (L-line) were grazed in a single flock from 1986 to the present, except at mating when single sires were allocated to groups of ewes within selection lines. Hogget rams available for selection as replacements were exposed to 5-6 ewes in oestrus. The latency to first mount (tmount) and first serve (tserve), the count of mounts (nmount) and services (nserve) as well as the proportion of services to mounts (success) were recorded during a 20-minute mating dexterity test. Count traits (nmount, nserve and success) were recorded from 1992 to 2024 and latency traits from 1993 to 2024. Record numbers ranged from 756 (latency traits) to 766 (count traits). Test weight (TWT), yearling weight (YW), as well as yearling testis circumference (TC) and diameter (TD) were also recorded. The effects of selection line and birth year, their interaction, as well as random animal additive effects were assessed in single-trait analyses using ASReml4. A proportion of 0.838 of 506 H-Line rams was interested in the ewes (characterised by nmount $\geq$ 1), compared to 0.700 from 260 L-Line rams (Chi²=18.90, P<0.001). Expressed to L-Line performance, behavioural latencies were reduced by 38.9 (tmount) and 39.0% (tserve) in the H-Line (P<0.05). In contrast, count traits and success in the H-Line exceeded those in the L-Line by respectively 30.9, 74.1 and 43.3% (P<0.01). TWT and YW were respectively 15.1 and 15.9% heavier in H-Line rams (P<0.01). Accordingly, H-Line rams had larger testis dimensions than their L-Line contemporaries in all but 11 of the 32 years recorded. Latency and count traits were zero to lowly heritable. Only the estimates ($\pm$ SE) for tmount (0.08 $\pm$ 0.06), nserve (0.09 $\pm$ 0.07) and success (0.11 $\pm$ 0.07) exceeded the corresponding SEs. Heritability estimates for weight and testis traits ranged from 0.21 $\pm$ 0.09 for TC to 0.33 $\pm$ 0.09 for TWT. Ram behavioural latency and count traits were lowly heritable. The derived estimates were of the same magnitude as ewe reproduction traits, though. Ram behaviour benefited from selection for an increased NLW in the H-Line. Selection to improve NLW did not cause unwanted correlated responses in traits assessed in this study. Further studies are indicated as more data become available as heritability estimates are still imprecise. A substantially larger data set is needed to estimate genetic correlations with acceptable levels of accuracy.

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Diurnal variation of rumen temperature in South African sheep breeds under mediterranean summer conditions

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The use of indwelling rumen boluses enables continuous, high-resolution monitoring of rumen temperature (RT) under field conditions. Comparing the diurnal patterns of RT of South Africa's most important sheep breeds under different scales of heat load could be insightful for characterising breed differences, especially concerning the potential tolerance of indigenous breed types to heat stress. The aim was to characterise diurnal RT patterns across thermal stress categories in indigenous, composite and exotic South African sheep breeds.: Ethical approval reference: ACU-2023-26750. A total of 129 intact ram lambs were evaluated over two consecutive summer seasons, the sum of 64 lambs in 2023 and 65 lambs in 2024, with each of the eight breeds represented by 7 to 9 animals within a season. The breeds included the indigenous Namaqua Afrikaner (NA); composite breeds with indigenous genetic content: Meatmaster (75%; MM) and Dorper (50%; DP); and breeds of predominantly exotic origin: Merino (MR), Dormer (DM; terminal sire composite), Dohne Merino (DH; wool composite), South African Mutton Merino (SAMM), and Ile de France (IDF). Temperature loggers were orally administered, encapsulated in standard release boluses, which were programmed to record RT at 5-minute intervals. The post-drinking dips were excluded from the raw data, and the data were averaged within each hour to generate hourly estimates. The daily mean temperature humidity index (THI) was subsequently used to classify days into three heat stress categories (THIcat; low, moderate, high). The data were analysed within a linear mixed model. Fixed effects were breed interacted with THIcat and the month as a sampling block. Random terms were animal and animal.month, while a first-order autoregressive function was added to account for dependence between adjacent measurements. Subsequently, the diurnal rhythm was predicted according to a cubic smoothing spline with seven knot points, nested within both breed and THIcat. All breeds displayed variations of the typical monophasic diurnal rhythm pattern, with minimum RT tending to occur at ~07:00 and maximum RT between 18:00 and 20:00. However, notable differences were visible across breeds, as supported by the breed interaction with THIcat ($P < 0.01$) and the linear and non-linear components of the spline ($P < 0.01$). Generally, trends for DH were higher, DP lower, and IDF exhibited the steepest rise to and decline from peak RT. Considering breed differences across THIcat was most informative. The majority of exotic breeds (DH, SAMM, MR, and IDF) showed an increase of approximately 0.3 to 0.4 °C in peak RT under severe heat stress compared with low heat stress conditions. In contrast, the MM, DP, DM and NA maintained similar peak RT across THI categories. Interestingly, breed differences also varied notably across the day within a THIcat, with greater variation during cooler periods, likely reflecting differences in endogenous heat production. These findings indicate that breed patterns and differences in diurnal RT are context-dependent, varying with environmental heat load and time of day. Heat load is clearly important, but not the only predictor of RT patterns. The more stable patterns seen for breeds such as the DP and NA support the contention that indigenous breeds are more tolerant to high heat stress.

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Effect of Kalahari melon (*Citrullus lanatus*) essential oil and butyric acid in grower pig diets on growth performance, meat quality and fatty acid profile

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The pig industry is one of the main sectors which use antibiotic growth promoters for improved production performance. The sudden shift and restrictions on their use had a negative impact on pig welfare, and it necessitates an urgent need to explore alternatives that are both consumer and environment friendly. A variety of compounds, including organic acids and essential oils have been proposed as potential alternatives to antibiotic growth promoters in pig production. A study was conducted to determine the effect of Kalahari melon essential oil and butyric acid as alternative growth promoters in growing pigs on growth performance, meat quality and fatty acid profile. Forty growing mixed sex large white weaner pigs were weighed and randomly allocated to five dietary treatments NC negative control (no growth promoter), PC- (antibiotic growth promoter, Zin Bacteriocin), KEO-Kalahari melon essential oil (0.4%), BA- butyric acid (0.6%) and KEOA Kalahari melon essential oil (0.4%) + Butyric acid (0.6%) and each pig was considered an experimental unit. Pigs were weighed weekly for growth performance. Feed intake and weight gain were recorded until the termination of the feeding trial. At the end of the feeding trial, pigs were slaughtered and carcass, meat and fatty acid analyses were carried out. All experimental procedures and designs were approved by the North-West University Animal Production Research Ethics committee (NWU-AnimProdREC), and it was granted ethics number NWU-02010-20-A5. Dietary treatments significantly influenced growth performance ($P < 0.05$). Dietary treatment significantly ($P < 0.05$) affected protein utilisation and growth efficiency, and growth efficiency (GE) was high in KEOA (4.89 ± 0.12) and lowest in NC (3.72 ± 0.12). Complementary effects of Kalahari melon essential oil and butyric acid influenced gut function, improving growth performance. Dietary treatments significantly affected carcass characteristics and some meat quality parameters except for meat yellowness (b^*), drip loss and water holding capacity. ($P < 0.05$). After 24 hours, NC remained with the highest meat pH value (6.22 ± 0.07) compared to other dietary treatments. Improved nutrient absorption and utilization due to the inclusion of essential oils and organic acids increases glycogen reserves and aids in the process of lactic acid formation after slaughter. Dietary treatments had a significant effect on SFA content ($P < 0.005$) and KEBA (2.266 ± 0.161) had the highest SFA content. Dietary treatment affected MUFA concentration ($P < 0.005$), and the n-6 / n-3 fatty acid ratio was affected by dietary treatments and was highest in NC (28.78 ± 3.104) and lowest in EOOA (13.14 ± 3.104). Essential oils and organic acids alter the fatty acid profile of pork, improving its healthiness. Results indicate that Kalahari melon essential oil, butyric acid and their blend affect growth performance, carcass characteristics and meat quality and nutritional composition of pork. Inclusion of Kalahari melon essential oil and butyric acid in growing pig diets improves growth performance, pork quality and its healthfulness.

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Effect of different varieties of rosemary (*Rosmarinus officinalis*) plant extracts on in vitro methane production of *Eragrostis curvula* hay

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Antibiotic growth promoters (AGP) are known to reduce methane production from ruminants but are also notorious for their residue in animal products. As such, efforts to shift from AGP to more organic sources are on the rise, such as plant extracts. Different plant extracts have been tested and have been proven to reduce methane without affecting feed digestibility in ruminants. The aim of this study was to evaluate the capability of different rosemary varieties and their phytochemicals on *in vitro* gas production, methane inhibition, and *in vitro* organic matter digestibility. The study was approved by the Animal Ethics Committee of the University of Pretoria (NAS316/2021). Three different varieties of rosemary leaves (McConnells blue, Tuscan blue, and Roseus) were harvested 8 weeks after planting (Season 1) and six varieties (McConnells Blue, Tuscan Blue, Roseus, Mountain Mist, Wild Rosemary and Silver Fox) were harvested at 50 % flowering (Season 2). Each variety had 10 plants which were all harvested from. The plant material was stored in a freezer immediately after harvest. The frozen plant material was freeze-dried, and leaves were separated from branches and ground into a powder. Leaf powder was extracted by adding 85 mL of methanol and 15 mL of distilled water to 10 g of leaf powder. The plant metabolites were identified and quantified using the untargeted Liquid Chromatograph-Mass Spectrometry method. The plant extracts were added to *Eragrostis curvula* at a recommended rate of 75mg/Kg DM feed (Akanmu, 2018). To prepare the dose, dried crude extract was reconstituted with water, 1.2 mg of dried extract was added to 120 mL of water. For gas production, 400 mg of substrate was used and 3mL of plant extract solution was added into serum bottles which were incubated for 48 hours using standard procedure by Meinke (1988). Methane samples were taken using 10mL luer lock syringes at every gas reading (3, 6, 12, 24 and 48hours) and measured for methane using a gas chromatograph. Samples for in vitro organic matter digestibility were prepared by adding 1.5mL of plant solution to 200 mg substrate, procedure was carried out using the two-stage digestion described by Tilley and Terry (1963). Principle component analysis was used to investigate the relationship between varieties, metabolites, gas production, methane and digestibility. Wild Rosemary was different to the other varieties in terms of the concentration and presence of most of the metabolites phytochemical profiles. Whereas McConnell's Blue was the only variety that showed seasonal difference in the concentration of metabolites. In season 1, McConnell's Blue variety increased total gas production (TGP) and Tuscan Blue variety decreased methane (CH₄) and in vitro organic matter digestibility (IVOMD). In season 2, all the rosemary varieties plant extracts reduced TGP, but no effect was observed for (CH₄). The study further identified positive correlations between some metabolites (such as rosmannol, rosmarinic acid, rosmannol, carnolic acid and carnolol) and TGP, CH₄ and IVOMD. The metabolites across the different varieties were similar in quantity, although, Tuscan Blue showed a higher relative concentration of several metabolites. Tuscan Blue varieties have superior anti-methanogenic effect compared to others. These findings underscore the potential of rosemary extracts as sustainable feed additives that support methane reduction.

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Genomic regions under selection in Ayrshire cattle identified using integrated haplotype score

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Improving the sustainability of the South African dairy industry requires a precise understanding of the genetic basis of economically important traits. While the Ayrshire breed is valued for its milk quality and environmental adaptability, the specific genomic regions contributing to these traits remain poorly characterized. Selection signature approaches, such as the integrated haplotype score (iHS), detect ongoing positive selection within a single population by measuring extended haplotype homozygosity. The aim of the study was to identify genomic regions under recent positive selection in South African Ayrshire cattle using iHS, providing a foundation for understanding the genetic drivers of resilience and productivity. Genotype data from 560 South African Ayrshire cattle (Ethical Clearance: 010411-009) were generated using the Illumina® BovineSNP50 genotyping panel (51 448 autosomal SNPs). Following merging with PLINK v1.9 and phasing with Beagle v5.5, 30 018 autosomal markers were retained for analysis in the *rehh* R package. Strong evidence of selection was defined as $|iHS| > 3$. Candidate regions were extended 1 Mb flanking significant SNPs. Genes were identified using the *Bos taurus* ARS-UCD1.2 annotation, and genomic patterns were evaluated via overlap analysis with the Animal QTL database. Significant selection signals were detected at 49 SNP positions across 21 autosomes, defining 38 candidate genomic regions. While the most intense selection peaks were localized on BTA2, 4, 9, 11, 21, and 23, high-density selection clusters were particularly evident on BTA13 and BTA19, which contained >25 significant SNPs each. Overlap analysis revealed that these regions are highly enriched for economically important production traits, including milk protein percentage (n=183 QTLs), milk yield (n=123), and milk fat percentage (n=115). Furthermore, selection signatures coincided with QTLs for physiological resilience, specifically tuberculosis susceptibility (n=84) and mastitis resistance (n=27). Candidate genes identified within these functional complexes include immune response (*CMKLR2*, *TCF7L1*), metabolic regulation (*PLAGL1*, *HIGD1A*), and cellular stress (*CLIC5*). These findings demonstrate a multi-trait selection pattern where productivity is closely integrated with environmental adaptation. These results indicate that South African Ayrshire cattle exhibit genomic signatures that simultaneously target metabolic function, disease resistance, and milk composition. These identified regions provide a data-driven baseline for breeding strategies. Future research should prioritize these high-density clusters to investigate potential biological trade-offs between intensive production and long-term environmental resilience.

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Empowering smallholder sheep farmers using data-driven body weight prediction algorithms in Dorper sheep from two villages in Limpopo province, South Africa

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In many rural smallholder farming systems, the lack of access to weighing equipment makes it challenging for farmers to determine sheep body weight accurately. This limitation affects key management decisions, including marketing, feeding, health care and breeding strategies, often reducing productivity and income. Data-driven algorithms provide a practical approach to support evidence-based decision-making, even in low-resource settings. The aim of the study was to evaluate the use of data mining algorithms to predict live body weight from linear body measurements in Dorper sheep, highlighting their potential to empower smallholder farmers. The study was approved by the University of Limpopo Animal Research and Ethics Committee (AREC) before the commencement of the data collection (AREC/22/2023: PG). A total of 306 Dorper sheep aged 1–2 years from two villages in Lepelle-Nkumpi Local Municipality, Limpopo Province, were assessed for heart girth, withers height, rump height, rump length, and body length. Four predictive models - classification and regression tree (CART), chi-square automatic interaction detection (CHAID), Exhaustive CHAID, and multivariate adaptive regression splines (MARS) were compared using standard goodness-of-fit criteria. The MARS algorithm demonstrated the highest predictive accuracy, identifying heart girth, withers height, rump height, body length, and sex as key contributors. Integrating such data-driven algorithms into smallholder livestock systems enables more reliable estimation of body weight, supporting informed decisions for feeding, health management, breeding and pricing. This approach links animal science with practical farm management and sustainable rural development. Using data mining algorithms to predict body weight provides an effective, accessible tool for smallholder farmer sheep, improving livelihoods, production, and resilience in rural livestock systems.

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Effect of replacing lucerne hay with *Seriphium plumosum* meal in diet on live weight gain, meat quality and sensory attributes of Nguni steers

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Meat constitutes a significant source of essential nutrients in human diets, with its consumption largely driven by product quality and sensory attributes. In rangeland-based production systems, seasonal feed shortages remain a major constraint to livestock productivity. Indigenous woody species, characterized by relatively high crude protein content and widespread availability, present a viable alternative feed resource. *Seriphium plumosum* has been shown to exhibit superior nutritional value relative to grasses during specific phenological stages. Therefore, its strategic incorporation as a supplementary feed in ruminant diets may mitigate seasonal feed deficits during drought or dry periods, while potentially improving meat quality. This study evaluated the potential of *Seriphium plumosum* as a dietary feed ingredient and its effects on growth performance and meat quality of Nguni steers. The experiment was conducted at the Agricultural Research Council – Animal Production (ARC-AP) facility following ethical approval from the ARC-AP Ethics Committee (APAEC–2020/16) and the University of Limpopo Animal Research Ethics Committee (AREC/01/2020: PG). All procedures complied with the South African National Standard (SANS 10386:2008) for the care and use of animals in research. Twenty-eight Nguni steers were individually housed and assigned to four dietary treatments containing *S. plumosum* meal at inclusion levels of 0%, 10%, 20%, and 30% over a 111-day experimental period. The study followed a completely randomized design with seven replicates per treatment. Live weight gain was measured fortnightly. Meat quality parameters assessed included meat colour (performed on two freshly cut steaks of 15 mm thickness using Minolta Chroma meter (Model CR200, Osaka, Japan) and water-holding capacity. Warner–Bratzler shear force was determined by cutting three steaks (25 cm thick, load cell 2000) at an internal diameter of 1.27 cm on the 10th rib, total cooking loss was calculated as the % difference in weight of the cooked and raw meat. Dietary inclusion of *Seriphium plumosum* had no significant effect ($P > 0.05$) on live weight gain, meat colour, tenderness, or cooking loss, indicating that its incorporation did not compromise animal performance or meat quality. This response may be attributed to the moderate levels of condensed tannins present in *S. plumosum*, which are known to stabilise rumen microbial activity and enhance protein utilisation without exerting detrimental anti-nutritional effects. The absence of treatment effects on meat colour suggests that myoglobin stability and pigment concentration were not adversely affected. This could be associated with reduced metmyoglobin formation and the maintenance of heme pigment integrity, thereby preserving desirable colour attributes. Similarly, the lack of significant differences ($P > 0.05$) in Warner–Bratzler shear force and cooking loss indicates that *S. plumosum* inclusion did not alter muscle fibre structure or water-holding capacity. These findings suggest that, at the inclusion levels evaluated, condensed tannins did not negatively influence post-mortem muscle properties or meat textural characteristics. Overall, the inclusion of *S. plumosum* meal in diet showed potential as an alternative feed resource for Nguni steers. However, further long-term studies are recommended to confirm its effectiveness and determine optimal inclusion levels under different production systems.

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Genomic characterisation of the South African Wagyu populations

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The Wagyu cattle breed was introduced to South Africa (SA) during 1999 and operates under an open herdbook for upgrading using beef breeds such as Bonsmara, Angus and Drakensberger. Two wagyu strains are recognized, namely the South African Japanese Black (JB) and Akaushi (AK). Wagyu cattle are highly valued for superior meat quality, particularly marbling. Since genotyping commenced in 2016, genomic characterisation has become important to the Wagyu Society of SA to assess genomic diversity, inbreeding and population structure within the South African population. The aim of this study was to perform a genomic characterization of the South African Japanese Black and Akaushi Wagyu cattle, using Australian Japanese Black as an outgroup. A total of 2517 (789 South African and 1728 Australian) genotypes from first cross to fullblood animals were available (Ethics approval NAS255/2022) for this study. Animals were genotyped using either Unistel BovineSNP50 v3 BeadChip or Neogen GGP Bovine 100K SNP arrays, and only common SNPs shared between platforms were retained for combined analyses. Only genotypes from fullblood and purebred animals were utilized for the genomic analyses. Four data sets were created, one for each population and one combined. Quality control removed samples and SNPs with call rates below 95% and Hardy–Weinberg equilibrium (HWE) with $P < 0.001$ using PLINK (Purcell *et al.*, 2007). 205 and 437 South African AK and JB and 624 Australian JB genotypes remained for analyses. PLINK (Purcell *et al.*, 2007) was used to estimate observed (H_o) and expected (H_e) heterozygosity, minor allele frequency (MAF) and linkage disequilibrium (LD). Genomic relationship matrices generated using GCTA, principal component analysis (PCA) was performed using eigenvalues from the first three principal components, and population structure was assessed using ADMIXTURE. The ideal K-value was visualised using Genesis to generate a bar plot for demonstrating relationships among the animals. The combined dataset indicated lower observed than expected heterozygosity ($H_e > H_o$); 0.310), suggesting population substructure, while the AK showed slightly higher heterozygosity (0.320) compared to the South African and Australian JB populations (0.300 and 0.280, respectively). These values indicate moderate genomic diversity comparable to other South Africa beef breeds. The overall inbreeding coefficient (F_{IS}) was 0.013, indicating limited genomic inbreeding, while average LD ($r^2 = 0.408$) reflected moderate marker association suitable for genomic diversity assessment. PCA identified two distinct clusters separating AK and JB with the South African AK distinct from both the South African and Australian JB populations. ADMIXTURE supported this separation and identified three distinct population groupings. Although the South African Wagyu society and breeders use the term Wagyu interchangeably for Japanese Black and Akaushi, genomic analyses confirmed that these populations are genetically distinct. Owing to their different ancestral origins, Akaushi and Japanese Black should be regarded and evaluated as separate breeds in future genetic evaluations.

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Genetic (co)variance components of faecal egg count and production traits in Elsenburg South African Mutton Merino and Dormer sheep

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Gastrointestinal nematode (GIN) infestation is a major constraint for sheep health and production in pasture-based systems. Anthelmintics are currently the primary control measure, but the emergence of resistant helminth strains threatens their effectiveness. Breeding for innate resistance, as part of an integrated parasite management strategy, can contribute significantly to a long-term solution. Faecal egg count (FEC), used as an indirect measure of GIN resistance, has been successfully leveraged in sheep breeding in Australia and New Zealand. In South Africa, FEC studies have been limited, predominantly focusing on Merinos, while popular breeds such as the South African Mutton Merino (SAMM) and Dormer remain understudied. No reports were found on the relationship between FEC and production traits in these breeds. The aim of the study was to estimate genetic (co)variance components for FEC, liveweight traits, and wool traits in SAMM and Dormer lambs. This study used FEC data recorded on 1393 SAMM and 2510 Dormer lambs managed as a single flock on the Elsenburg Research Farm [DAEC: R12/55 and R12/59]. Production traits analyzed were weaning weight (WW), yearling weight (YW), clean fleece weight (CFW), staple length (SL), fibre diameter (FD), and coefficient of variation of fibre diameter (CVFD). Raw FEC data were skewed and leptokurtic; therefore, a logarithmic transformation, $LFEC = \ln(FEC + 100)$, was applied to normalise the distribution and account for zero values. Univariate and multivariate mixed-model analyses were performed using ASREML V4.2, fitting fixed effects including birth year, sex, breed, birth type, age of dam, and two-factor interactions, tested sequentially according to F-statistics. Random effects tested were direct additive, maternal additive, and maternal permanent environmental effects, using log-likelihood tests. Dormer lambs showed a lower LFEC mean (6.69 ± 0.03) than SAMM (6.89 ± 0.04) lambs, with this breed difference suggesting a genetic basis for nematode resistance. The direct heritability (h^2_a) of LFEC was 0.14 ± 0.04 , showing that a useful portion of the variation observed in LFEC is attributable to genetic differences, thereby allowing selection for reduced FEC. Production traits exhibited moderate to high h^2_a , except for WW where variation partitioned predominantly to maternal components. Phenotypically, correlations were generally weak, with LFEC showing significant and favourable correlations only with YW (-0.06 ± 0.02) and WW (-0.04 ± 0.02). Genetically, LFEC was favourably correlated with SL, WW, YW, CFW and CVFD; however, only the favourable correlation with CVFD (0.37 ± 0.12) was significant. FEC was unfavourably, but non-significantly, correlated with FD. These genetic relationships indicate that FEC and production traits could be improved simultaneously in the present flock, but also that no promising proxy traits for FEC exist. This study provides further evidence that FEC is variable and heritable in South African sheep, indicating that selection for reduced FEC should be feasible in this resource flock, with minimal risk of unwanted correlated responses in other economically important traits. However, wide-scale selection will require FEC recording beyond research flocks, which is currently lacking. The observed breed differences in response to GIN challenge warrant further investigation.

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Evaluation of factors influencing the detection of selection signatures in populations selected for traits with different genetic architectures using simulated data

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Detection of selection signatures in livestock is challenging due to inconsistencies across methods, sample sizes, and genetic architectures. Commonly used approaches include runs of homozygosity (ROH), integrated haplotype score (iHS), fixation index (FST), cross-population extended haplotype homozygosity (XP-EHH), and integrated haplotype deviation (iHDSel). Their effectiveness varies with population characteristics, while choice of detection thresholds can strongly influence the results. Evaluating these factors using simulated data, where true selection signatures are known, allows rigorous comparison of methods, thresholds, and false-positive burden. The aim of the study was to evaluate how statistical method, QTL number, trait heritability, sample size, and detection thresholds affect power and false discovery on declared regions in simulated sheep populations under divergent and random selection. Sheep populations were simulated in AlphaSimR with six scenarios varying QTL number (3, 20, 200 per five chromosomes) and heritability (0.15 and 0.40). Subpopulations were selected for high or low phenotypic values or random mating over 50 generations. Subsamples of 5, 10, 20, 30, 50, 200, 250, 500, and 1000 individuals were analysed. Selection signature analyses used FST, ROH, iHS, XP-EHH, and iHDSel with multiple thresholds per method (e.g. FST top 0.1%, 1%, 10%; ROH length and incidence rules; iHS and XP-EHH absolute and percentile cut-offs; iHDSel p-value thresholds). Each scenario was replicated 50 times. Declarations were validated against simulated QTL positions (100 kb window); power and false discovery rate on declared candidates were summarised. FST achieved higher mean power for high–low than for selected–random contrasts at primary thresholds, yet genome-wide false discovery rates stayed very high for tail-based FST, iHS, and XP-EHH, illustrating a strong power–FDR trade-off. Non-zero signals involving the random control line are therefore a poor index of successful selection recovery: under liberal rules they chiefly reflect non-truth declarations and threshold behaviour, because those QTL were not under directional selection. Intermediate to large subsamples (200–500 individuals) generally stabilised estimates; very small samples (5–20) reduced power. Fewer QTL improved contrast strength across methods. XP-EHH mirrored FST-like contrast effects and sample-size responses. ROH showed lower overall power but line-specific patterns that depended on QTL count, heritability, and ROH rules. iHS was relatively stronger under some oligogenic, lower-heritability conditions at larger n. iHDSel provided complementary, more conservative signals. Stricter thresholds reduced hit counts and improved precision; relaxed thresholds increased apparent detection at the cost of higher false positives. Threshold sensitivity analyses supported these patterns. Results are qualitatively consistent with multi-statistic livestock scans, though field studies lack simulation's known-truth benchmark. Transparent reporting should pair power on validated targets with false discovery on declared windows, contrast type, and thresholds. Divergent selection strengthens interpretable inter-population signal; random-line contrasts mainly expose false-positive risk under liberal genome-wide rules. FST and XP-EHH dominate marginal power under primary tails but need conservative follow-up; ROH and iHDSel are more specialised. Multi-threshold, multi-outcome summaries support informed design and interpretation of selection signature studies in livestock breeding programmes.

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Preliminary results on the influence of enzyme-treated insect meal on growth and gonad development of abalone (*Haliotis midae*)

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Important ingredients in abalone diets include a good quality protein source, carbohydrates, and a low lipid, fatty acid and fibre content. Fishmeal has a favourable protein content, making it ideal to be used in aquaculture and terrestrial animal feeds to ensure optimal growth. Concern about the sustainable use of fishmeal in animal feeds necessitates the investigation of alternative protein sources such as insect meal to ensure growth in production animals. It is important to consider how alternative protein sources will affect the growth and reproductive development of abalone, an important aquatic species in the South African aquaculture sector. The aim of the study was to determine the potential of enzyme-treated insect meal supplemented to abalone diets, to maintain growth and reproductive development in abalone. No ethical approval was required for the trial as abalone are considered invertebrates. The ethics committee was, however, notified of the project (ACU-2025-33687). A total of 5120 South African abalone (*Haliotis midae*) were randomly allocated to 16 different treatments (8 baskets per treatment) consisting of varying inclusion levels (i.e. replacing fishmeal) of enzyme-treated insect meals i.e. 20, 40, 60, 80 and 100% and a control without insect meal (IM). The IM was hydrolysed prior to inclusion using three different enzymatic treatments, i.e. chitinase, amylase and autolyse. The shell width, length and abalone weight were taken monthly of three tagged abalone per basket throughout the 6-month trial. At the termination of the trial, two females and one male per basket were selected for processing. The processing involved weighing of the individual abalone, shucking the abalone, followed by weighing the foot and viscera. The foot muscle and viscera (digestive gland and gonad) were then separated and weighed individually. The viscera of the male and one female were used for physical gonad measurements. XLSTAT was used to compute descriptive statistics, conduct ANOVA and ANCOVA analyses respectively, and determine regression coefficients. The treatment diet that consisted of amylase-treated IM included at 60% (i.e. 40% fishmeal) resulted in the best growth, and the diet consisted of autolysed IM included at 20% (i.e. 80% fishmeal) resulted in the poorest growth ($34.72 \pm 1.64\text{g}$ vs $25.40 \pm 1.69\text{g}$; $P < 0.05$). The diet consisting of amylase-treated IM included at 60% (i.e. 40% fishmeal) similarly had the most beneficial effect on gonad development, compared to the autolysed IM included at 20% (i.e. 80% fishmeal) which resulted in the poorest gonad development ($15.51 \pm 0.74\text{g}$ vs $9.77 \pm 0.77\text{g}$; $P < 0.05$). No differences were observed between male and female abalone. From the preliminary results, it can be deduced that amylase treatment of the insect meal rendered the nutrients more accessible, thereby resulting in the more pronounced live weight and gonad development. Preliminary results indicate that the enzyme treatment of insect meal using amylase, potentially allows for the abalone feed to be metabolised more efficiently, resulting in sustained growth and related gonad development. Follow-up studies will investigate the partitioning of nutrients towards gonad development, and whether this occurs at the expense of growth in pre-harvest abalone.

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Feather harvesting methods influence feather quality and yield in South African Black breeder ostriches (*Struthio camelus* var. *Domesticus*)

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The ostrich feather industry is an important component of South Africa's agricultural economy, providing stability for commercial enterprises and job opportunities for rural sectors. Feather harvesting is commonly carried out through gathering ripe feathers or clipping plumes, however, there is limited scientific evidence comparing the effects of these harvesting strategies on feather quality and yield. The aim of the study was to determine the influence of different feather harvesting approaches on feather quality and yield. Ethical approval for the study was granted by the Western Cape Department of Agriculture's Animal Ethics Committee (DAEC, reference number 6/2020). Breeder ostriches (N=222), stratified according to weight and sex, were assigned to five different feather harvesting treatments across 4 annual production cycles (2019-2022). Treatments included no harvesting of feathers (control), feather gathering of 5 types of wing feathers and tail feathers, feather clipping of white plumes and subsequent quill removal 4 weeks later, feather clipping of white plumes, followed by feather gathering at quill removal 4 weeks later, and feather clipping with delayed quill removal 3 months later. The number of plumes, plume length, plume width, total feather weight, five feather quality characteristics of the white plumes (scored on a 9-point scale) and the income generated from the plumes were recorded. Linear models were used to assess the fixed effects of feather treatment, bird sex, production year, cumulative years in treatment, and age in a factorial statistical design. All fixed effects significantly influenced feather quality, -yield and income generated. Males produced more plumes than females (52 ± 1 vs 47 ± 1 ; $P < 0.001$), and plume number increased with time in treatment, from 46 ± 1 after two years to 51 ± 1 after three to four years of treatment ($P < 0.001$). Plume weight was higher in males (282 ± 6 g) than in females (213 ± 7 g; $P < 0.001$) and showed an age $\times$ treatment interaction, with delayed quill removal resulting in higher yields in older birds (8-10 years old) compared to younger breeders (5-7 years old at the end of the study). Younger birds produced longer plumes than older birds (659 ± 4 vs 634 ± 5 mm; $P < 0.05$), while plume width showed a sex $\times$ treatment interaction ($P < 0.05$). Sex ($P < 0.001$), treatment ($P < 0.001$) and years in treatment ($P = 0.038$) influenced total feather weight, with males producing 32% more feathers than females (926 ± 17 g vs 702 ± 21 g). Feather damage was the most prominent in untreated birds ($P < 0.001$), reflecting poor plumage condition and more exposure to environmental wear and tear across years. Fault bars were more prevalent in harvested birds ($P = 0.01$), possibly caused by stress associated with harvesting practices. Plume value was improved by feather harvesting (1138–1269 ZAR vs. 536 ± 120 ZAR; $P < 0.001$) and were higher for males compared to females (1217 ± 58 vs 880 ± 68 ZAR, $P < 0.001$). Annual feather harvesting of 6 types of ostrich feathers maximised feather yield, without compromising key quality traits, resulting in improved financial returns, whereas feather yield and value were reduced when feathers were left to moult naturally.

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The effect of Mopane worm (*Imbrasia belina* meal) and multienzyme inclusion on gut morphology, digesta pH, and growth performance of Ross 308 broiler chicks

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Edible insects have emerged as a novel primary protein source and /or feed additive in poultry nutrition. However, the broiler chicks cannot digest insect chitin; hence, the inclusion of multienzyme in insect-based diets could improve the utilisation of insects. Therefore, the present study aimed to evaluate the effect of dietary graded levels (12, 14, 16, or 18 %) of mopane worm (*Imbrasia belina*) and/or 50g/kg DM multienzyme in broiler diets on gut morphology, digesta pH, and growth performance of broiler chicks during the starter phase. A total of 300 unisex day-old broiler chicks were randomly assigned to 5 dietary treatments in a completely randomised design for 14 days. Each treatment was replicated 5 times with 12 chicks per replicate. Treatments included: 1) basal diet without mopane worm meal and multienzyme (*Trt1*); 2) basal diet with only 12% of mopane worm meal without multienzyme (*Trt2*); 3) basal diet with 14% of mopane worm meal and 50 g/kg DM multienzyme (*Trt3*); 4) basal diet with 16% of mopane worm meal and 50 g/kg DM multienzyme (*Trt4*), and 5) basal diet with 18% of mopane worm and 50 g/kg DM multienzyme (*Trt5*). The collected data were subjected to the one-way analysis of variance using SAS software. The obtained results indicated that the experimental diets did not affect ($P < 0.05$) the digesta pH of duodenum; however, the digesta pH of proventriculus, gizzard, jejunum, ileum and caeca were affected ($P > 0.05$). The proventricular and gizzard pH were lower ($P < 0.05$) in broiler chicks on diets *Trt3*, *Trt4*, and *Trt5* than those on diets *Trt1* and *Trt2*. The jejunum pH was lower ($P < 0.05$) in broiler chicks on a diet *Trt4* than those on diets *Trt1*, *Trt2*, *Trt3*, and *Trt5*. Subsequently, ileum and caeca pH were lower ($P < 0.05$) in broiler chicks on a diet *Trt2* than those on diets *Trt1*, *Trt3*, *Trt4*, and *Trt5*. The gut lengths of gastrointestinal, small intestine, duodenum, jejunum, ileum were longer ($P > 0.05$) in broiler chicks on diets *Trt2*, *Trt3*, *Trt4*, and *Trt5* than those on diet *Trt1*. However, experimental diets did not affect ($P < 0.05$) the length of the large intestine and caeca. The gastrointestinal, crop, gizzard, spleen, pancreas, heart, liver, small intestine, duodenum, jejunum, ileum, large intestine and caeca gut weights were lighter ($P < 0.05$) in broiler chicks on a diet MW_{0%} than those on diets *Trt2*, *Trt3*, *Trt4*, and *Trt5*. The feed intake (FI) was lower ($P < 0.05$) in broiler chicks on a diet *Trt4* than those on diets *Trt1*, *Trt2*, *Trt3*, and *Trt5*. The body weight gain (BWG) was lower ($P < 0.05$) in broiler chicks on diets *Trt1* than those on diets *Trt2*, *Trt3*, *Trt4*, and *Trt5*. The feed conversion ratio (FCR) was lower ($P < 0.05$) in broiler chicks on a diet *Trt5* than those on diets *Trt1*, *Trt2*, *Trt3*, and *Trt4*. It can be concluded that incorporating 12, 14, 16, or 18 % mopane worm meal and 50 g/kg DM of multienzyme into broiler starter diets improved gut morphology, BWG, FCR, FI, gut weight and gut length with little effect on digesta pH. However, more studies on mopane worm meal are required to confirm these results.

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Nutritional and phenolic characterisation of Spineless Cactus (*Opuntia ficus-indica*) cladodes as a functional feed resource for slow-growing goats

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Spineless cactus (*Opuntia ficus-indica*) cladodes are emerging as viable drought-adapted feed resource for goats under semi-arid conditions; however, comprehensive information on their nutritional composition and phenolic profile remain limited. Understanding both nutrient composition and bioactive compounds is essential in evaluating their suitability as a functional feed resource for slow-growing goats under resource-constrained environments. The aim of the study was to evaluate the nutritional composition, amino acid profile, and phenolic compound characterisation of spineless cactus cladodes as a functional feed resource for slow-growing goats. The nutritional composition and phenolic characteristics of the spineless cactus cladodes were assessed. All cladodes were harvested from naturally growing *Opuntia spp.* plants in the University of Limpopo fields, at the early reproductive stage and without any human intervention. Sampling was conducted at the end of wet season between April and May 2025. The Official Methods of Analysis (AOAC) were used for nutrient composition determination, whereas Quadrupole Time-of-Flight Mass Spectrometer (QTOF-MS) was used to assess the phenolic compounds suitable for goat feeding. All procedures were approved by the University of Limpopo Animal Research Ethics Committee (AREC-290914-017). The cladodes contained 6.32% crude protein, 29.64% neutral detergent fiber, 11.27% acid detergent fiber, 14.63% crude fiber, 18.06% ash, and gross energy of 12.12 MJ/kg, indicating moderate nutritive value suitable for supplementary goat feeding. Essential amino acids such as leucine (0.38%), lysine (0.38%), and valine (0.23%) were present, while glutamic acid (0.71%) and aspartic acid (0.50%) dominated the non-essential amino acid profile. Phenolic profiling revealed diverse flavonoid compounds, with typhaneoside, 1-O-feruloglucose, and robinin identified as dominant constituents, suggesting potential antioxidant functionality. Although fat content was low (1.63%), the combined nutrient and phytochemical composition support the use of cladodes as a climate-resilient functional feed ingredient in semi-arid goat production systems. The crude fiber levels observed in the present study further indicated that this plant has potential as a valuable dietary supplement for goats, as adequate fiber intake is essential for maintaining normal rumen function, promoting rumination, and reducing the risk of digestive disorders such as acidosis and enterotoxemia. This further suggests the cladodes carry the capacity to improve productivity in smallholder settings through their moderate nutritive value, essential amino acid profile, and phenolic compounds that may contribute to enhanced health and resilience under climate variability. Spineless cactus cladodes provide a nutritionally relevant and phytochemically rich supplementary feed resource for slow-growing goats and hold strong potential as a climate-smart feeding strategy in semi-arid environments where conventional feed resources are limited. Further studies are envisaged comparing the feedlot production performance and efficiency of ruminants such as in ruminants' production under intensive feeding systems since they are the biggest contributors of ruminal methane gas.

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The effect of climatic factors on calving percentage of Bonsmara cows in the Eastern Kalahari Bushveld

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Reproductive performance is an important factor in extensive beef production systems. South African climatic conditions such as high temperature and humidity during the summer breeding season may negatively affect fertility in Bonsmara cows. However, limited long-term information is available on the relationship between weather variables and calving percentage. The aim of the study was to determine whether average maximum and minimum temperature, relative humidity and rainfall before, during and after the breeding season affected the calving percentage of the Bonsmara breed over 33-year period. The study was conducted at the Vaalharts Research station of the Northern Cape Department of Agriculture, Environmental Affairs, Rural Development and Land Reform (DAERL). The calving data of extensively managed Bonsmara cows (n=3904) from 1986 to 2019 were extracted from the INTERGIS. The climatic data for the same period, collected from the local Vaalharts weather station included: average monthly minimum and maximum temperature, minimum and maximum relative humidity, temperature humidity index (THI) and rain within the three-month breeding season and a month prior to the breeding season (November to February). Pearson's correlation coefficient was used to correlate the weather data variables with the calving percentage. A stepwise multiple linear regression model was subsequently fitted to predict the calving percentage (dependent variable), using the weather data for the four months as independent variables. The experimental procedures were approved by DAERL ethics committee (NC/AEREC/19/11/008). Calving percentage variation between 74 and 99 % over a 33 year period was recorded. A negative correlation between the calving percentage and the second month of the breeding season-January maximum temperature ($r = -0.459$; $p = 0.006$); February maximum relative humidity ($r = -0.196$; $p = 0.265$); February THI ($r = -0.239$; $p = 0.173$) was recorded. The summary regression of weather patterns and the calving percentage contributed cumulatively to the R^2 . The contribution of NovHmin to the R^2 is 22.7%, JanTmax 17.3%, FebHmax 17.8%, JanTHI 8.1% and FebTHI 8.3%. The model that was fitted had an R^2 of 78.6%. These results indicate that during the summer breeding season, high temperatures and humidity levels could exert a detrimental effect on the Bonsmara calving percentage in warmer regions of South Africa. The calving percentage of Bonsmara cows that were kept in the eastern Kalahari bushveld over the past 33 years was influenced by temperature and humidity during the summer breeding season. The results demonstrated a definite relationship between climatic variables and calving percentage and consistently supported the initial findings.

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The effect of moisture content on the sensory properties of rabbit biltong

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Value addition within the meat sector has become an increasingly important marketing strategy in promoting the utilisation of sustainable protein sources and enhancing the use of underexploited livestock species. Rabbit meat is well characterised by its favourable nutritional profile and production efficiency yet remains underutilised in South Africa. This is partly due to limited product development and low consumer exposure. Therefore, adding value to rabbit meat by processing it into familiar meat product forms such as biltong may offer a clear route to improving its consumer acceptability and demand. However, an understanding of how moisture content affects the sensory quality of dried meat products is required. This is critical for optimising processing conditions for rabbit meat to achieve the desirable quality of the innovative product (rabbit biltong). This study investigated the effect of two moisture content levels on the sensory properties of rabbit biltong, with the objective of optimizing product quality for consumer acceptance. Twelve rabbits were purchased from a commercial farm, slaughtered under standard conditions and processed into biltong. The rabbits were electrically stunned, exsanguinated, and processed, with carcasses subsequently chilled, sealed and transported under controlled cold-chain conditions to the University of KwaZulu-Natal for further laboratory analysis. The rabbit meat samples were marinated in a formulated spice and vinegar mixture and dried at 25°C for different times to achieve two target moisture content levels: 40% and 50%. The moisture content was confirmed using the AOAC oven-drying method. A sensory evaluation was then conducted by a 15-member consumer panel using a 9-point hedonic scale to assess appearance, aroma, texture, juiciness, flavour and overall acceptability. The data was analysed using paired-samples t-tests and a Wilcoxon signed-rank test, where appropriate, with significance set at $p < 0.05$. All ethical clearance was obtained from the University of KwaZulu-Natal Animal Research Ethics Committee (AREC/00008071/2024) and the Human Science Research Ethics Committee (HSSREC/00029565/2025). The mean sensory scores ranged from 5.80 to 7.00, which included a good overall acceptability for both moisture content levels. The rabbit biltong that was dried to 40% moisture recorded higher scores for appearance (6.40 ± 1.60), aroma (6.80 ± 1.70) and flavour (5.93 ± 1.71). However, the rabbit biltong dried to 50% moisture content recorded higher scores for juiciness (7.00 ± 1.51) and texture (6.87 ± 1.60). Significant differences in aroma and juiciness between the two moisture levels were observed. There were no significant differences ($p > 0.05$) between the two moisture content levels for appearance, texture, flavour and overall acceptability. These findings indicate that higher moisture retention enhances juiciness and tenderness, while greater dehydration intensifies aroma. The rabbit biltong dried to either moisture content level (40% and 50%) was acceptable to the consumer panel. The 40% moisture level was associated with stronger aroma, while the 50% level enhanced juiciness. These results suggest that moisture content can be adjusted to influence specific sensory attributes of rabbit biltong, although further research with larger consumer panels is needed to validate its broader market potential.

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The maternal heritability of ewes to reunite with their lambs during the neonatal period

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The ewe-lamb bond, formed through the behavioural interactions between the dam and her offspring, is critical for adaptation during the neonatal period and is thus a prerequisite for a good chance of lamb survival. Previous studies have reviewed ewe temperament and behaviour during this period as possible indirect selection strategies for improved lamb survival. The aim of this study was to examine maternal heritability for the ability of ewes to reunite with their lambs during the neonatal period after temporary separation. The data was obtained from two lines (High-line: selected for and Low-line: selected against) of a Merino research flock that has been divergently selected for lambs reared per ewe mated from the same base population since 1986 [DAEC: R112/57]. The study was conducted over 10 years (1998 to 2007) by screening a subset of ewes for a maternal behaviour test recorded at 1 and 3 days after birth. At 1 day old, lambs were individually tethered 20m away from their dams, and performance was recorded as the time interval (seconds) ewes took to reunite with their lambs (ETOL1). At 3 days old, lambs were randomly placed into one of three different pens, with the remaining pens containing progeny of another ewe. The ewes to these lambs were then individually recorded for the time interval it required to reunite and identify their correct lambs (ETOL3). The dataset contained 1331 repeated measures for ETOL1 and 947 for ETOL3 recorded on 579 ewes. Data based on time intervals were skewed and transformed to natural logarithms before analysis. ASREML was used to estimate fixed effects and derive direct maternal variance and maternal permanent environmental (PE) variance components in respective single-trait analyses. The High-line ewes had a lower predicted ETOL1 compared to the Low-line ewes, suggesting that ewes selected for rearing success showed a stronger tendency to bond with their lambs. ETOL1 decreased with ewe age, and ETOL3 decreased with ewe age up to age 4 where it started to increase again. The largest margin of decrease with ewe age was from the primiparous stage (2 years) to the multiparous stage (3+ years). The increased performance with experience is interesting when considering the poor performance of primiparous ewes in survival traits. ETOL1 had a moderate maternal repeatability ($\pm$ SE) of 0.21 ± 0.03 , with a low but significant (p -value < 0.05) direct maternal heritability of 0.08 ± 0.05 as well as a moderately-low ewe PE variance ratio of 0.13 ± 0.05 . Corresponding values for ETOL3 were respectively 0.08 ± 0.04 , 0.06 ± 0.05 , and 0.02 ± 0.05 . The results obtained for the maternal repeatability for both traits indicate permanent individual effects underpinning mothering behaviour as tested by ETOL1 and ETOL3. Results obtained in the study support the importance of the ewes' individual role in developing an exclusive ewe-lamb bond that should reflect positively on ewe mothering ability and, possibly, lamb survival. The tests conducted for this study are not executable outside the stringent scientific environment of an Institutional resource flock, but the results motivate further research on genetic selection for a favourable ewe temperament.

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Temporal dynamics of ruminal metabolome, degradability, and fermentation in response to molasses-treated guinea grass–cowpea silage

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The inclusion of protein-rich legumes such as cowpea (*Vigna unguiculata*) and the use of molasses are recognized strategies to improve silage quality and enhance nitrogen content, particularly in mixed systems. However, little is known about how molasses inclusion in tropical forages ensiling affects the temporal dynamics of the ruminal metabolome and degradability responses during subsequent microbial fermentation. The aim of this study was to evaluate, through an *in vitro* approach, the effects of molasses treatment on the ruminal degradability kinetics of Guinea grass (*Panicum maximum*)–cowpea silage over incubation time, and the corresponding shifts in the downstream metabolomic profile. Cowpea and Guinea grass were grown at the Yanagido Experimental Farm, Gifu University, Japan. Cowpea was sown at 0.13 kg/a and harvested at 50% flowering, while Guinea grass was sown earlier at 0.12 kg/a and harvested at 1–1.5 m height. After 20 h of wilting and chopping to 5 cm, the forages were mixed in a 65:35 ratio (Guinea grass: cowpea). The treatments included a control without molasses (GC) and addition of 8% molasses (GCM). GC and GCM were vacuum-sealed and stored for 60 d. The resulting silage samples were oven-dried at 60 °C for 48 h, ground to pass a 1 mm sieve, and 0.5 g of each sample was incubated in buffered rumen fluid obtained from four Saanen × Shiba wethers. All animal procedures were approved by the Committee for Animal Research and Welfare of Gifu University (Approval ID: AG-P-N-20240057 and 20250122). The pH, NH₃-N concentration and short chain fatty acids production were determined at 4, 8, 12 and 24h. Ruminal metabolites were assessed through UPLC-QTOF-MS, and the data was processed using MS-DIAL and MetaboAnalyst. A nutrient disappearance test was performed for 72 h, and the data was fitted to the nonlinear model: $y = a + b(1 - e^{-ct})$. Effective degradability (ED) and potential degradability (PD) were calculated. GCM exhibited higher dry matter (DM), water-soluble carbohydrate, and metabolizable energy contents, but lower neutral detergent fiber and acid detergent fiber contents than GC, with no significant differences in crude protein (CP) and hemicellulose contents. The ED, PD, and soluble fractions of DM and organic matter (OM) were consistently greater in GCM across all incubation times, particularly at 24 and 48 h ($P < 0.001$). In contrast, the CP degradability and its soluble fraction were greater in GC at 8, 12, and 48 h ($P < 0.001$), which coincided with elevated branched-chain fatty acid production (8–12 h) and higher NH₃-N concentrations (12–24 h). Metabolomics revealed that molasses supplementation increased the abundance of several bioactive compounds identified in the rumen fluid, including biochanin A-β-D-glucoside, crocetin, mellein, and carveol. This suggests that molasses enhances antioxidant capacity and stabilizes specific plant-derived secondary metabolites within the rumen microenvironment. Beyond serving as a simple, readily fermentable energy source, molasses therefore acts as an inhibitor of the microbial degradation of bioactive phytonutrients during the ensiling process. Conversely, indole derivatives, 2-hydroxy-4-methylpentanoic acid, and fatty acids such as 9-HODE, ricinoleic acid, and 2-hydroxystearic acid were consistently decreased under GCM. This indicates a metabolic shift in the rumen microenvironment away from lipid and amino acid metabolism towards carbohydrate-driven fermentation. Molasses supplementation of Guinea grass–cowpea silage enhances *in vitro* ruminal fermentability by reshaping substrate-driven microbial metabolism toward more efficient carbohydrate utilization while preserving protein.

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Effects of a novel *Bacillus subtilis*-based probiotic blend on jejunal histomorphology and phylogenetic composition of cecal microbiota in densely stocked broilers

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Bacillus subtilis has attracted considerable interest as a promising probiotic alternative to antibiotic growth promoters (AGPs) in poultry production, primarily due to its ability to form resilient spores and its beneficial effects on gut health regulation. Nevertheless, the ideal inclusion rates and the effectiveness of multi-strain *B. subtilis* formulations are not yet fully understood, especially under high stocking-density conditions, where birds are more vulnerable to environmental and physiological stress. Supplementing broiler diets with a multi-strain *Bacillus subtilis* probiotic improved digestion, health, and growth under crowded conditions. The optimal dose (0.5%) led to better weight gain, feed efficiency, nutrient digestibility, and meat quality. This study investigated the optimal dosage of a novel *Bacillus subtilis* probiotic blend as a replacement for antibiotic growth promoters (AGP) by assessing its impact on some gut functionality parameters. All procedures implemented in this study were performed following the guidelines and regulations approved by the Institutional Animal Care and Use Committee (IACUC) of the University of Mpumalanga Research Ethics Committee – Animal Sciences (UMP REC-AS, approval no. UMP/Mlambo/1/2024) and North-West University Animal Production Research Ethics Committee (NWU – ANIMPROD REC, approval no. NWU-00818-24-A5). In a completely randomized design, 900-day-old Ross 308 broiler chicks (43.21 ± 0.372 g live weight) were allocated equally across 36 pens measuring 0.75 m² each with 13 birds per pen. Six dietary treatments were randomly assigned to the pens and provided from the starter to the finisher phase. The diets were comprised of a basal broiler diet without AGP or the *B. subtilis* probiotic mixture (NEGC); the basal diet supplemented with 0.5% (w/w) zinc bacitracin (POSC); and four versions of the basal diet supplemented with *B. subtilis* probiotic mixture at 0.3% (PRB3), 0.4% (PRB4), 0.5% (PRB5), or 0.6% (PRB6). After slaughter, 5 cm sections of the jejunum were sampled for histomorphological measurements, and cecal digesta were collected to assess the phylogenetic composition of the cecal microbiota. There was a significant dietary influence ($p < 0.05$) observed on jejunal morphology, where broilers on PRB5 exhibited the largest villi absorptive surface area (VASA), while those on PRB6 showed the smallest. A significant dietary effect ($p < 0.05$) was noted on microbial diversity, but there was no effect ($p > 0.05$) on alpha-diversity. The cecal microbiota was dominated by phyla Verrucomicrobiota, Bacillota, and Asgardarchaeota, while genera *Akkermansia*, *Limosilactobacillus*, *Collinsella*, SOKP01, *Exiguobacterium*A, and *Rhizomicrobium* were most dominant across and in specific diets. The PRB6 treatment group exhibited the presence of a scientifically unknown phylum, SOKP01. Beneficial microbes (i.e., *Bacillota* and *Limosilactobacillus*) were most abundant in broilers that received diet PRB5, which indicated a healthy gut. PRB5 improved nutrient uptake by promoting the largest VASA. Hence, the *B. subtilis* probiotic blend is recommended for supplementation at 0.5% (w/w) in broiler diet to improve intestinal VASA and microbiota. Also, *Rhizomicrobium* requires further investigation for its role in broilers.

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Gestational and early-life rainfall effects on lifetime reproductive output in two sheep breeds farmed under arid conditions

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The value of a breeding ewe in a commercial sheep flock is largely determined by her lifetime reproductive output. It has been documented in the literature that environmental conditions during pregnancy and early development can influence lifetime reproductive performance. The aim of this study was to determine if the rainfall level during maternal gestation and the first year of life affected lifetime reproductive output in Namaqua Afrikaner and Afrino ewes kept under extensive conditions in an arid region. Since the study utilised historical data, no ethical clearance was required. Individual reproduction records for the Klerefontein Namaqua Afrikaner and Afrino flocks, collected between 1979 and 2019, were used to calculate lifetime reproductive performance and first-time lambing performance. Performance traits included number of lifetime lambing opportunities (NLLO), lifetime number of lambs born (LNLB) and weaned (LNLW) as well as lifetime total weight weaned (LTWW) and lifetime average weaning weight (LAWW). Rainfall records were used to calculate mean long-term annual and gestation period (April-September) rainfall. Based on these values, five rainfall classes, dry, below average, average, above average and wet were created for gestation period and first year of life. Lifetime reproductive performance, first-time lambing performance and Afrino wool traits were then compared among these rainfall classes. A Kruskal-Wallis test followed by multiple comparisons *post-hoc* tests with corrections was conducted in Tibco Statistica to determine if ewe performance differed between the rainfall classes. In Namaqua Afrikaner ewes, rainfall during maternal gestation significantly affected all lifetime reproduction traits ($P \leq 0.002$), but the effects were inconsistent and not linearly related to rainfall. Afrino ewes were similarly inconsistently affected, except for NLLO ($P = 0.099$) and LTWW ($P = 0.090$), which were not affected by rainfall during maternal gestation. All lifetime reproduction traits in both breeds were significantly ($P < 0.001$) but inconsistently affected by the amount of rainfall received during the first year of life. Similarly, first-time lambing performance in both Namaqua Afrikaners ($P \leq 0.001$) and Afrinos ($P \leq 0.002$) showed significant but inconsistent rainfall effects. Wool traits of the Afrino ewes at 14 months of age were also affected by rainfall during the first year of life ($P < 0.001$). Overall, it was found that both rainfall during maternal gestation and the first year of life had a significant effect on reproductive performance, but these effects were intermittent and did not follow a clear pattern. Although the exact degree of influence remains obscured, there is a definite link between rainfall and lifetime reproduction, pointing to the presence of some degree of fetal or developmental programming in the traits considered. These findings highlight the importance of environmental conditions in affecting lifetime performance under extensive farming conditions. It also clearly links predicted declining rainfall in the region to decreased lifetime reproduction, a major concern for livestock farmers in the region.

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The genetic diversity and breed composition of South African Bosvelders sheep

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The Bosvelders sheep, was developed in 2009 through strategic crossbreeding of the Bapedi, White Dorper, and Van Rooy sheep breeds. The development of the Bosvelders sheep represents a promising indigenous resource for sustainable sheep production in Southern Africa. Despite its growing importance in smallholder and emerging farming systems, there remains a significant gap of scientific information regarding its genetic diversity and population structure. This study assessed the genetic diversity, population structure and within-population selection signatures of the Bosvelders sheep to inform its breed standards, subsequent registration and conservation strategies. The methodology and materials of this study were approved by the ethics committee of the University of Zululand (UZ-REC 0691-008bPGD 2024/25). Blood samples (n=189) of Bosvelders sheep (n=132) and the ancestral breeds including Bapedi (n=21), White Dorper (n=15) and Van Rooy (n=20) were collected from four South African provinces (KZN, Mpumalanga, Limpopo and Western Cape) for genotyping analysis. The samples were genotyped using the Illumina OvineSNP60K BeadChip. Hierarchical analysis of molecular variance (AMOVA) was conducted using the poppr package in R. Principal component analysis (PCA) was performed with the SNPRelate package, population admixture was analysed using the GENESIS package (version 0.2.6), and signatures of recent positive selection were assessed using the extended haplotype homozygosity (EHH)-based Integrated Haplotype Score (iHS) implemented in the rehh package in R. Differences within individuals explained most of the genetic variation (89.98 %), whereas a smaller proportion (10.69 %) was attributed to differences among populations. The observed heterozygosity ranged from 0.31 ± 0.00 in Bapedi to 0.39 ± 0.01 in the Bosvelders sheep, whereas the expected heterozygosity remained consistent (0.38 ± 0.00) across all populations. The Bosvelders sheep showed higher observed heterozygosity than the ancestral breeds. Principal Component Analysis (PC 1 and PC 2) showed that the Bosvelders sheep were mainly located in the centre of the plot, suggesting an intermediate relationship with the founder breeds which aligns with patterns observed in developed breeds. In the admixture analyses, the founder populations confirmed at K=2. Using the within-population iHS, chromosome 10 and chromosome 18 showed the number of significant ($-\log_{10}(p) > 3$) SNPs. Candidate genes found in chromosome 10 and chromosome 18 were *RXFP2*, *BMP15*, *KITLG*, and *DLK1-DIO3/RTL1*, *MEG3*, respectively and they were associated to traits such as polledness, fertility, parasite resistance, and carcass muscling. Chromosomes 2, 3, 4, 15, and 19, also showed loci under selection, and these were associated with meat quality, muscle growth and body condition, corroborating earlier genomic studies highlighting these regions as targets of selection in meat-producing sheep breeds. The genetic analysis of Bosvelders sheep revealed intra-population variation, reflecting outcomes of a structured breeding development strategy. Future work should expand the founder breeds of Van Rooy and White Dorper as developed breeds and integrate their founder breeds for a deeper insight into ancestral signatures we see in the Bosvelders sheep today.

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Poster Presentation Abstracts

Adaptive growth responses of indigenous goats to water restriction

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Water scarcity is an increasing constraint to livestock production in arid and semi-arid regions under climate change. While limited water availability negatively affects livestock, goats, especially indigenous breeds, are generally more tolerant to water scarcity than many other livestock species due to physiological and behavioural adaptations that support survival in harsh environments. However, comparative evidence on the growth responses of indigenous goat breeds under varying levels of water restriction remains limited. The Nguni goat and Xhosa goat are indigenous to South Africa and are widely raised in semi-arid regions where seasonal water shortages occur. We hypothesized that water restriction would reduce growth performance and feed intake in both breeds, but that differences would exist between breeds in their ability to cope with water stress. This study therefore evaluated the effects of different levels of water restriction on growth performance of Nguni and Xhosa goats. Eighteen female goats per breed (Nguni: 19.43 ± 0.26 kg; Xhosa: 15.92 ± 1.12 kg) were assigned to three watering treatments: *ad libitum* water intake (W0), 70% of *ad libitum* intake (W70), and 50% of *ad libitum* intake (W50). Each treatment group consisted of six animals per breed. Goats were housed individually in pens and fed a total mixed ration containing 70% lucerne hay and 30% concentrate at 4% of body weight (BW) on a dry matter basis. The experiment consisted of a 14-day adaptation period followed by a 75-day data collection phase. Growth performance parameters measured included final body weight (FW), total weight gain (TWG), average daily gain (ADG), and total dry matter intake (TDMI). Data was analysed using a two-way analysis of covariance (ANCOVA) with breed and water restriction level as fixed effects and initial body weight included as a covariate. Statistical significance was declared at $P < 0.05$. Ethical approval: Ref. No. MUCO11SAKI01. Under moderate water restriction (W70), Nguni goats maintained a higher ($P < 0.05$) FW (16.76 kg) than Xhosa goats (15.74 kg). Under severe water restriction (W50), Nguni goats maintained a FW ($P < 0.05$) of 16.60 kg compared with 15.03 kg in Xhosa goats. At W70, Nguni goats lost less ($P < 0.05$) BW (-0.87 kg) compared with Xhosa goats (-1.89 kg). Under severe restriction (W50), the weight loss ($P < 0.05$) was -1.02 kg in Nguni goats and -2.61 kg in Xhosa goats. Xhosa goats experienced a larger ADG reduction ($P < 0.05$) (-34.75 g/day) compared with Nguni goats (-13.68 g/day) under W50. Water restriction also significantly reduced TDMI ($P < 0.05$). However, Nguni goats consistently consumed more feed ($P < 0.05$) than Xhosa goats across all treatments. The observed decline in body weight gain and average daily gain confirms that water scarcity negatively affects growth in goats. Despite this, Nguni goat showed greater tolerance to water stress than Xhosa goat, with smaller reductions in body weight, ADG, and feed intake. These findings suggest better physiological adaptation to dehydration and metabolic stress by Nguni goats and thus its selection potential climate-resilient livestock production.

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Macadamia oil cake as an alternative feed ingredient in pork production

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Rising feed costs, climate volatility and increasing sustainability pressures on raw materials challenge modern pork production systems. Soybean oil cake (SOC) and maize remain the primary protein and energy sources in grower–finisher diets in Southern Africa. This creates competition between the human food and animal feed sectors, reducing food security and increasing feed costs. Macadamia oil cake (MOC), a by-product of the expanding South African macadamia industry, contains moderate crude protein levels and high concentrations of monounsaturated fatty acids (MUFA). Inclusion of MOC in pig diets may enhance by-product utilisation, reduce feed–food competition, and potentially influence pork fatty acid composition. However, limited data are available regarding its effects on growth performance, carcass characteristics, and economic returns in pigs. This 84-day study evaluated MOC as a partial replacement for SOC and maize in grower–finisher pig diets. Effects on average daily gain (ADG), feed conversion ratio (FCR), carcass characteristics, fatty acid composition and economic outcomes were assessed. All study methods were approved by the Animal Ethics Committee of the University of Pretoria (NAS038-24). A total of 480 grower–finisher pigs were allocated to six dietary treatments formulated to be isocaloric and isonitrogenous, with graded inclusion levels of MOC (0%, 3.5%, 7.5%, 10.5%, 14% and 17.5%). Growth performance parameters; ADG, feed intake and FCR were recorded. Carcass characteristics were measured post-slaughter, and subcutaneous fat samples were analysed for fatty acid composition using gas chromatography. Statistical analyses were done using SAS and the GLM model for the average effects within treatments and significant differences using Fischer's least significant difference test at a 95% confidence interval. No significant differences were observed in the slaughter weight and overall growth performance across the six treatments. During the third and final phase, pigs with moderate MOC inclusion achieved higher ($P < 0.05$) ADG than those in the highest inclusion group, suggesting a possible optimal inclusion level. Feed intake decreased ($P < 0.05$) at the highest MOC inclusion level compared to the control, likely due to the higher fibre content of the MOC. Feed conversion ratio significantly improved from 2.33 in the control to 2.26 at the highest inclusion level ($P < 0.05$). Carcass yield, dressing percentage and backfat thickness were not affected by dietary treatment ($P > 0.05$). Fatty acid analysis showed increased ($P < 0.05$) MUFA concentrations at the highest inclusion level; however, variability among treatments limited clear dose-response interpretation. The second-highest MOC inclusion resulted in a significantly higher margin over feed costs than the control. MOC can partially replace SOC and maize in grower–finisher pig diets, without compromising growth performance or carcass characteristics at moderate inclusion levels. The inclusion of MOC improved feed efficiency and enhanced economic returns in pork production under the conditions of this study. Strategic feed formulation is required to optimise nutrient utilisation and maximise benefits. MOC is a viable alternative feed ingredient for pork production systems in South Africa.

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The use of a multi- enzyme complex in grower pig diets containing maize distillers dried grains with solubles

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South African pork producers face rising feed costs, prompting the use of alternative ingredients. Maize distillers dried grains with solubles (DDGS), a co-product of the bioethanol production industry, is a potentially cost-effective ingredient for swine diets. However, maize DDGS contains high concentrations of non-starch polysaccharides (NSP) and exhibits variability in nutrient composition, which may limit its inclusion in pig diets due to reduced nutrient digestibility. Exogenous enzyme supplementation may mitigate these limitations by improving nutrient release and digestibility. This study firstly aimed to determine the maximum inclusion level of maize DDGS in grower–finisher pig diets, without negative effects on growth performance and carcass characteristics. Secondly, the study aimed to evaluate the efficacy of a multi-enzyme complex in grower pig diets containing 20% maize DDGS on growth performance and carcass traits. Ethics approval was obtained (NAS361/2022). Two consecutive trials were conducted using commercial crossbred pigs (Topigs TN-70 × Tempo). In Trial 1, 528 pigs were allocated to 12 treatments in a 3 × 2 × 2 factorial arrangement (0%, 15% or 30% DDGS; sex; ± protease enzyme), with four replicates per treatment and 11 pigs per pen. In Trial 2, 480 pigs were assigned to eight treatments in a 2 × 2 × 2 factorial design (standard vs reduced nutrient density; sex; ± multi-enzyme complex containing carbohydrases); all diets contained 20% DDGS. There were six replicates per treatment, and 10 pigs per pen. Growth performance over four phases, carcass characteristics, and economic parameters were evaluated in both trials. Data were analysed using PROC GLM (SAS). In the first trial, inclusion of maize DDGS up to 30% did not affect ($P > 0.05$) final body weight, average daily gain (ADG), feed conversion ratio (FCR), or carcass characteristics. Although feed intake differed among treatments ($P < 0.05$), efficiency was not compromised. Importantly, DDGS inclusion reduced total feed cost ($P < 0.05$) without affecting margin over feed cost. In Trial 2, reducing nutrient density had limited effects on overall performance, although pigs fed the standard nutrient density diet achieved higher ADG during Phase 3 ($P < 0.05$). Enzyme supplementation increased body weight in Phases 3 and 4 (+2.1 kg overall; $P < 0.05$), and improved overall ADG ($P < 0.05$), without affecting overall FCR. Carcass characteristics were unaffected by nutrient density, while enzyme supplementation increased warm and cold carcass weights ($P < 0.05$) without altering lean percentage or backfat thickness. Economically, enzyme supplementation increased income and margin over feed cost ($P < 0.05$). Maize DDGS can be included at levels up to 30% in grower pig diets without compromising growth performance or carcass characteristics. Supplementation with a multi-enzyme complex improved growth performance and carcass weight in diets containing 20% maize DDGS and enhanced economic returns. These findings support the use of maize DDGS, combined with enzyme supplementation, as a nutritionally and economically viable feeding strategy for pork production systems.

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Evaluation of the antioxidant and antimicrobial roles of underutilized medicinal leaves in fortified beef sausage

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The high nutrient density of beef sausage serves as a catalyst for rapid spoilage, necessitating the use of effective preservative to maintain quality. While synthetic preservatives are commonly employed, concerns regarding their residual toxicity have driven a strategic shift toward natural alternatives. Consequently, medicinal plants such as Stonebreaker leaves (SBL) are emerging as viable replacements, aligning with the meat industry's focus on developing 'clean-label' meat products. The aim of this study was to evaluate the preservative potency of aqueous extracts and dried stonebreaker leaves (*Phyllanthus niruri*) at 0%, 5% and 10% inclusion levels in comparison with synthetic preservative (sorbic acid). Stonebreaker leaves (SBL) were identified, verified, assigned identification number (IFE – 18429) and deposited at IFE Herbarium, Department of Botany, Faculty of Science, Obafemi Awolowo University. A total of 500 gram of verified *P.niruri* was sourced in Teaching and Research Farm, Osun State University and processed into aqueous extract (E) and dried (D) forms, they were portioned into 5% (2 g) and 10% (4 g). A total of 40g of dried *P.niruri* was evaluated for phytochemical (flavonoid, saponin, alkaloids, steroid, polyphenol, tannin) and vitamins (A, D, B₁ and E). A total of 6 kg of beef from the thigh of White Fulani cattle was purchased from mini abattoir of Teaching and Research Farm to process beef sausage (B) and to evaluate the impacts of synthetic (SP) and natural (SBLE/SBLD) preservatives on beef sausage. Raw beef was divided into six batches: T1: 5% BSBLD, T2: 5% BSBLE, T3: 10% BSBLD, T4: 10% BSBLE, T5: BSP, T6: B, for proximate, minerals, vitamins, cholesterol, TBARS, microbial load and sensory evaluation in a completely randomized design fitted into 2 x 2 factorial design using two-way ANOVA. Laboratory analysis was conducted at Faculty Scientific Laboratory, Faculty of Agricultural Production and Management, Osun State University. Result for phytochemical and vitamin analysis shows that, SBL contained flavonoid –8.39mg, saponin –15.16mg, alkaloids – 6.32mg, steroids – 24.13mg, polyphenols –56.77mg, tannin –9.54mg, vitamin A –14.82mg, vitamin D –35.08mg, vitamin B₁ – 0.38mg and vitamin E –48.65mg. Result for proximate composition of beef sausage revealed that, T3 is significantly ($p<0.05$) higher in protein, ash with the least fat, moisture, cholesterol and TBARS. For minerals, the highest phosphorus, potassium, magnesium and zinc were recorded in T1 while iron peaked in T3. T4 exhibited significant amounts of B-vitamins (B₁, B₂, B₃, B₆ and B₁₂) followed by T3. Microbial load reduced with higher inclusion of SBL with the least TBC, TFC and TCC in T4 followed by T3. T5 was preferred by the panelist while T2, T4 and T6 were equally accepted with no significant ($p>0.05$) difference. SBL enhanced the nutritional profile and shelf life of beef sausage especially at higher inclusion while unfortified beef sausage had the lowest nutrient and shows higher susceptibility to spoilage. Incorporation of SBL, specifically at 10% inclusion level in dried (proximate, cholesterol and TBARS) and extract (B-vitamins and microbial load) forms, demonstrated superior efficacy in maintaining the nutritional quality and shelf life of beef sausage.

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Bone quality parameters, including medullary bone scraping, to establish reference benchmarks in cage- and floor-reared layer flocks

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Medullary bone is a specialised, highly labile calcium reservoir that supports eggshell formation and reflects skeletal mineral status in laying hens. Repeated mineral mobilisation during the production cycle increases susceptibility to skeletal depletion and structural damage. Practical tools for monitoring bone health and establishing reference benchmarks across ages and rearing systems remain limited, especially for assessing medullary bone dynamics under commercial conditions. This study evaluated medullary bone scraping as a practical indicator of bone health across ages and examined relationships between medullary, cortical parameters in cage- and floor-reared commercial layer flocks. The study was approved by the Animal Ethics Committee of the University of Pretoria (NAS216/2024). A total of 800 Amberlink laying hens were randomly allocated at hatch to either a floor- or cage-reared system (400 hens/system). Hens were randomly selected at 12 weeks and then were monitored daily for oviposition and sampled 10 h post-oviposition 25, 31, 51, and 71 weeks of age. At each time point, 20 hens per system were euthanised by cervical dislocation, and right tibiae were excised. Cortical and medullary bone densities were quantified using computed tomography. Mechanical integrity was assessed using three-point bending test (Instron testing system). Medullary bone was scraped, defatted, and ashed to determine mineral composition. Data were analysed using JMP 17.0 with the fit model platform. Pearson correlation coefficients (r) were used to evaluate relationships among bone parameters, with correlation strength categorised as very weak (< 0.20), weak ($0.20\text{--}0.39$), moderate ($0.40\text{--}0.59$), strong ($0.60\text{--}0.79$), or very strong (>0.80). Medial cortical bone density was moderately negatively correlated with the wet weight of the tibial medullary bone ($r = -0.41$; $p < 0.0001$). In contrast, medial medullary bone density showed strong positive correlations with full bone wet weight ($r = 0.61$; $p < 0.0001$), dry cortical weight before ashing ($r = 0.61$; $p < 0.0001$), and the medullary bone ash percentage ($r = 0.64$; $p < 0.0001$). Moderate associations were observed between medullary density and wet and dry cortical and medullary weights ($r = 0.56\text{--}0.58$) and wet and dry medullary percentages ($r = 0.47$ and 0.49). Moderate negative correlations were observed between medullary density and wet and dry cortical percentages ($r = -0.48$), while positive correlations were noted with ashed cortical weight ($r = 0.52$) and full bone weight ($r = 0.58$). Wet cortical percentage was moderately negatively correlated with ashed cortical weight ($r = -0.49$), full bone percentage weight ($r = -0.53$), and medullary ash percentage ($r = -0.48$). Rearing system had minimal effects on skeletal parameters, with minor early differences, whereas prolonged egg production was the primary driver of bone health. Medullary bone scraping is a practical and sensitive method for assessing skeletal mineral status in layers throughout the production cycle. Strong associations between medullary bone density, mineral content, and whole-bone measures support its use for establishing reference benchmarks across ages and rearing systems. This approach offers a practical tool for improving bone health management in commercial laying flocks.

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Evaluation of the proximate composition, nutritional quality, and sensory attributes of different shaped *patsey* products from chevon

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The meat industry continues to evolve in response to increasing consumer demand for convenient, nutritious, and appealing food products. Chevon (goat meat) is widely recognized as a valuable source of high-quality protein and essential minerals, especially in developing countries. However, its utilization in processed snack-type products remains relatively limited when compared to beef and poultry. "*Patsey*," a value-added chevon-based product, presents an opportunity to enhance the marketability and consumption of goat meat. This study investigated the effects of product shape and processing methods on the quality, shelf stability, and consumer acceptability of chevon *Patsey*. Specifically, it evaluated three product shapes (rectangle, square, and sponge) and two processing techniques (frying and oven-drying). The study focused on determining their influence on proximate composition, oxidative stability, microbial quality, micronutrient content, and sensory attributes. Fresh goat meat (5 kg) obtained from the thigh muscle of West African Dwarf goats was used for the experiment. The meat was cut into chunks, soaked in an apple cider mixture for four hours, and cooked for ten minutes. It was then shaped into the three forms, and ingredients were added to the shaped meat and subjected to the two processing methods. A 3 × 2 factorial experimental design was used, resulting in six treatments: fried rectangle (T1), oven-dried rectangle (T2), fried square (T3), oven-dried square (T4), fried sponge (T5), and oven-dried sponge (T6). Laboratory analyses were conducted to determine proximate composition, including protein, fat, ash, moisture, and nitrogen-free extract. Oxidative stability was assessed using TBARS and lipid peroxidation tests, alongside cholesterol determination. Microbial quality was evaluated through total bacterial count (TBC), total fungal count (TFC), and total coliform count (TCC). Selected micronutrients such as vitamins B1 and B6, as well as iron, magnesium, and phosphorus, were also analyzed. Sensory evaluation was carried out by a panel using a 9-point hedonic scale to assess colour, flavour, tenderness, juiciness, texture, and overall acceptability. The results showed significant differences ($p < 0.05$) among treatments, mainly due to variations in processing methods and product structure. Oven-dried rectangle (T2) had the highest protein content (55.31%), suggesting that oven-drying helps preserve or concentrate protein. Fried sponge (T5) recorded the highest fat content (33.17%) due to its porous structure, which increased oil absorption during frying. Moisture content was higher in fried samples, while oven-dried samples generally had lower moisture levels, indicating better shelf stability. In terms of oxidative stability, fried rectangle (T1) had the highest cholesterol level, whereas fried sponge (T5) recorded the lowest. TBARS values indicated slight variations, with oven-dried sponge (T6) showing relatively higher oxidative levels. Microbial counts were generally low across all treatments, indicating good hygienic practices during processing. Micronutrient analysis revealed that oven-dried sponge (T6) had the highest levels of vitamin B1 and phosphorus, while oven-dried square (T4) had the highest iron content. Sensory evaluation showed that T6 (oven-dried sponge) received the highest ratings for all attributes, including overall acceptability. In conclusion, both product shape and processing method significantly influence the nutritional quality and acceptability of chevon *Patsey*. While oven-dried rectangles offer higher protein content, oven-dried sponge provides the best overall balance of sensory quality, nutrient retention, and consumer preference, making it the most suitable option for commercial production.

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The use of a partially activated vitamin D₃ source at differing phytase doses to improve calcium and phosphorus digestibility in broilers

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Leg abnormalities remain a major challenge in the broiler industry despite efforts to improve skeletal health through improved Ca and P nutrition. Vitamin D₃ plays a central role in regulating Ca and P absorption, and using its partially activated form may enhance its bio-efficacy and improve Ca and P utilisation. The interaction between vitamin D₃ metabolites and phytase, which increases phytate hydrolysis and mineral availability, warrants further investigation. The study evaluated the effects of a partially activated vitamin D₃ source (α -D₃) and/or phytase at differing inclusion levels on apparent ileal digestibility (AID) of Ca and P in broilers. The study was approved by the Animal Ethics Committee of the University of Pretoria (NAS088/2023). A 3×3 factorial arrangement of treatments was used, where 1500 male Ross 308 broilers were fed increasing doses of α -D₃ (0, 2.5, 5.0 µg/kg diet), and phytase (0, 1000, 2000 FTU/kg diet). Broilers were sampled on d 10 (24 h experimental feeding period) and d23 (36 h experimental feeding period). Ileal digesta were collected and analysed for Ca and P to determine their AID. Data were analysed with JMP 17.0 using the fit model platform. When the model was significant ($P < 0.05$), means were separated using a protected Tukey HSD (Tukey, 1949). Where no interactions were present, main effects were reported. At d10, no interaction between phytase and α -D₃ was observed. However, phytase dose exerted a main effect ($P < 0.001$) on both AID Ca and P. There is a stepwise increase in AID P ($P < 0.001$) as the phytase dose increases (19.91%, 80.04% and 86.56% with phytase at 0, 1000 and 2000 FTU/kg diet respectively). However, an increase in phytase dose does not have a notable effect on the AID Ca over 1000 FTU/kg diet. A main effect of α -D₃ was also noted, where increasing α -D₃ improved ($P < 0.001$) AID Ca with a stepwise increase, however there was no effect on AID P. At d23, an interaction ($P < 0.001$) between phytase and α -D₃ was noted for both AID Ca and P. The highest AID Ca was reported when 1000 or 2000 FTU/kg diet phytase was added with 5.0 µg/kg α -D₃ (68.22 and 71.57%, respectively); or when 2000 FTU/kg diet phytase was combined with 2.5 µg/kg α -D₃ (71.34%). In the absence of phytase, increasing α -D₃ supplementation increased ($P < 0.001$) AID Ca in a stepwise manner (32.60, 43.67, and 51.63%, for 0, 2.5, and 5.0 µg/kg, respectively). AID P at d23 was primarily affected by phytase supplementation ($P < 0.001$) with less consistent responses to α -D₃. Supplementation with a partially activated vitamin D₃ source improved Ca digestibility, particularly when phytase is absent or included at low levels. At higher phytase inclusion levels, the benefit of additional α -D₃ in the diet was reduced. These results highlight the importance of considering interactions between vitamin D₃ and phytase in broiler diets.

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Observational study of commercial sow behaviour in mid-gestation during summer and winter seasons in South Africa

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Heat Stress (HS) is a major challenge in both the welfare and productivity of commercial pig production in South Africa and worldwide. Modern pigs may experience HS at lower temperatures than those from the 20th Century. The thermal comfort range of modern sows in gestation is estimated between 13.2-16.4 °C, a range much lower than current production conditions in South Africa. The identification of behavioural HS indicators such as posture allows for early implementation of mitigation strategies which will ensure the negative effects associated with HS are minimized. The aim of this study was to monitor the effects of heat stress on sows in mid gestation in a commercial piggery subjected to high average summer temperatures using behavioural parameters for improvement of sow welfare. Ethical approval for this study was granted by the Animal Ethics Committee at the University of Pretoria (NAS255/2024). Mid-gestation sows (n=45) used in this study were housed across 8 pens with a maximum of 7 sows per pen. Sows housed on a commercial farm in group housing and were observed for behavioural changes during winter (House Temperature Range 11°C -26.1°C) and summer (House Temperature Range 21.8°C -39.5 °C). Behavioural observations were recorded twice daily at 08:00 and 12:00 for a period of two weeks with posture (standing, sitting, lateral lying & sternal lying) being recorded from each individual animal in a pen as an indicator of HS. This allowed animal behaviour to be linked to specific environmental conditions. Differences in animal posture between 08:00 and 12:00 were analysed using repeated-measures ANOVA. Significant differences were observed between the number of sows standing ($p < 0.05$) and lying laterally ($p < 0.001$) between 08:00 and 12:00 daily. Average internal house temperatures increased from morning to midday in both seasons, winter (08:00: 13.42 °C; 12:00: 21.81 °C) and summer (08:00: 28.85 °C; 12:00: 32.87 °C). The proportion of sows observed standing and lying laterally in winter was $14.9 \pm 2.1\%$ and $45.9 \pm 3.5\%$, respectively, where the same postures were observed at $4.6 \pm 1.8\%$ and $59.6 \pm 6.1\%$ for the summer season. Values are presented as mean $\pm$ standard error (SE). Standing behaviour differed significantly between seasons ($p < 0.05$), whereas no significant difference was observed for lateral lying. Sows seemed to adjust their posture according to the daily temperatures, spending more time standing in the cooler morning conditions and more time lying laterally in the warmer afternoon temperatures. There was no significant difference between the behaviour of animals exposed to morning sunlight and those in the centrally located pens ($p > 0.05$). Overall, posture is a simple and easily observable indicator of HS, with high environmental temperatures being associated with increased lateral lying and decreased standing behaviour. These findings show that posture is a practical and easily observable indicator of HS in commercial production and can contribute to improved sow welfare and production.

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Effects of dam parity and foal sex on birth, weaning and survival parameters of the Elsenburg Percheron horse stud

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The South African Percheron horse population is limited in size with a restricted genetic base and a limited number of breeders. This draught breed is present in small conservation-oriented studs of which the long-established Elsenburg herd is the oldest in South Africa. In these limited-size populations, reproductive efficiency and foal survival is important for genetic retention of the breed. Early-life indicators like birth weight, weaning weight and survival to weaning can be used to evaluate the effectiveness of breeding strategies. Dam parity and foal sex may influence birthing outcomes, growth and the survival of the foals. This study investigated the effects of dam parity and foal sex on birth, weaning and survival parameters of the Elsenburg Percheron Conservation Stud. Data from 183 parturitions of Percheron mares from 1985 until 2023 were analyzed for birth and weaning weights of foals as well as foal survival up until weaning. Dam parity was classified as primiparous (first foaling) or multiparous (≥ 2 foalings). Foals were weighed 24 hours after birth and kept with the mares until weaning at an age of 6 months. Mares with their foals were kept together as one herd each year until time of weaning. While foals were at foot, mares grazed irrigated kikuyu grass 24 hours a day with no supplementary feed except in the dry summer months when they received *Eragrostis* hay if grazing deteriorated. On the day of weaning, the foals were first weighed, then separated from the mares and raised as a herd on their own. The data was analysed using the general linear model procedure of TIBCO Statistica 14 to determine the effect of dam age (in years), parity (primi- vs. multiparous) and foal sex on birthweight, weaning weight and survival to weaning. This project was approved by the DAEC of the WCDoA under registration number R12/72. Foals from primiparous mares were significantly ($P < 0.05$) lighter at both birth and weaning than foals from multiparous mares ($63.9\text{kg} \pm 1.36$ and $358.2\text{kg} \pm 7.7$ vs $67.1\text{kg} \pm 0.71$ and $375.8\text{ kg} \pm 3.9$). The survival rate of the foals did not differ between primiparous and multiparous mares (70% vs 77%). Primiparous mares were therefore able to rear foals successfully under the prevailing management conditions. Foal sex had no significant effects on birth weights (males 67.2kg and females 65.6kg), weaning weights (males 375.1kg and females 369.0kg) and survival rates (males 73% and females 79%) of Percheron foals. Dam ages had no significant effects on birth weights, weaning weights and survival rates of Percheron foals. This study indicated that in this small conservation herd, primiparous mares can be effectively incorporated into breeding programmes without compromising foal survival, although reduced early growth should be considered in management and selection decisions aimed at long-term genetic conservation.

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Concentration analysis of trace minerals of veterinary importance in cattle grazing in the Mpumalanga province

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To optimise production in grazing cattle, it's essential to consider several factors, with adequate trace mineral levels in their diet being crucial for growth, immunity, and reproduction. Research indicates that soil trace mineral concentrations significantly influence forage quality, which directly impacts livestock health. Trace mineral deficiencies develop gradually and rarely display obvious symptoms. Cattle that depend only on pasture often experience shortages of essential trace minerals, including manganese, iron, cobalt, copper, zinc, selenium, iodine, and molybdenum. Although testing soil and plant materials may have limited diagnostic value, scientific evidence indicates that trace mineral concentrations in groundwater are correlated with those in cattle livers. Consequently, we must prioritise the trace mineral status of grazing cattle to safeguard their health and productivity. Trace mineral deficiencies in grazing livestock in South Africa, aside from selenium, are largely unknown. The study aimed to determine whether there are trace mineral deficiencies of veterinary significance in grazing cattle across three municipalities in Mpumalanga Province. The study was carried out in the municipal districts of Govan Mbeki, Msukaligwa, and Lekwa, within Mpumalanga Province, and included 21 cattle farms selected as a representative sample for groundwater and cattle liver testing. Groundwater samples were collected from boreholes on each farm, and liver samples were collected from the right lobe at abattoirs from healthy cull cows. The cattle chosen for the study were all cull cows at the end of their production cycles, as trace mineral deficiencies develop gradually and are rarely accompanied by symptoms, making these animals ideal subjects. Both groundwater and liver samples were analysed for trace mineral concentrations, specifically manganese, iron, cobalt, copper, zinc, and molybdenum, using an inductively coupled plasma mass spectrometer. Ethical approval for this research was granted by the Animal Research Ethics Committee of Tshwane University of Technology (Reference number AREC202304006). Previous research has demonstrated a correlation between trace minerals in groundwater and the liver. Results from this study found that only groundwater zinc correlated with liver zinc ($p < 0.05$). Liver data also showed that the highest proportions of marginal deficiencies were for manganese and copper, with 75% of liver samples falling below the prescribed minimum for manganese and 55% indicating a marginal copper deficiency. Zinc concentrations in the liver were sufficient in 95% of samples. Govan Mbeki and Lekwa exhibited marginal manganese deficiencies, while Msukaligwa showed a marginal copper deficiency. Multiple comparisons across districts revealed significant differences in cobalt, copper, zinc, and molybdenum ($p < 0.05$). The groundwater results showed that only two samples exceeded the manganese and copper limits. The study revealed that 75% of grazing cattle had marginal manganese deficiency, while 55% exhibited marginal copper deficiency. The levels of manganese and copper antagonists found in liver and groundwater samples did not significantly influence the bioavailability of these minerals; therefore, further research is necessary to investigate other antagonists not covered in this study that could affect their bioavailability. The only trace mineral found adequate was zinc, with 95% of the liver samples meeting or exceeding the recommended minimum concentration. These findings will aid veterinarians and nutritionists working with cattle farmers in the region to diagnose manganese and copper deficiencies, improving supplementation strategies, and monitoring related symptoms.

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Validation of survival EBVS for young merino sires using the LR-methodC.S. Carter^{1,2#}, C.L. Nel^{1,2}, S.W.P. Cloete²

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Early lamb mortality is a major contributor to reproductive inefficiency. The inclusion of survival as a trait for genetic selection of Merino sires has potential to reduce lamb mortality with associated economic and welfare benefits. In sheep breeding, genetic progress leans heavily on the selection of superior sires at hogget age. Targeting survival traits at this age poses some difficulty. In addition to a very low heritability, all sires will present with the same phenotype (survived), and EBVs depend solely on family information, excluding progeny tests. Given limited information on selection candidates, it is appropriate to critically evaluate the expected merit of young, unproven sires (sires without progeny) by considering the accuracy and dispersion of EBVs at this stage. The aim of the study was to assess the inclusion of survival as a potential trait in the index of young sires using the 'LR-Method' to validate the predicted merit of unproven sires. The data were recorded on the Elsenburg Merino resource flock. Pedigree (10358 identities) and progeny records for survival to weaning (8468 animals) as a binary trait have been recorded since 1986. All genetic analyses were performed using an animal model with ASReml V4.2 software. Fixed effects used in the model were: year, line, year x line interaction, birth type, sex, age of dam, and birth mass squared. Random effects were additive animal (genetic) and maternal (identity) terms. For the forward cross-validation, validation and training data sets were constructed. Proven (Whole) EBVs were generated using the complete data set (validation set) while training sets were produced to estimate unproven (Partial) EBVs for sires born between 2014-2018. Training sets were produced by removing progeny data of sires on a stepwise basis (Progeny data for 2020 was removed to produce training set for sires born in 2018 and so on). Candidate sires were then screened to ensure sufficient progeny (>15) in the validation dataset. 32 sires were retained for validation according to the 'LR-Method'(Legarra-Reverter Method) to determine accuracy(ACC_{LR}), bias(B_0), and dispersion(B_1) by benchmarking the unproven($\hat{a}_p$) EBVs to proven($\hat{a}_w$) EBVs of retained sires as described

$$ACC_{LR} = \sqrt{\frac{cov(\hat{a}_w \hat{a}_p)}{(1+F-2f)\sigma_g^2}}$$

The mean survival heritability was low(0.08 ± 0.02), but slightly higher than many previous results reported from the observed scale. The accuracy of the unproven EBVs was moderate at 0.27 which is promising given the very low heritability broadly accepted for survival traits but is not comparable to similar metrics of accuracy in other studies given the particular cross-validation design used. The metric of dispersion was 0.35, demonstrating a large margin of under-dispersion against the benchmark value of $B_1=1$. This reflects a strong shrinking effect that occurred due to the removal of progeny data, and would bias older, proven sires if compared to new candidates. This study supports the potential inclusion of survival traits for genetic selection in young sires by demonstrating useful accuracy in unproven EBVs by cross-validation. Under-dispersion will be an issue only if selection decisions compare proven and young sires. However, the results of this study need to be replicated on a larger, across-flock dataset.

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Wound healing and weight gain in Bonsmara weaner calves following dehorning

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Dehorning is a routine farm management practice to ensure the safety of cattle handlers and reduce bruising and carcass damage. All methods of dehorning involve tissue destruction and are painful and stressful procedures. In beef cattle, under extensive conditions, wounds may take up to 13 weeks to fully heal and pose a risk for infection. Despite the availability of polled genetics, dehorning is routinely performed and raises welfare concerns. Research to date has focused on dairy calves, with no research on the welfare implications of dehorning beef calves. The aim of this study was to assess wound healing and weight gain of calves dehorned on a beef stud farm. 69 Bonsmara calves, three to four months of age, were included in this study representing first and 2nd parity plus cows. 35 polled calves comprised the control, while 34 calves were dehorned as part of routine management practices on a Bonsmara stud farm in the Northern Cape. Calves were dehorned with a hot disbudding iron and treated with an aerosol ectoparasiticide. Dehorning wounds were photographed (Canon 500D digital camera) and measured (sagittal and frontal length) using a 150mm vernier caliper, directly after the procedure, the following day, and once a week for five weeks thereafter. Polled and dehorned calves were weighed before dehorning, the following day, and then once a week for five weeks thereafter. Statistical analysis was conducted in R implementing a linear mixed-effects model, with calf included as a random effect and treatment, week, and their interaction as fixed effects. At first measurement, wound lengths were 24.1 ± 2.27 mm (mean $\pm$ SD; left) and 23.7 ± 2.73 (right), with the length remaining similar after five weeks (23.9 ± 2.99 mm). During week three wound lengths increased due to necrotic tissue falling off - five calves' wounds increased (15%). In week four, 23 calves' wound increased (68%) due to necrotic tissue falling off. Out of the 34 calves, 23 calves re-bled over the five-week observation period, due to either re-injury or the necrotic tissue falling off. Wound healing in this study is similar to previous research in dairy calves where necrotic tissue fell off on average 24 days; in this study necrotic tissue began falling off between 21 to 28 days after dehorning. Body weight increased significantly over time ($P < 0.001$), reflecting normal calf growth. However, there was no significant overall difference in weight between horned and polled calves ($P = 0.18$). The wounds from dehorning took several weeks to fully heal. For several weeks following dehorning, there is a risk of wounds re-bleeding due to injury or necrotic tissue falling off, which increases the risk of infection. Weight differences were observed between polled and horned groups, however no significant differences were observed between treatments.

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Economic implications of age at first calving in TMR Holstein herds

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Age at first calving (AFC) is widely recognized as one of the most influential determinants of lifetime profitability in Holstein dairy herds. Although often treated primarily as a reproductive milestone, AFC has direct economic consequences because it defines the duration of the non-productive rearing phase and the magnitude of capital invested before milk income is generated. Delayed calving extends rearing costs, postpones the break-even point, and shifts the lifetime profit trajectory of the cow, thereby influencing the probability of achieving positive net returns. The aim of the study was to investigate the economic implications of AFC under South African conditions, with particular emphasis on break-even dynamics and the milk yield required for cost recovery. Rearing costs were estimated using commercial benchmarks and farmer records from total mixed ration (TMR) Holstein herds. Cost components included feed, housing, labour, veterinary care, and opportunity costs associated with raising replacement heifers. Feed requirements were quantified across the pre-weaning, growth, and pre-calving phases. Economic performance was evaluated by comparing total rearing costs with milk income generated during the first lactation. Average rearing costs were estimated at approximately R26,135 per heifer, with feed representing the largest cost component. A detailed breakdown included milk replacer (350 L, R2,275), calf starter (120 kg, R960), silage (7,000 kg DM, R8,400), concentrates (1,200 kg, R7,800), minerals and additives (R1,000), veterinary care (R1,200), housing and bedding (R4,000), and labor (R500). Regional variation (Durbanville, Malmesbury, Darling, Caledon, Swellendam) was observed, with Western Cape herds benefiting from lower feed costs due to access to irrigated pasture compared with inland systems reliant on purchased concentrates. First lactation expenses totalled R45,700, largely driven by feed costs of approximately R40,000. With an average yield of 9,000 kg milk generating R67,500 in revenue, the net balance after rearing and first lactation costs remained slightly negative (≈R4,335), highlighting the importance of subsequent lactations for cost recovery. In a study on the effect of age at first calving involving 100 herds with 25,000 cows' lactations, it was found that heifers that first calved at 24 months were the most efficient. Earlier age at first calving reduces rearing costs, shortens the non-productive period, and accelerates break-even, whereas delayed calving increases feed and housing expenses and heightens the risk of negative margins. Optimizing AFC is essential for sustainable dairy production in South Africa. Management practices that promote efficient rearing, balanced nutrition, and earlier calving can significantly improve herd economics. By aligning biological performance (such as age at first calving and longevity) with economic sustainability, producers can enhance profitability and resilience in Holstein herds managed under total mixed ration systems.

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Effects of dietary fossil shell flour supplementation on growth performance, serum biochemistry, and carcass characteristics of broiler chickens

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Feed additives are increasingly being explored as sustainable strategies to enhance growth performance, nutrient utilisation, and health status in broiler chickens. Fossil shell flour has gained attention as a potential natural feed additive due to its mineral composition and possible physiological benefits in poultry nutrition. The aim of the study was to evaluate the effects of graded levels of dietary fossil shell flour supplementation on growth performance, serum biochemistry, and carcass characteristics of broiler chickens. Ethical approval for the current study was obtained from the Animal Research Ethics Committee of the University of Fort Hare, Alice; Ethical clearance number: MPE01SGAJ01/23/A. A total of 300-day-old Ross 308 broiler chicks were randomly allocated to five dietary treatments containing 0, 2, 4, 6, or 8% fossil shell flour. Each treatment consisted of six replicates with 10 birds per replicate. Birds were reared for 35 days under standard management conditions. Growth performance parameters were recorded weekly. Serum biochemical indices and carcass characteristics were evaluated at the end of the feeding trial. Data were analysed to determine linear and quadratic responses to increasing inclusion levels. Dietary fossil shell flour significantly ($P < 0.05$) influenced growth performance. Inclusion at 2% improved feed intake, body weight gain, and final body weight, whereas levels $\geq 4\%$ resulted in reduced growth performance. Feed conversion ratio was not significantly affected. Serum biochemical parameters remained largely stable, indicating no severe metabolic disturbances. However, fossil shell flour supplementation reduced calcium and LDL cholesterol concentrations, increased bilirubin levels, and exhibited quadratic effects on potassium concentration, suggesting possible modulation of mineral balance and lipid metabolism. Carcass evaluation revealed that inclusion levels above 2% reduced live weight, hot and cold carcass weights, and certain primal cuts (thigh, drumstick, and wing). Breast weight and dressing percentage were not significantly affected. Among organ weights, only heart weight increased at 4% inclusion, while large intestine weight decreased at 8%. These findings suggest that moderate supplementation may support growth and metabolic efficiency, whereas excessive inclusion may impair nutrient utilisation and growth performance. Dietary supplementation of fossil shell flour at 2% improved broiler growth performance and lipid metabolism without negatively affecting carcass quality. However, inclusion levels above 2% impaired growth and reduced carcass yield. Therefore, 2% fossil shell flour is recommended as the optimal inclusion level under the conditions of this study.

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The carbon footprint of Bonsmara cattle grazing natural rangeland

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The perception that beef has a higher carbon footprint compared with other foods negatively impacts the sector. It is therefore essential to obtain local data of the whole system to shed light on the soil-plant-animal interactions relating to the carbon balance of the system. The aim of the study was to establish a realistic baseline carbon footprint for extensive beef production under natural grazing conditions by taking into account enteric methane emissions as well as the grassland and soil carbon components. The study was conducted using 10 multiparous Bonsmara cows grazing approximately 50 ha of undisturbed rangeland in the Sourish mixed bushveld of South Africa. Stocking density was maintained at 0.2 large stock units (LSU) per hectare. Methane emissions were estimated based on the enteric methane emission factor for commercial beef cattle in South Africa (78.9 kg CH₄ LSU⁻¹ year⁻¹). Annual methane emissions per cow were converted to carbon dioxide equivalents (CO₂-eq) using the 100-year global warming potential (GWP₁₀₀). Gross seasonal carbon input from the rangeland was determined from above-ground dry matter production measured over the three growing seasons. Veld evaluation was done by both the step-point and quadrant veld evaluation methods. Above- and below-ground carbon stocks were derived using weighted root-to-shoot ratios for grass species, calculated according to their relative abundance in the veld. A carbon fraction of 0.45 was assumed for dry biomass. Dry-season contributions were considered negligible due to minimal plant growth. Net seasonal vegetation carbon was calculated as the difference between gross carbon input and estimated decomposition losses. Soil organic carbon (SOC) stocks were determined to a depth of 60 cm from measured SOC concentration and bulk density. Soil respiration was measured during the growing season to quantify soil respiration CO₂ flux. The seasonal carbon emission fraction (f-emission) was calculated as the ratio of measured soil respiration C-flux to total estimated decomposed carbon, estimating the proportion of decomposed biomass carbon released to the atmosphere. Net seasonal carbon balance (soil + vegetation) was converted to CO₂-eq using the Intergovernmental Panel on Climate Change (IPCC, 2006) molecular mass ratio (44/12). Total system CO₂-eq per hectare, including cattle methane emissions combined with soil and vegetation carbon fluxes over a 12-month period, was then calculated. All procedures involving animals were approved by the Agricultural Research Council, Animal Production Ethics Committee (APIEC21/12) and conducted under Section 20 authorisation of the Animals Protection Act No. 71 of 1962 (Ref nr 12/11/1/1/15 (2167JD)). The total carbon footprint of the system, including enteric methane emissions from the animals and measured soil and vegetation carbon losses, was calculated at approximately 20.5 kg CO₂-eq kg⁻¹ live weight. The total system CO₂-eq ha⁻¹ was calculated at 244 kg CO₂-eq ha⁻¹. The carbon footprint measured in this study is therefore in line with other published values (15–30 kg CO₂-eq kg⁻¹ live weight) from Argentina, Brazil and Spain for extensive, low-input rangeland systems under semi-arid conditions. This agreement suggests that similar trends are observed across semi-arid natural grazing systems, while the present study provides local data under South African Sourish mixed bushveld conditions. The results show that under semi-arid South African conditions, an extensive beef production system can maintain near carbon-neutral dynamics within the rangeland.

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Heritability estimates and genome-wide association study of coat colour and patterns in Nguni cattle

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Nguni cattle display diverse coat colours and patterns that make their hides valuable for leather production. Genetic selection based on relevant genomic variants offers an opportunity to produce animals with preferred coat colours and patterns, thereby improving the value of Nguni cattle. The aim of the study was to estimate the heritability of colours and patterns and to detect genomic regions influencing these traits in Nguni cattle within and across countries. Data comprised of 705 Nguni animals sampled from seven regions in Southern Africa: Loskop ($n = 124$), Roodeplaat ($n = 143$), Mukhathini Community farm ($n = 224$), Mara ($n = 104$), Swaziland ($n = 48$), Mozambique ($n = 26$) and ARC-Eastern Cape (EC) ($n = 82$). Samples from Loskop, Roodeplaat and Mukhathini were genotyped on the 50K Bovine SNP array; samples from Mara, Swaziland, Mozambique and ARC-EC were sequenced at a coverage of 0.5X low-pass whole-genome sequencing to build up a reference genome for imputation. Quality control of the genotypes was undertaken using Plink software to exclude genotypes with call rate ≥ 0.95 , missingness of individuals ≥ 0.90 , minor allele frequency of ≥ 0.02 and deviation from HWE ≥ 0.0001 . Subsequently, 43 446 SNPs from 432 animals were retained. Genotypes from the 50K SNP BeadChip were imputed with LP-WGS variants using BEAGLE software. The imputed genotypes were filtered based on Dosage R-Squared ($DR^2 \geq 0.8$), resulting in 72 820 336 SNPs. A chi-square test was performed on genotypes to assess associations between coat colour and patterns, sex of the animal, and region. Heritability (h^2) of coat colour and patterns was estimated using a single-trait pedigree model in BLUPF90. A genome-wide association study with a significance level of ($-\log_{10}[P]$) was performed using linear mixed models in GAPIT to detect association between the genomic variants and coat colours and patterns. The chi-square test of independence between coat colour and patterns and region indicated that there was a significant association between coat colour and patterns and region ($p < 0.001$). Heritability estimates for coat colour and patterns were 0.34, 0.45 and 0.34 for Loskop, Roodeplaat and Mukhathini populations, respectively. GWAS on black coat colour detected one indicative SNP on BTA4 (6 7615 775 bp; p -value = $1.642220e-23$). The *CREB5* gene, involved in melanogenesis and melanocyte differentiation, was identified as a candidate gene for black coat colour. White coat colour was associated with the *GNG7* gene on BTA 7 (21 022 281 bp; p -value = $3.714210e-06$), which is involved in the PI3K-Akt signaling pathway, which contributes to melanin synthesis. The *BNC2* gene on BTA8 was identified as influencing patchy patterns (27 945 079 bp; p -value = $2.431293e-09$). Moderate to high heritability and candidate genes revealed strong genetic control of coat colour and patterns, supporting effective selection in Nguni cattle. Selection informed by identified genomic regions and candidate genes from this study can be used to produce preferred coat colours and patterns in Nguni cattle, thereby improving the value of Nguni cattle.

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Effect of different limestone sources and phytase doses on Ca and P digestibility in broilers

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Current efforts to develop a digestible calcium (Ca) system have primarily focused on factors affecting Ca digestibility from limestone. Limestone is the primary Ca source supplemented into broiler diets, but variation in the physical and chemical properties of limestone, particularly particle size and solubility, influence Ca digestibility and the utilisation of phytate-bound phosphorus (P). While the supplementation of exogenous phytase improves phytate hydrolysis and thereby increases the availability of P and other phytate bound nutrients, phytase efficacy may be influenced by limestone Ca release rate and phytase dosage. This study therefore evaluated the effects of limestone sources with different solubilities, phytase dose and the interaction on Ca and P digestibility in broilers. All animal husbandry and experimental procedures were approved by the University of Pretoria Animal Ethics Committee (NAS290/2024). The experiment was a 3 × 3 factorial design with limestone-free diets included to calculate digestibility, yielding 12 treatments with 10 replicates each. Diets contained one of three limestone sources or no limestone and were supplemented with 0, 1,000, or 2,000 FTU/kg of a novel-consensus bacterial 6-phytase. The limestone sources exhibited differing solubility profiles at 5, 15, and 30 min (LS1: 95.5%, 96.4%, 96.5%; LS2: 49.5%, 80.5%, 95.0%; LS3: 31.0%, 54.2%, 77.4%). A total of 972 male Ross 308 broilers were reared in floor pens until d 19 or 21 (sampling block 1 and 2, respectively), after which 360 birds were transferred to a metabolic facility for ileal digestibility assessment. Birds received the treatment diets for 36 h in order to prevent the up/down regulation of Ca digestion. Ileal samples were collected from the distal half of the ileal, and then analysed for Ca and P using ICP methodology, to determine the apparent ileal digestibility (AID) of Ca and P. Data were analysed using JMP 17.1, with block included as a random effect. Tukey's test was used for separations, with significance reported at $P < 0.05$. No interaction between limestone and phytase was noted, though there were main effects of phytase dose and limestone source. The inclusion of LS1 improved ($P < 0.05$) AID Ca when compared with LS2 and LS3. Conversely, LS1 showed a decreased ($P < 0.05$) AID P relative to LS2 and LS3. Increased limestone solubility led to a increased Ca digestibility and decreased P digestibility. Phytase supplementation resulted in a stepwise increase ($P < 0.05$) in AID P as dose increased from 0 to 1 000 and 2 000 FTU/kg diet (25.14%, 70.01%, and 74.38%, respectively) as well as AID Ca (44.83%, 50.8% and 54.44% respectively). The positive effect of phytase on mineral digestibility increases as phytase dose increases. Limestone solubility influenced mineral digestibility, with rapid solubilisation enhancing Ca but reducing P digestibility. Phytase improved Ca and P digestibility in a dose-dependent manner, supporting higher inclusion levels to optimize mineral utilization in broilers.

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Effects of fermentation period and amino acid supplementation of pigeon pea seed-based diets on the performance, carcass traits, and blood characteristics of Ross 308 broiler chickens

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Pigeon pea (*Cajanus cajan*) is a locally available legume with potential as an alternative protein source in poultry diets; however, anti-nutritional factors limit its utilisation. Fermentation and amino acid supplementation may enhance its nutritional value. This study evaluated the effects of fermentation duration and methionine–lysine supplementation of pigeon pea–based diets on growth performance, carcass traits, intestinal biometry, and blood profiles of Ross 308 broilers during the starter phase. A total of 300 day-old Ross 308 broiler chicks were randomly allocated to six dietary treatments in a completely randomised design, with five replicates of ten birds each. Diets included a commercial control, unfermented pigeon pea, and 72-hour and 120-hour fermented pigeon pea diets, with or without amino acid supplementation. Growth performance, nutrient utilisation, carcass traits, intestinal biometry, and blood (haematological) parameters were evaluated. The study complied with institutional animal ethics standards (Reference: 2022/CAES_AREC/121). Fermentation duration and amino acid supplementation significantly ($p < 0.05$) improved crude protein digestibility and overall nutrient utilisation, while reducing anti-nutritional factors in pigeon pea–based diets. Broilers fed the 120-hour fermented and amino acid-supplemented diet (T5) achieved the highest final body weight (653.22 g) and the best feed conversion ratio (1.7). Improvements were also observed in carcass traits and intestinal biometry. Increased white blood cell counts suggest enhanced immune status, while reduced digesta pH likely contributed to improved nutrient utilisation. Optimally fermented pigeon pea, combined with methionine and lysine supplementation, improves nutrient utilisation, growth performance, and physiological health of broilers. These findings demonstrate the synergistic value of processing and amino acid balancing in enhancing the nutritional quality of alternative plant protein sources, contributing to more sustainable and cost-effective poultry feed formulation in South Africa.

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The effect of space allowance and marketing strategy on production performance of grower-finisher pigs

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Stocking density and space allowance are key factors influencing welfare, growth performance, and profitability in grower–finisher pig production systems. Current space allowance recommendations are largely based on older genotypes and lower slaughter weights than those used and achieved in modern production systems. In addition, marketing strategies such as pre-selecting heavier pigs before slaughter are frequently implemented to optimise space utilisation. Increasing global demand for high-quality pork, together with societal concerns regarding animal welfare, requires producers to maximise production efficiency while minimising facility cost and maintaining sustainable systems. However, the combined effects of stocking density and marketing strategy on productivity and economic returns remain poorly defined. This study evaluated the effects of space allowance and marketing strategy on growth performance, carcass characteristics, and economic returns of grower-finisher pigs, with a specific focus on meat production per unit of available barn space. All procedures involving animals were approved by the Animal Ethics Committee (Approval No. NAS275/2024). The study was conducted at the Baynesfield SwiNE Research Unit, KwaZulu-Natal, South Africa, using 528 grower–finisher pigs (Topigs TN70 × Tempo; 31.7 ± 0.15 kg initial body weight; 70 days of age) over 84 days. Pigs were randomly allocated to six treatments with eight replicates (n=8) per treatment. Treatments 1-3 evaluated different space allowances expressed as k-values derived from allometric scaling (BW^{0.67}). Treatments 4-6 evaluated different marketing strategies that involved removing pigs one week prior to slaughter. All pigs received the same phase-fed maize-soybean-based diets. Body weight and feed intake were recorded at defined intervals. At slaughter, carcass weight, dressing percentage, and lean meat percentage were measured. Economic parameters were calculated based on feed costs and carcass revenue. Data were analysed using PROC GLM in SAS. Pigs housed at the highest space allowance (i.e. lowest stocking density) achieved greater (P < 0.05) average daily gain and feed intake compared to pigs housed at higher stocking densities. Early removal of pigs to correct space allowance did not result in compensatory growth sufficient to offset reduced total production. When performance was expressed per 1000 m² of barn space, higher stocking densities resulted in greater total carcass output and improved margin over feed cost per unit area. Marketing strategy had no effect (P > 0.05) on overall grower-finisher performance. However, pigs provided with additional space during the final week before slaughter exhibited improved (P < 0.05) growth rate and feed efficiency during that period, indicating a short-term positive response to increased space availability. Optimising pork production requires a shift from maximising individual pig performance toward maximising meat output per unit of available facility space. Strategic manipulation of space allowance and marketing strategy can improve economic returns without compromising growth performance or carcass quality. These findings highlight space efficiency as a key driver of sustainable grower-finisher pig production.

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Optimal dietary lysine concentration for pigs during summer and winter

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Modern high-lean pig genotypes exhibit high protein accretion rates and require precise lysine supply to maximise growth efficiency and carcass quality. Seasonal variation may influence voluntary feed intake and metabolic responses, while sex-related differences in lean growth potential may alter lysine requirements. Defining optimal standard ileal digestible (SID) lysine concentrations under varying seasonal conditions is essential for efficient pork production. This study evaluated the growth and carcass responses of pigs to graded dietary SID lysine concentrations during summer and winter, with all other essential amino acids maintained at constant ratios relative to lysine. Ethics approval (NAS110/2022) was obtained. A total of 528, 70-day-old Topigs TN60 pigs were assigned to six dietary treatments, with sex included as a fixed effect (four pen replicates per treatment, 11 pigs per pen, and equal numbers of males and females in separate pens). Diets were isocaloric and supplied 70, 80, 90, 100, 110 and 120% of the Topigs Norsvin SID lysine recommendation. The 84-day trials were conducted during winter and summer (Baynesfield SwiNE Research Unit, KwaZulu-Natal). Growth performance was evaluated, and carcass characteristics were recorded at slaughter. Data were analysed using the GLM procedure of SAS and treatment means were separated using Fisher's LSD test ($P < 0.05$). Quadratic regression analysis was performed to describe the response to graded SID lysine levels. Reducing SID lysine to 70% significantly limited final body weight (≈ 102 kg), and average daily gain (≈ 0.88 kg/d). Increasing SID lysine to 90% restored growth performance (final body weight ≈ 113 – 115 kg; ADG ≈ 1.01 – 1.03 kg/d). Further increases to 100–120% did not enhance growth, indicating that lysine at $\geq 90\%$ was no longer limiting protein accretion. Strong quadratic relationships were observed between SID lysine concentration and both final body weight and ADG ($R^2 = 0.95$ and 0.97 , respectively). Feed conversion ratio improved markedly between 70% (≈ 2.70 g/g) and 90% SID lysine (≈ 2.42 g/g), reflecting improved efficiency of nutrient utilisation when amino acid supply supported lean tissue deposition. Only minimal improvements above 90–100% lysine were observed, indicating diminishing returns once maximal protein deposition capacity was reached. Average daily feed intake was only marginally affected. Cold carcass weight increased from 76 kg at 70% to 85–87 kg at $\geq 90\%$ SID lysine, while dressing percentage improved modestly. Carcass leanness exhibited only small increases at 100–120%.

Winter pigs generally showed higher absolute growth rates than summer pigs; however, the lysine response was consistent across seasons. No sex $\times$ lysine interactions were observed, and response patterns were similar in gilts and boars. Reducing SID lysine to 70% of the recommended level impaired performance in both sexes and seasons. Increasing dietary SID lysine improved performance up to approximately 90% of the recommendation, beyond which responses plateaued. These findings indicate that 90–100% of the recommended SID lysine level is sufficient to support optimal grower–finisher performance under both seasonal conditions, highlighting the importance of precision lysine formulation to optimise nutrient efficiency without unnecessary oversupply.

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Hempseed oil supplementation: effects on meat production and quality in *Haemonchus contortus* infected lambs

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The use of hempseed oil (HSO; *Cannabis sativa* L.) in ruminant production is an emerging strategy for meat quality enhancement owing to its nutraceutical potency. Due to its high energy density, antioxidant and antimicrobial properties, HSO may influence parasite–host–diet interactions, thereby improving animal performance and meat quality. Nevertheless, evidence remains limited regarding benefits for meat production and quality. The aim of the study was to assess the interactive effects of *Haemonchus contortus* infection and HSO supplementation in finisher diets on growth, carcass, and meat quality parameters of feedlot lambs. Following ethical approval (REC: ACU-2025-32362), 60 three-month-old Dohne Merino ram lambs (25 ± 2.0 kg) underwent a 42-day feeding trial after a 28-day drug clearance and diet adaptation phase. Lambs were randomly assigned to six treatment groups ($n=10$ / treatment). Infected groups were orally inoculated with 4000 third-stage *H. contortus* larvae. Treatments combined two infection statuses (infected, non-infected) and three parasite control strategies [control diet (0% HSO), 5% HSO diet, and synthetic anthelmintic (2.5 mg/kg monepantel + 0.2 mg/kg abamectin)]. Dry matter intake (DMI) and average daily gain (ADG) were monitored throughout and used to calculate feed conversion efficiency (FCE). At slaughter, carcass traits including hot carcass weight, dressing percentage, pH and temperature at 45 minutes and 24 hours were assessed. The left *longissimus thoracicus* muscle was sampled for the analysis of physical meat quality traits. Data was analysed using the GLIMMIX procedure in SAS v9.4, with diet, infection status, and their interaction as fixed effects, animal as a random effect, and initial body weight as a covariate. Treatment means were compared using Tukey's post hoc test ($P \leq 0.05$). No differences ($P > 0.05$) in growth performance were observed among treatments, likely due to the low worm infection dose. Dietary HSO increased ($P \leq 0.05$) temperature at 45 minutes and only reduced ($P \leq 0.05$) meat redness among the colour coordinates. HSO-fed infected lambs displayed the lowest ($P \leq 0.05$) shear force values. The elevated early carcass temperature likely impaired metmyoglobin reductase activity and accelerated metmyoglobin production, reducing redness and subsequent chroma values. Concurrently, this higher temperature accelerated postmortem tenderisation, a process driven by calpains I and II, which degrade muscle proteins at an increased rate as temperatures rise. Regardless of worm infection, replacing maize with HSO as an energy source-maintained growth performance, with minimal effects on meat physical quality. The emerging hemp industry in South Africa presents a promising future for implementation of HSO as a nutraceutical feedstuff.

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Oral use of probiotics for ostrich chicks

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Artificial hatching and rearing of ostrich chicks limit natural gut colonization with beneficial microbes. Probiotic preparations can potentially be helpful in assisting with the initial gut colonization of ostrich chicks with beneficial bacteria to reduce disease and mortalities. The aim of the study was to determine whether the use of probiotics with different bacterial strains can improve ostrich chick health, survival and growth in an artificial environment, and to investigate the social transmission of bacteria within groups. Ethical approval was granted by the Western Cape Department of Agriculture's Ethics Committee (DAEC, reference number 10/2020). Individual chicks (n = 210) were randomly assigned to treatment groups. Three main treatments, namely control (no probiotic), Probiotic A (*Bacillus subtilis*, 2×10^9 CFU/g) and Probiotic B (BIOREMTM-culture consisting of a broad spectrum of lactic acid producing organisms, 2×10^8 CFU/ml) treatment, were each repeated in 5 groups in a randomised complete block design with 15 groups of 14 chicks each. Chicks were dosed from day-old, with 1 ml for the first three days after hatch, and thereafter 2 ml weekly up to eight weeks of age, with either distilled water (control) or one of two commercial probiotics (0.1 g probiotic/day). Within the probiotic treatment groups, only half of the chicks, randomly chosen, were dosed with the probiotic, however, while the other half were dosed with distilled water only to determine whether there would be social transmission of the probiotic bacteria within the groups. Chicks were weighed weekly up to eight weeks of age and mortalities were recorded to three months of age. Faecal samples of individual chicks were collected at the end of the treatment period. VIT® Field test kits were used to test for *Clostridium perfringens*. Standard statistical procedures for a randomised block design were followed with treatments within pens as experimental units. Three-month cumulative mortality in the untreated control groups exceeded that of the probiotic-treated groups ($P = 0.01$). In absolute terms mortality was lowest for water-dosed chicks in the Probiotic A treatment groups. Growth of probiotic treated groups to eight weeks of age were improved ($P < 0.05$) relative to the control groups, irrespective of treatment within the group. Results from field test kits for *Clostridium perfringens* in faecal samples showed significant differences between the untreated control groups and probiotic-treated groups ($P < 0.01$). Faecal samples from birds that were dosed with Probiotic A compared to those of birds in the same groups dosed with water only, had longer reaction times with the test kits, indicating lower *Clostridium perfringens* numbers ($P = 0.04$). There was no significant difference in reaction times between those dosed with the probiotic compared to those dosed with water only for birds in the Probiotic B treatment groups ($P = 0.31$). This could indicate that social transmission of bacteria did occur within groups. Early-life probiotic treatment of groups of individuals benefited group survival and growth and can therefore be utilized to address the challenges with ostrich chick rearing. Results indicate that social transmission of bacteria associated with the probiotics occurred within groups.

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Peripartum supplementation of *Moringa oleifera* leaf meal improves antioxidant status and reproductive recovery in transition dairy cows

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The transition period in dairy cows is associated with profound metabolic, physiological, and oxidative stress that may negatively affect milk production, immune competence, and reproductive performance. Oxidative imbalance during this phase often contributes to delayed uterine involution, increased susceptibility to infections, and impaired ovarian activity. Nutritional strategies involving phytogetic feed additives have gained increasing interest as sustainable approaches to improve animal health and productivity. *Moringa oleifera* leaf meal (MOLM) contains high levels of bioactive compounds such as polyphenols, flavonoids, vitamins, and phytosterols with recognised antioxidant, antimicrobial, and metabolic regulatory properties. However, information regarding its effects on oxidative status and reproductive recovery in transition dairy cows remains limited. This study evaluated the effects of peripartum supplementation of *Moringa oleifera* leaf meal on lactation performance, antioxidant status, metabolic responses, uterine microbial dynamics, and ovarian activity in Holstein dairy cows during the transition period. This study conformed to the regulations of the Agricultural Research Council Ethics Committee (APIEC #14 of 2017) and of North-West University (NWU 481-18-A5). A total of 48 Holstein cows were randomly allocated to three dietary treatments consisting of different levels of MOLM supplementation: M0 (control), M10 (1 g MOLM per 12 kg body weight per day), and M30 (1 g MOLM per 6 kg body weight per day). *Moringa oleifera* leaf meal (MOLM) was administered during the peripartum period (-21 to +21 days in milk). Before dosing, the supplement was mixed with lukewarm water and administered individually to each cow. Lactation performance parameters, including feed intake, milk yield, milk composition, and somatic cell count, were monitored during early lactation. Milk samples were analysed for total antioxidant capacity, while blood samples were analysed for antioxidant enzymes such as glutathione peroxidase (GPx), superoxide dismutase (SOD), and malondialdehyde (MDA), as well as metabolic indicators including cholesterol, blood urea nitrogen, and creatinine. Postpartum uterine microbial populations were assessed through bacterial isolation, and reproductive activity was evaluated using progesterone concentrations and indicators of ovarian cyclicity. Statistical significance was declared at $P < 0.05$. Feed intake and milk yield were not significantly affected by MOLM supplementation ($P > 0.05$), indicating no negative impact on lactation performance. However, supplemented cows exhibited lower somatic cell counts and increased milk antioxidant capacity, suggesting improved udder health and oxidative stability ($P < 0.05$). Glutathione peroxidase activity increased in MOLM-supplemented cows, indicating enhanced antioxidant defence mechanisms during the transition period. Additionally, serum cholesterol, blood urea nitrogen, and creatinine concentrations were reduced ($P < 0.05$) in supplemented cows, suggesting improved metabolic stability and reduced muscle protein mobilisation. MOLM supplementation also enhanced uterine health by promoting earlier microbial clearance, with reduced detection of *Escherichia coli* and *Trueperella pyogenes* postpartum. Reproductive recovery was improved, as indicated by earlier progesterone elevation and a higher proportion of cows exhibiting normal ovulation patterns. Ovarian cyclicity improved in a dose-dependent manner, increasing from 25% in M0 to 63% in M30 by 60DIM. Peripartum micro-supplementation of *Moringa oleifera* leaf meal improved antioxidant status, metabolic responses, uterine health, and ovarian activity in transition dairy cows without compromising feed intake or milk production. These findings suggest that MOLM may serve as a promising phytogetic feed additive for improving reproductive efficiency and physiological resilience in dairy production systems.

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Detection of putative lethal haplotypes and their associated candidate genes in South African Brahman cattle

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Deleterious recessive alleles can persist at low frequencies in livestock populations, where their recessive inheritance makes them difficult to detect using single-marker approaches. Haplotype-based analyses improve detection by identifying regions with reduced or absent homozygosity, pointing to putative recessive lethal or sublethal variants. However, the biological significance of these regions is often not investigated. Linking detected haplotypes to underlying genes and their functional roles provides biological context that can support informed breeding decisions and the management of deleterious variation in livestock populations. The aim of the study was to detect putative recessive haplotypes and characterize the functional roles of candidate genes located within these genomic intervals. A total of 399 animals were genotyped for 141 716 SNP markers. The following QC measures were performed, minor allele frequency (MAF ≤ 0.01), call rates (≤ 0.95), and non-autosomal SNPs were removed. The final datasets for downstream analyses comprised 315 animals with 91,752 SNPs. Haplotype phasing was performed using Beagle v5.4.0. Putatively lethal haplotypes were identified using R statistical software and subsequently characterized overlapping genes within these haplotype regions. These haplotypes were detected based on the criteria: population frequency $>1\%$, expected homozygote count ≥ 5 and zero observed homozygotes. The haplotypes were derived from merged overlapping windows, indicating regions of consistent absence of homozygosity across different sliding windows. Gene annotations and associated phenotypes were retrieved from Ensembl, while known quantitative trait loci (QTL) were identified using the Cattle QTL database. Eight putatively recessive haplotypes were identified across six chromosomes. The identified haplotypes mapped to gene dense regions across several Bos Taurus autosomes (6, 9, 10, 17, 21, and 26). The candidate genes were associated with embryonic or prenatal lethality (CC2D2A, PDIA3, STRC, SERF2 and MTG1) and abnormal sperm physiology (CATSPER2), while others were linked to neuronal development (MAP1A and SORCS3). The identification of SORCS3 within a candidate haplotype region on BTA 26 provides strong evidence for its potential biological relevance in cattle. This gene has been mapped to QTL for milk fat yield and body weight, traits that are under strong positive selection in beef and dairy breeding programs. The overlap between production related QTL and a haplotype showing absence of homozygosity suggests that selection for economically favourable traits may inadvertently be maintaining deleterious recessive alleles in the population. This study identified several recessive haplotypes associated with reduced homozygosity, indicating putative effects on embryonic survival and early developmental processes in Brahman cattle. Potential integration of haplotype-based recessive variant detection into breeding strategies could provide both practical benefits for livestock productivity and fundamental insights into the genetic basis of embryonic viability. Integrating such information into genomic selection programs could provide an opportunity to manage deleterious alleles, maintain herd reproductive performance, and promote sustainable genetic improvement.

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Effect of Kalahari melon (*Citrullus lanatus*) meal inclusion in lamb diets on growth performance and meat quality characteristics

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Kalahari melon (*Citrullus lanatus*) is often produced for the extraction of seed essential oils, which are mainly used in the cosmetic industry. The remaining oilcake meal was initially considered an environmental nuisance. Nevertheless, the oilcake meal contains considerable amounts of protein (up to 35%) and some important fatty acids, and hence it can be a protein source for livestock. Therefore, the study was carried out to investigate the feasibility of integrating such protein sources in lamb diets, as they may allow for the least-cost diet formulations and sustainable feeding strategies. This study was carried out to evaluate the effect of substituting Soyabean meal (SBM) with different inclusion levels of Kalahari melon oilcake (KMOC) on growth performance and meat quality characteristics of lambs. Forty (40) Meatmaster lambs were randomly assigned to 5 dietary treatments with 8 replicates—a completely randomised design and fed in individual pens for 54 days. In the test diets, SBM was replaced with KMOC meal at the following graded levels of KMOC: 100 % SBM (T1), 25% (T2), 50% (T3), 75% (T4), and 100% (T5). Data on growth performance were analysed using the mixed models for repeated measures, taking into account the effect of diet and week (SAS version 9, 2010). Data on carcass characteristics and meat quality were analysed using the general linear models of SAS (2010). The ethical number NWU-00822-21-A5 for the experimental procedure was approved by the NWU-ANIMPROD REC. Lambs in different treatments had an initial weight (IW) of 27.6±3.21 kg. There were significant differences ($P < 0.05$) in overall feed intake (FI), average daily feed intake (ADFI), average body weight gain (ABWG), average daily gain (ADG) and feed conversion ratio (FCR) on lambs fed KMOC in between treatment groups. Lambs fed a 50% KMOC diet had the highest ($P < 0.05$) body weight gain (BWG), ADFI, and ADG. The results indicate that there was a significant effect ($P < 0.05$) on dressing%, hot carcass weight (HCW), and cold carcass weight (CCW). Nevertheless, the lambs fed 25% of KMOC in diets marginally had higher dressing percentages (50.30±2.23), although it was significantly different and declined as inclusion levels increased. The carcass length was high in lambs fed 50% KMOC (70.43cm ±2.07), followed by those fed a 25% KMOC (67.06.cm±2.07). Diet levels did not influence spleen-somatic indices (SSI); the spleen and lungs were significantly higher (69.37±5.74 and 380±23.55) in 50% KMOC. Diet significantly affected ($P < 0.05$) meat colour coordinates, water holding capacity, cooking loss, dripping loss, and meat shear force in response to incremental levels of KMOC. Findings of the current study indicate that Kalahari oilcake meal can partially replace soybean meal in the weaner lambs' diet without any negative effects on growth performance or meat quality. The use of 50% KMOC in lamb fattening can be a viable option, especially during periods when the cost of conventional protein sources is high due to high demand and limited supplies.

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Influence of defatted winged termite (*Macrotermes natalensis*) meal inclusion on gut morphology and carcass characteristics of Ross 308 broiler chickens

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Winged termites (*Macrotermes* spp.) are highly nutritious edible insects containing 53,34% crude protein, minerals and essential fatty acids that could be nutritionally beneficial when included in poultry diets. The present study aimed to evaluate the partial replacement of soyabean meal (SBM) with defatted winged termite meal (WTM) on gut intestinal morphology, carcass quality traits of Ross 308 broilers reared for 42 days. 150 one-day-old, unsexed Ross 308 broiler chickens were randomly allocated to 3 treatments x 5 replicates x 10 birds/pen in a completely randomized design. Three (3) isonitrogenous and iso-energetic diets were formulated to replace SBM with WTM as follows: WTM0 = basal control diet without WTM; WTM5 = WTM0 diet with 5% WTM; WTM10 = WTM0 diet with 10% WTM. At the end of starter (day 1-14), grower (day 15-28) and finisher (day 29-42) phases, 2 chickens per treatment were slaughtered using cervical dislocation method for visceral organ weights and gut morphology measurements. However, carcass traits were only evaluated on day 42 after slaughter. Data was analyzed using one-way ANOVA (SAS, 2019). This study was approved (2022/CAES_AREC/150) by the Animal Research Ethics Committee of the College of Agriculture and Environmental Science at the University of South Africa. The findings showed WTM diets had no effect ($p>0.05$) on gut morphological indices, carcass characteristics and meat quality traits of broilers fed incremental levels of WTM throughout the growth stages with exception of small intestines (SI), caeca (CW) and hot carcass (HCW) weights which were affected ($p<0.05$) by the inclusion of WTM in chicken diets after 42 days. Broilers on WTM5 had heavier ($p<0.05$) SI than those on WTM0 and WTM10 diets. However, birds fed WTM10 had reduced ($p<0.05$) CW and HCW than other treatment groups. The non-significant effect of WTM inclusion on gut morphological indices and carcass traits of broilers suggest that WTM could be safely included in broiler diets without adverse effects on gut morphological indices, carcass traits and meat parts. Possible explanation of heavier SI of chickens fed WTM5 compared to WTM0 at finisher phase could be due to the anatomical and physiological mechanism for utilizing high dietary fibre content observed in WTM. However, reduced HCW of broilers fed WTM5 and WTM10 diets than WTM0 could be attributed to chitin content found in termite alates, which has been reported to reduce digestibility and performance of broilers (Kim et al., 2021). Thus, up to 10% WTM could be supplemented in diets as a partial replacement for SBM without adverse effects on gut morphological and carcass quality of broiler chickens. However, further studies are encouraged on the inclusion of above WTM 10% to determine optimal inclusion level.

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The effects of small contemporary groups and limited pedigree depth on estimation of variance components in South African beef cattle

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The accuracy of Estimated Breeding Values (EBVs) relies heavily on the precise estimation of (co)variance components. This estimation is frequently challenged in smaller livestock populations by limited pedigree depth, small contemporary groups (CGs), and unbalanced datasets. Accurately partitioning phenotypic variance into additive genetic, maternal, and environmental components is critical, yet difficult when data structure is compromised. The study aimed to evaluate the effect of pedigree depth and contemporary group (CG) size on (co)variance components and heritability estimates for weight traits (birth, weaning, 12-, and 18-month weights) and post-weaning growth traits (average daily gain, hip height, body length, scrotal circumference) in South African Angus, Charolais, and Hereford cattle. Data for the three breeds was obtained from the SA Stud Book LOGIX system across 10-year (2012–2022) and 20-year (2002–2022) datasets. The 20-year unedited data represented 106 Angus, 38 Charolais, and 33 Hereford registered breeders. After editing, the total records analysed per breed across the various datasets ranged from 1,565 to 12,295 for Angus, 71 to 8,776 for Charolais, and 719 to 13,376 for Hereford. Genetic connectedness between herds was ensured by restricting the data to CGs with at least five animals, containing progeny from at least two unique sires, and ensuring those sires were present in at least two other CGs. Variance components were estimated via VCE6 using REML procedures. Multi-trait animal models incorporated direct and maternal additive genetic effects, dam permanent environmental (PE) effects, and sire-by-herd (SXH) interactions. Analysing data over the 20-year time frame improved genetic evaluations not by drastically inflating individual CG sizes, but by significantly increasing the number of CGs (e.g., Angus weaning CGs increased from 440 to 605) and providing more data points across which environmental effects could be distributed. Multi-trait analyses of sequential weights revealed strong positive genetic correlations between traits (e.g., weaning and yearling weight direct $r=0.91$ for Angus). Across breeds, heritability (h^2) for post-weaning weights was lower than expected (e.g., Charolais 12-month direct $h^2 = 0.07–0.13$). This was attributed to a decline of data as animals aged, recording depth dropped from over 96% at birth to just 12–24% by 18 months, resulting in smaller CGs and reduced statistical power to detect genetic variance. Pedigree completeness varied across breeds. In the Hereford 20-year dataset, suspected incorrect parentage forced the exclusion of maternal components, deflating direct heritability estimates (e.g., birth weight h^2 dropped from 0.32 to 0.21). Additionally, models demonstrated that dam PE accounted for significant environmental variance from birth to 18 months. Where significant, the inclusion of SXH effects consistently increased residual variance; omitting this effect when necessary, would have otherwise inflated genetic variance by failing to account for the extensive use of specific selected sires within certain herds. While larger datasets improve the contemporary group structure by increasing data volume, they cannot compensate for poor pedigree integrity. Accurate genetic evaluations for smaller populations require complete recording through all sequential growth phases, alongside genomic-based parentage testing to resolve pedigree limitations and accurately partition maternal and direct variance components.

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Effect of dried water hyacinth supplemented rations on feedlot steers

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Water hyacinth (*Eichhornia crassipes*, WH), is an invasive aquatic plant that invaded open water ways and dams in South Africa. Water hyacinth has potential as a ruminant feed ingredient; however, its ability to accumulate pollutants that are then fed to ruminants raises food-safety concerns. This study evaluates the nutritive value of dried WH in iso-nitrogenous feedlot rations and assessed the presence of heavy metals in WH and in tissues of cattle consuming WH. Ethical approval was granted by the ARC-AP Animal Ethics Committee (APaec 18/18). Water hyacinth was harvested from Hartbeespoort Dam, Northwest Province, South Africa. The WH was dried and chemically analysed (DM basis: CP 16%; GE 15 MJ kg/DM; NDF 47%; Cu 11 mg/kg; Fe 2073 mg/kg; As 0.75 mg/kg; Pb 2 mg/kg; Cd and Hg not detected). Thirty-four Bonsmara weaner cattle (18 steers and 16 heifers), aged 6–8 months and averaging 180 kg liveweight, were used in the study. Weaners were individually housed in stanchions and offered one of the four experimental iso nitrogenous rations containing: 0%, 25%, 35%, or 45% WH respectively, in a completely randomized block design. Each treatment consisted of four to five steers and four heifers. The feeding trial was conducted over 98 days. The crude protein contained in either dry (16%) or fresh WH is ideal to be utilised in rations for growing cattle. Water Hyacinth has potential for livestock feed owing to its nutrient value; however, the fodder may contain toxic materials from the source of biomass. Average daily gain decreased significantly with increasing WH inclusion ($P < 0.001$), with cattle in the control group achieving 1.60 kg/day compared with 0.83, 0.70, and 0.30 kg/day in the 25%, 35%, and 45% WH treatments, respectively. Feed intake showed a similar declining pattern, and feed conversion ratio worsened at higher levels of WH inclusion. Heavy metals, arsenic (As), cadmium (Cd), or lead (Pb), were not detected in liver or muscle samples, although copper and iron concentrations decreased numerically as dietary WH increased. The calculated Fe concentration in the treatment diets (treatments 2 (562 mg/kg), 3 (766 mg/kg) and 4 (962 mg/kg)) were above the maximum tolerable concentrations, whilst Cu concentrations were 6, 6.5 and 6.8 mg/kg respectively for the same treatments. The high Fe concentrations can interfere with Cu absorption and lead to Cu deficiency and reduced animal performance. Gender did not influence results ($P > 0.1$). Routine screening of WH-fed livestock products remains advisable due to the plant's capacity to absorb environmental contaminants. Further research is needed to identify post-drying additives or processing strategies that reduce the effect of high iron content on copper availability and improve the palatability and intake of WH to enhance its value as a cost-effective feed resource for beef cattle.

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The influence of habituation on temperament traits of Namaqua Afrikaner rams

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Behavioural reactivity represents the observable expression of temperament in farm animals. The Namaqua Afrikaner breed has a strong flocking instinct, and separation from flock mates can result in an acute stress response when individual animals are being handled. Consistent, positive human-animal interactions, such as those encountered during routine husbandry tasks, have been shown to reduce fear responses in livestock over time. The aim of the study was to determine the influence of habituation on the docility of Namaqua Afrikaner (NA) rams. Ethical clearance (number ACU-2022-24147) was obtained from the Research Ethics Committee: Animal Care and Use (REC: ACU) of Stellenbosch University and from the Grootfontein Animal Ethical Committee (number AP10/2/1/3). Sixteen low reactive NA rams and 44 high reactive NA rams were subjected to a three-minute docility test. At the start of the test, the ram was brought into a 5 m x 5 m pen as calmly as possible. At this stage, the handler stood in the pen in the corner out of direct sight of the ram as he was brought into the pen. Recording of the data commenced after the ram was given a 30 second adaptation period. The handler then started to slowly guide the ram into a 1.5 m x 1.5 m square in the middle of the pen by using a very soft voice and slow arm movements. Reactive behaviours of the rams in the pen and the time they spent or stood still in the square were recorded by two assessors located under a shaded area of the kraal behind a shade netting screen. Data were analysed with Chi-square and ANOVA procedures of XLStat Essentials software version 2025.2.0. There was no difference in the frequency of urination, defecation or bleating between habituated and non-habituated rams. The time lapse until entering the square ranged from 11 to 168 seconds. More habituated than non-habituated rams entered the square (75.00% vs 20.45%) and stood still in the square (50.00% vs. 11.36%; $P=0.002$). Most of the rams that entered the square, did so once, while fewer rams did so twice. More non-habituated rams jumped out of pen (43.18% vs. 6.25%) and more of their tests had to be terminated (31.82% vs. 0.00%; $P=0.001$). The habituated rams spent a longer time standing still in the square upon first entering the square (25.34 ± 8.74 vs 7.00 ± 4.90 seconds; $P < 0.05$), as well as the total time that the ram stood still in the square (36.96 ± 10.18 vs 8.18 ± 5.70 seconds; $P < 0.05$) than the non-habituated rams. Habituated rams spent longer time in total in the square (49.36 ± 11.09 vs 10.14 ± 6.22 seconds; $P < 0.05$) than non-habituated rams. Habituation of the NA rams induced calmer behaviours, reduced fear and higher tolerance to handling and human presence. The study supports the adoption of habituation protocols as a practical strategy to improve animal welfare and handling efficiency in sheep production systems.

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Genomic assessment of non-descript cattle in three districts of KwaZulu-Natal province, South Africa

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Smallholder farmers in KwaZulu-Natal (KZN) depend on cattle for food security and livelihoods, yet face productivity challenges from climate change, disease outbreaks, and unstructured crossbreeding within smallholder systems which results in the erosion of genetic integrity and heightened inbreeding risk in localised herds. While province-wide genomic characterisation of KZN non-descript cattle exists, district-level diversity remains uncharacterised, creating a gap in literature in this regard. The northern (Amajuba), central (uMzinyathi), and southern (Harry Gwala) districts, which collectively represent the geographic distribution of KZN, remains absent from literature. The aim of the study was to assess genetic diversity and quantify inbreeding levels of non-descript cattle populations from Amajuba, Harry Gwala, and uMzinyathi districts of KZN using SNP array data. For this study, ethics approval was granted by the Agricultural Research Council Animal Production Ethics Committee (APIEC 24/08). A total of 281 cattle were genotyped across Amajuba (n=91), Harry Gwala (n=94), and uMzinyathi (n=96). Quality control was conducted in PLINK v1.9, applying thresholds for single nucleotide polymorphism (SNP) missingness, individual missingness, minor allele frequency (MAF), and Hardy-Weinberg equilibrium deviation, retaining 47 668 SNPs and 276 individuals. Observed (H_o) and expected heterozygosity (H_e), and inbreeding coefficients (F_{IS}) were derived from PLINK's heterozygosity output, with population-level means and standard errors summarised per district in R software using the 'dplyr' package. MAF was similarly estimated and summarised per district using the same software. Pairwise fixation indices (F_{ST}) were computed using 'StAMPP' by applying the Weir and Cockerham method with 100 bootstrap replicates at a 95% confidence interval. Mean MAF ranged from 0.237 ± 0.001 (uMzinyathi) to 0.250 ± 0.001 (Harry Gwala), averaging 0.242 ± 0.001 across districts, confirming polymorphic SNP variation consistent with values reported for non-descript cattle in South African smallholder systems. H_e was uniform across all three districts (0.325 ± 0.000), while mean H_o (0.316 ± 0.003) was slightly lower, indicating populations near Hardy-Weinberg Equilibrium. Overall inbreeding was low (mean $F_{IS} = 0.030 \pm 0.008$), though uMzinyathi showed a modest heterozygote deficit ($F_{IS} = 0.073 \pm 0.012$), consistent with localised inbreeding within a geographically isolated herd, while Harry Gwala showed a heterozygote excess ($F_{IS} = -0.007 \pm 0.008$), reflecting active outbreeding. Minimal genetic differentiation among districts (pairwise $F_{ST} = 0.005-0.008$), albeit lower than anticipated given the geographic distribution of sampling, suggests a shared genetic background likely due to unrestricted cattle movement across district boundaries. District-level estimates were similar with a previous province-wide study within KZN but indicated slightly lower inbreeding and comparable diversity when accounting for differences in marker density and sample size. Despite the absence of formal breed management, this study provides a district-level genomic baseline for non-descript KZN cattle, demonstrating that moderate genetic diversity and low inbreeding levels have been sustained. The district-level baseline established here provides a foundation for future studies integrating performance data which could support the development of breeding strategies tailored to the specific genetic profiles of KZN smallholder systems.

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Evaluating two feeding programs for feedlot cattle: The potential use of supplementing *Lithothamnium glaciale*, a rumen buffer (Acid Buf), on top of an ionophore antibiotic within high-starch diets fed to finishing cattle

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Increasing starch concentration in cattle diets improves metabolizable energy supply and performance but also increases the risk of ruminal acidosis. Supplementing high-starch diets with a calcareous marine algae buffer in combination with an ionophore antibiotic could enhance rumen stability and performance of finishing bulls. This study evaluated the effect of a standard finishing diet with acceptable starch content versus a high-starch diet on performance, organ health and blood parameters of finishing bulls. *Lithothamnium glaciale* (Acid Buf), a long-acting rumen buffer, was used to reduce the risk of rumen acidosis in the high-starch diet. All procedures were approved by the Interfaculty Animal Research Ethics Committee of the University of the Free State (UFS-AED2023/0001/23). Ninety-six Bonsmara bulls were used in a randomized trial design. Animals were weighed and randomly allocated into light and heavy groups. Light animals had an average starting weight of 290.7±15.8 kg (n=48) and a feeding period of 111 days, while heavy animals had an average starting weight of 343.6±22.7 kg (n=48) and a feeding period of 77 days. Within each weight group, bulls were fed either a control diet (normal starch – 433 g/kg DM: CON) or a treatment diet (high-starch – 484 g/kg DM: ACID BUF) supplemented with Acid Buf to supply ≈60 g/animal/day during the starter (10.0 g/kg DM), grower (7.4 g/kg DM) and finisher (6.0 g/kg DM) phases. Six pens per treatment (4 animals/pen) served as experimental units for intake measurements, while individual animals were the experimental units for performance traits. Rumen, liver and lung lesions, as well as inflammation, were scored at slaughter. Blood samples (jugular vein) were collected from a subset of four animals per treatment on days 0, 7, 14 and 28 for analysis of serum amyloid A, haptoglobin, cortisol, calcium and phosphorus. Production data were analysed using ANCOVA with starting weight as covariate. Categorical data were analysed using a Chi-square test and other continuous data using ANOVA. Significance was declared at P <0.05. Starch intake was higher in both weight groups fed the ACID BUF treatment, while phosphorus intake was lower compared with the CON diet (P <0.05). None of the performance parameters (dry matter and metabolizable energy intake, daily gain and feed efficiency), cold carcass weight, dressing percentage, carcass grading or faecal score were affected by dietary treatment (P >0.05). Across both weight groups, no treatment effects were observed for organ pathology, blood biomarkers or mineral concentrations. Increasing dietary starch did not improve performance of finishing Bonsmara bulls, and no negative effects on organ health or metabolic status were observed. Future research should focus on conditions of greater acidosis risk to better elucidate *Lithothamnium glaciale*'s potential role in rumen health modulation and nutrient utilisation.

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Effect of mastitis incidence on milk production and SCC in Swedish dairy herds

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Mastitis remains one of the most economically important and welfare-compromising diseases in dairy cattle. Beyond production losses, mastitis is associated with impaired udder health and increased inflammatory response, commonly measured through somatic cell count (SCC). In Sweden, research on the phenotypic and genetic relationships among mastitis, milk yield, and SCC puts emphasis on designing balanced breeding and management strategies that improve both productivity and animal welfare. The aim of the study was to (1) To evaluate the effect of mastitis incidence on milk yield and SCC; (2) To estimate genetic parameters for milk yield, log-transformed SCC (logSCC), and mastitis incidence in Swedish dairy cattle using pedigree-based animal models. The dataset comprised of 317 lactation records of 190 Holstein cows across seven Swedish commercial dairy herds (2018–2024). Mastitis incidence was defined per lactation as a binary trait (1 = ≥ 1 occurrence per lactation; 0 = no mastitis occurrences during the lactation). Total lactation milk yield (L) and average lactation SCC were obtained from herd management systems; SCC was log-transformed for the analysis. Phenotypic comparisons between mastitis groups were conducted using Welch's t-tests and Wilcoxon rank-sum tests. A general linear model was run to assess the effects of mastitis incidence, lactation number, herd, lactation start year, and season on milk yield and logSCC. Genetic parameters were estimated using ASReml-R, fitting pedigree-based animal models. A repeated-measures threshold animal model (logit link) was used for the analysis of mastitis incidence. There was no significant difference in total lactation milk yield between cows with and without mastitis incidences (12,596 L vs 12,303 L; $P = 0.14$), indicating no measurable reduction in milk yield. In contrast, mastitis had a clear effect on udder health, as cows with mastitis incidences showed significantly higher log-transformed SCC (2.13 vs 1.97; $P < 0.01$), confirming increased inflammation. Linear models further showed that lactation numbers and herd had stronger effects on milk yield than mastitis itself, highlighting the importance of management and environmental factors. Genetic analyses revealed moderate heritability for milk yield ($h^2 = 0.29 \pm 0.25$) and moderate heritability for logSCC ($h^2 = 0.24 \pm 0.08$), suggesting that both traits can respond to selection. In contrast, mastitis incidence showed very low heritability ($h^2 \approx 0$), supported by near-zero additive genetic variation ($\sigma^2_a = 1.6 \times 10^{-6}$). However, repeatability was moderate ($r = 0.36$), indicating that cows experiencing mastitis were more likely to be affected again due to permanent environmental factors rather than genetics. These findings suggested that in small daughter groups, selection for lower SCC may be a more effective strategy for improving udder health and welfare than selecting directly for mastitis incidence. Mastitis did not significantly affect total milk yield but was strongly associated with elevated SCC, indicating reduced udder health. Selection for lower SCC, combined with improved herd management, offers a practical strategy to enhance dairy cow health and welfare.

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Case-control genome-wide association analysis of dermatosparaxis in South African Drakensberger cattle

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Dermatosparaxis is an autosomal recessive disorder associated with heritable collagen abnormalities, due to mutations in the *pNPI* and *ADAMTS2* genes within various cattle breeds. Animals affected with dermatosparaxis are characterized by extreme skin fragility, tearing, and poor wound healing. Milder symptoms of the disorder, such as joint laxity and abnormalities in blood vessels, have been suspected in South African Drakensberger cattle, but the exact genetic mechanism and causative mutations of dermatosparaxis in Drakensberger cattle are unknown. The aim of the study was to identify genomic regions associated with dermatosparaxis in South African Drakensberger cattle using a case-control genome-wide association study (GWAS). A case-control GWAS was performed using 54 affected animals (cases), 250 unaffected animals (controls), and 40 612 SNPs genotyped with the Illumina BovineSNP50 BeadChip. Following dataset merging and restriction to autosomal chromosomes (1–29), quality control was conducted using PLINK v1.9 to exclude markers with missingness rate greater than 10%, minor allele frequency below 0.01, and Hardy–Weinberg equilibrium deviation at $p < 0.0001$. Animals with individual missing genotype rate exceeding 10% were excluded and the final dataset resulted in 300 animals, with 53 affected animals (cases) and 247 unaffected animals (controls), and 38 890 SNPs available for downstream analysis. The genetic structure of the sample group was assessed by principal component analysis (PCA) using GCTA software. The case-control GWAS analysis was performed with PLINK v1.9, implementing an allelic test. Results were visualised using a Manhattan plot, generated with R using the ‘qqman’ packages, with the genome-wide significance level set at $-\log_{10}(5e-8)$. Association testing was conducted using a case-control allelic chi-square test. A highly significant association signal was identified on bovine chromosome 1 (BTA1) within the 55–58 Mb region. The most significant marker, ARS-BFGL-NGS-34519, showed a P-value of 2.02×10^{-31} and allele frequency differences of 0.115 and 0.755 for cases and controls, respectively, were observed. Additional significant SNPs within the same region, including ARS-BFGL-NGS-85105 and BTA-25809-no-rs, formed a consistent linkage disequilibrium block. Several additional loci on chromosomes 6, 9, 11, 18, 21 and 22 reached genome-wide significance. The strong and concentrated association on BTA1, possibly suggests segregation of a major-effect locus underlying dermatosparaxis in the Drakensberger cattle population. The magnitude of the allele frequency shift and clustering of significant markers support the presence of a shared haplotype, as the genes close together on the same chromosome tend to evade recombination during meiosis. The use of case-control GWAS revealed a substantial association signal on BTA1. This shows that a major-effect locus may be the underlying cause of dermatosparaxis in South African Drakensberger cattle. Future work should focus on increasing the number of affected animals genotyped to improve power and refine the associated interval.

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Targeted supplementation with bioactive plants sustainably improves goat health and decreases antiparasitic drug use

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Goats play a significant role in semi-arid tropical farming communities with limited cropping capacity. Endoparasites, especially gastrointestinal nematodes (GINs), however, limit goat production. Control of GINs is typically mediated by anthelmintic drugs which can be costly, incorrectly used, or ineffective if anthelmintic-resistant GINs are present. To manage anthelmintic resistance and improve herd health at lower costs, farmers can implement Targeted Selective Treatment (TST); only treating a portion of the herd based on performance or health traits. *Viscum rotundifolium* known to contain condensed tannins and flavonoids and *Terminalia sericea* with known anthelmintic properties were selected for plant-TST. The study aimed to quantify the impacts of nutraceutical plant-based interventions on goat health, nutrition, and parasite infections when applied in a TST regime. We trialled a farmer-led TST scheme using a worm diagnostic tool for small ruminants, based on checking five points on the animal body: nose (purulent discharge), eye (colour of the conjunctivae), jaw (subcutaneous pitting oedema), back (body scoring condition, and tail (mild to severe diarrhoea). This diagnostic method, termed the Five Point Check or FAMACHA, was used to periodically assess goat health, with TST-anthelmintic interventions provided only to goats in poor condition. Plant-TST was trialled on 50% of the small-scale farms where goats in borderline or poor condition were supplemented with local bioactive plants (*Viscum rotundifolium* L. or *Terminalia sericea*). All experiments were carried out in accordance with the ethical standards and guidelines approved by the Biosafety and Research Ethics Committee, Botswana International University of Science and Technology, research permit reference # ENT8/36/4 XXXX II (5), additionally, all experiments were guided by ARRIVE international guidelines. Plant-TST treatment significantly reduced worm burden ($P < 0.001$) from a mean of 485 egg counts per gram (EPG) pre-treatment to 269 EPG post-treatment, with 75% of goats having a FEC of ≤ 400 EPG. Further, goats under Plant-TST had significantly better health outcomes ($p < 0.001$, FAMACHA scores) than those under TST-anthelmintic. Goats under plant-TST were 46.6 % less likely to require any anthelmintic treatment. Plant- and anthelmintic-TSTs had similar FEC reductions (55.5% and 52.5%, respectively). Plant-TST offers a low-cost resource to sustainably manage GINs in goats in semi-arid regions.

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Evaluation of breeding practices and trait preferences of Bapedi sheep farmers in Sekhukhune district, Limpopo province, South Africa

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Bapedi sheep breed is predominantly kept by the Bapedi people, for the sustainable livelihoods of resource poor rural communities of the Sekhukhune area. They are hardy and adapt to various climatic conditions and have low feed requirement as do other small stock due to their small body size (Kunene et al., 2014). This in turn makes Bapedi sheep breed user friendly to their keepers. Despite their major roles, sheep production remains generally low (Phaladi et al. 2025). Several studies have attributed these low productions to limited farmer knowledge in livestock genetic improvements (Bekuma & Tadesse (2025). Knowledge of farmer's breeding objectives and trait preferences helps farmers in developing and improving their livestock. However, there is limited information available on breeding objectives, practices, and trait preferences of Bapedi sheep farmers in Sekhukhune District. This study was aimed at identifying and documenting the breeding practices and trait preferences of Bapedi sheep farmers in Sekhukhune District. The study was approved by the University of Limpopo Animal Research Ethics Committee under the project number AREC/04/2025: PG. The study was conducted following a census research approach design method. Farmers were purposively sampled based on distribution of sheep population and presence of Bapedi sheep in the area. Data were collected on Bapedi sheep farmers' breeding knowledge and socioeconomic profile through face-to-face interviews using a structured questionnaire. Data were analysed using Statistical Analysis System (SAS, version 9.4). Chi-square (χ^2) statistics were used to compare categorical variables between four municipalities in Sekhukhune District. Selection criteria for rams and ewes were calculated for the importance of each criterion and estimated by computing the index of ranking as explained by Zewdu et al. (2018). Index = $\text{sum}(3 \times \text{rank}_1 + 2 \times \text{rank}_2 + 1 \times \text{rank}_3)$ for individual trait/ $\text{sum}(3 \times \text{rank}_1 + 2 \times \text{rank}_2 + 1 \times \text{rank}_3)$ for overall traits. Socio-economic characteristics and breeding objectives of respondents were significantly different ($P > 0.05$) between the four municipalities. Breeding season, selective breeding, castration, reason for castration, source of breeding rams, exchange of breeding rams were significantly different ($P > 0.05$) between the four municipalities. Body size (1.382), fertility (0.692), coat colour (0.663), conformation (0.538), growth rate (0.352), mature weight (0.284), disease tolerance (0.050), drought tolerance (0.032) and prolificacy (0.007) were indicated as important traits for selecting breeding rams while body size (1.226), fertility (0.583), coat colour (0.573), growth rate (0.503), conformation (0.500), prolificacy (0.198), disease tolerance (0.141), growth rate (0.140) and drought tolerance (0.138) as important traits in selecting breeding ewes in all the municipalities of Sekhukhune District. Breeding practices and trait preferences identified in the current study need to be considered when designing and developing community-based breeding programs for Bapedi sheep farmers in Sekhukhune District.

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Gut microbiota and transcriptome profiling analysis of indigenous chickens infested with *Ascaridia galli* parasite

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Ascaridia galli is a nematode parasite that produces gross pathological lesions and is considered the most important helminth parasite affecting village chickens. These parasitic nematodes inhabit the intestinal tract of the host and interact with the hosts intestinal microbiota. Infection with *A. galli* affects productivity, health and welfare of village chickens significantly with *A. galli* modulating the immune response of the host. This increases the severity of bacterial infection and fatal outcome associated with *A. galli* infection in village chickens. The study aims to profile the genome-wide microbiome-transcriptome analysis in non-descript village chickens naturally infected with *A. galli* parasite. Prior to conducting the study, ethics approval was obtained from the research ethics committee of the College of Agriculture and Environmental Sciences (2021/CAES_AREC/171) and Section 20 permit from the Department of Agriculture, Land Reform and Rural Development (12/11/1/1/23 (1892 RJ). Intestinal tissue samples were collected from *A. galli* infected and uninfected non-descriptive village chickens. In this present study, microbial DNA was isolated from non-descript mixed gender matured village chickens' intestinal contents followed by high throughput Illumina sequencing targeting 16S rRNA gene. For transcriptome analysis, pieces of the small intestines were collected, and RNA isolation was performed in duplicate for RNA-Seq. The library was sequenced utilizing MGI Sequencing technology (DNBSEQ-G400) at Agricultural Research Council (ARC) biotechnology platform, Pretoria, South Africa. Differential gene expression analysis was performed using pooled sequence data from biological replicates. Gene count data generated using PrepDE were analyzed using the DESeq2 package from Bioconductor within R version 3.2.2. The findings show that the gut microbiota of the analysed chickens infested with *A. galli* parasite indicated varying levels of diversity patterns with the diversity indices ranging from 2.42 to 5.41. Chickens that were *A. galli* positive displayed more balanced profiles, with proportions from *Akkermansia*, *Lactobacillus*, *Treponema*, *Phascolarctobacterium*, and *Serratia*. The scatter plot analysis of taxa prevalence versus abundance across phyla identified *Firmicutes* and *Bacteroidota* as core phylum of the chicken gut microbiome, with many taxa showing both high prevalence and abundance. The study findings also identified 191 genes with 52 Differentially Expressed Genes (DEGs) identified and shared between positive and negative chickens. Of the 52 DEG's, only ten genes were identified with log2fold change of above 1.0 with nine unpredicted genes, implying gaps in current annotation of the indigenous chicken genome that warrant further characterization. Genes meeting the significance threshold after multiple testing correction (FDR < 0.05) were considered significantly differentially expressed. The Gene Ontology (GO) analysis revealed significant genes involved in key biological processes, including biological regulation (RRBP1, CANX, MBTPS1) and metabolic process (TXNDC5 and MAN1B1). A total of 34 Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways were identified, of which eight pathways showed notable enrichment. Among these, the protein processing in the endoplasmic reticulum pathway exhibited the highest enrichment (fold enrichment = 3.7) and was the only pathway to reach statistical significance (p < 0.05). *Ascaridia galli* infected chickens that showed reduced microbial diversity, also showed transcriptomic signatures indicating immune activation and host stress responses. This relationship suggests that *A. galli* parasites infections may disrupt gut microbial homeostasis which in return may reduce the microbial evenness and richness while concurrently triggering host immune and inflammatory pathway. The findings give valuable insights into host-parasite interactions by highlighting molecular strategies employed by indigenous chickens to respond to *A. galli* infection.

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Comparative recovery and quality of *Bos indicus* cauda epididymal sperm influenced by retrieval technique and equilibration duration

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Cauda epididymal sperm is often used in livestock reproductive biotechnology, particularly when genetically valuable bulls die unexpectedly. Since these cells represent the final stage of sperm maturation, their successful recovery offers an important opportunity to preserve elite genetics that would otherwise be lost. Optimising retrieval and handling protocols is therefore essential to maximise post-processing viability and ensure the highest possible fertilising potential. This study aimed to determine the effects of retrieval technique and equilibration duration on the recovery and quality of *Bos indicus* cauda epididymal sperm across different evaluation periods. Ethical approval for this study was granted from the Agricultural Research Council Animal Ethics Committee prior to sample collection (approval number APIEC 23/10). Testes from *Bos indicus* bulls ($n=32$; ≥ 22 –24-months old), identified by sexually mature testicular dimensions (scrotal circumference 28–31 cm; testicular length 10–12 cm; width 4.0–5.5 cm), were collected post-mortem at a slaughterhouse, transported at 5 °C, and processed 6 hours following slaughter. Cauda epididymal sperm were retrieved using either retrograde flushing or slicing float-up technique in egg-yolk citrate extender (fraction A). Samples were equilibrated for 120 or 240 minutes at 5 °C, diluted at 1:1 with fraction B (containing 12% glycerol), loaded into 0.25 ml French straws, and cryopreserved in liquid nitrogen vapour. Sperm motility parameters were assessed post-retrieval, post-first equilibration, pre-freezing, and post-thaw with the aid of computer-assisted sperm analysis – Sperm Class Analyzer[®] system. Sperm recovery rate was calculated as the proportion of total motility at each evaluation period (post-first equilibration, pre-freezing, and post-thaw) to total motility immediately after retrieval, multiplied by 100. Statistical differences among variables were considered significant at $P < 0.05$, and all results were presented as Mean $\pm$ STD. Retrograde flushing yielded significantly higher sperm total motility (84.9 ± 4.1) than the slicing technique (72.0 ± 4.0) post-retrieval ($P < 0.05$). At both 120 and 240 minutes of equilibration period, flushed samples consistently showed higher total sperm motility throughout post-first equilibration (63.0 ± 0.9 ; 68.0 ± 2.4) and pre-freezing period (70.5 ± 1.6 ; 73.0 ± 1.7), compared with sliced samples post-first equilibration (55.1 ± 2.9 ; 64.0 ± 3.4), and pre-freezing (63.0 ± 2.1 ; 68.4 ± 1.5 ; $P < 0.05$). Extending equilibration time from 120 to 240 minutes enhanced sperm performance for both retrieval techniques, as shown by increased motility and improved recovery rates. The highest post-thaw motility (58.4 ± 2.3) and robust recovery (68.8 ± 2.2) were achieved with retrograde flushing combined with 240 minutes equilibration. Although slicing at 240 minutes produced the greatest pre-freezing recovery (95.0 ± 3.4) than retrograde flushing (86.0 ± 2.6), post-thaw motility (46.1 ± 3.8) remained significantly lower than that of retrograde flushing ($P < 0.05$). Bull cauda epididymal sperm quality remained satisfactory when using the retrograde flushing technique combined with a 240-minute equilibration period. Thus, further research is warranted to focus on identifying markers of cryotolerance, evaluating actual fertility outcomes, and testing improved extender formulations to enhance post thaw epididymal bull sperm survival.

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The effect of early weaning on performance, health parameters, and carcass traits of Bonsmara bull calves under feedlot conditions

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Early weaning is used in beef production to improve cow efficiency and manage nutritional constraints, but it may affect calf performance, health, and carcass development during feedlot finishing. These effects are particularly relevant for Bonsmara bull calves, which are widely used in South African feedlot systems. However, limited local data are available on the impact of early weaning under feedlot conditions. To evaluate the performance, health, and carcass traits of early-weaned calves (EWC) compared to traditionally weaned calves (TWC) of Bonsmara bull calves. The study was approved ethically under strict veterinary supervision, with due regard for animal welfare, ethical research conduct, and industry best practice. A total of 285 Bonsmara bull calves were sourced from different reputable stud breeders, backgrounded and finished concurrently. During backgrounding arrival, EWC were 196±18.0 kg (178 days old) and TWC were 248 ±18.9 kg (255 days old). The feedlot arrival body weight was 255 ±27.30 kg (n = 136) and 308 ±24.60 kg (n = 149) for EWC and TWC groups, respectively. The grower-adaptation and finisher ration provided *ad libitum* at 3% body weight. The SAS (2023) version 9.4 (SAS Institute Inc., Cary, NC) was used for analysis and Shapiro–Wilk’s test was performed before analysis (Shapiro and Wilk, 1965) for normality test. For analysis of variance, Student t-test was used, and the significant levels were observed at $P < 0.05$. The average IBW and EBW of the EWC were lower ($P < 0.001$) by 54 kg and 69 kg, respectively, compared to the TWC. Similar results were observed by Hudson *et al.* (2010) when compared yearling- and calf-fed steers. The overall growth of EWC was 8.96% higher than that of TWC, this was supported by Wolcott *et al.* (2010) as potential indicator by EWC. The TWC group had 7.23% (1.66 vs 1.78 kg; $P < 0.001$) greater ADG and 5.08% (5.79 vs 5.51; $P < 0.001$) lower FCR than the EWC group with no impact on DMI (9.59 vs 9.81; $P > 0.05$). Similarly, Hudson *et al.* (2010) found that yearling steers had greater DMI (1.36 kg per animal; $P < 0.001$) and ADG (0.13 kg; $P = 0.003$). Although TWC had 14.87% heavier carcasses than EWC ($P < 0.05$; 328.41 vs. 285.89 kg), no significant differences ($P > 0.05$) were noted in other carcass traits. Similar to Barker-Neef *et al.* (2001) and Abitante *et al.* (2024) and in contrast with that Myers *et al.* (1999a), Arthington *et al.* (2005), and Wolcott *et al.* (2010) who found no differences in HCW. As hypothesized, the TWC exhibited higher total morbidity, mortality, and case fatality rates by 0.83%, 0.67%, and 10% than the EWC, respectively. Early weaning resulted in lighter BW and carcass weights, lower ADG, and higher FCR than those of the TWC. Farmers should consider finishing TWC due to heavier BW, which results in heavier carcasses and better performances than EWC.

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Preliminary study: genomic regions for immune response in South African non-descript cattle from Mpumalanga and KwaZulu Natal provinces

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Non-descript cattle are known to be resistant to diseases and parasites and can withstand unfavorable climatic conditions. Runs of Homozygosity (ROH) are contiguous stretches of homozygous genotypes formed when parents transmit identical haplotypes to their offspring. For this reason, ROH are used to detect potential candidate genes influencing traits of economic importance. The aim of this study was to detect and identify runs of homozygosity underlying immune response in South African non-descript cattle populations from Mpumalanga (MP) and KwaZulu Natal (KZN) provinces. Ethical clearance was obtained from Agricultural Research Council-Animal Production (APIEC24/07). Genotype data from non-descript cattle in MP (n=96) and KZN (n=96) were generated using Bovine SNP50K BeadChip. Quality control was performed to remove non-autosomal SNPs, those with genotype rate of <0.05, minor allele frequency of <0.01 and Hardy Weinberg Equilibrium of $P = 0.0001$ using PLINK v2.0, resulted in 47 193 SNPs and 192 animals remaining for downstream analysis. ROH was identified using R package detectRUNS (sliding window). ROH parameters were set as follows; minimum ROH length set to 1Mb, 1 missing SNP and up to one possible heterozygous genotype allowed within the ROH, minimum number of SNPs was 50, minimum SNP density/ROH was one SNP for every 100 kb, and the maximum gap between the consecutive homozygous SNPs being 250 kb. Ensemble (Biomart), Genome Browser 115 was used to identify genes from the ROH regions. Cattle Quantitative Trait Loci (QTL) database was used for QTL detection. For this study, 705 ROH counts were obtained, the highest count in KZN (391) and lowest MP (314). Collectively, top counts were reported on BTA6, BTA19 and BTA20. Across the ROH classes, KZN presented a count of 252, 136 and 3 within the 0-2 Mb, 2-4 Mb and 4-8Mb classes respectively, while MP had ROH counts of 208, 102 and 4 in the corresponding classes. Eleven genes overlapping with these ROH regions were identified as putative candidates for immune response and parasite resistance. In the MP population, 3 genes (*SOS1*, *MAP4K3* and *AIF1L*) were detected, while the KZN population, harbored 8 genes (*IFNGR2*, *IL10RB*, *ADAM10*, *AQP9*, *IL1R2*, *IL1R1*, *ILR18R1* and *IL18RAP*). DAVID gene pathways analysis revealed that these genes are involved in immunological processes such as inflammatory response, antiviral defense, host immune defense, cytokine signaling, cell surface receptor signaling pathway, neutrophil extracellular trap formation, MAP signaling pathway and parasite resistance. Interestingly, *MAP4K3* gene was previously detected in N'Dama cattle and was associated with trypanosome resistance – the overlap of these regions with known disease-resistance QTLs, suggests that these homozygous regions may represent genomic footprints of natural selection for environmental adaptation. Candidate genes for immune regulation and parasites resistance were identified within ROH regions across both provinces, highlighting the potential for genomic-led improvement in smallholder systems. These homozygous regions may harbor adaptive traits maintained through environmental pressures, offering an opportunity to align livestock productivity with local sustainable goals. However, integrating these putative markers into breeding strategies will require further functional validation.

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Application of high-potency white-rot fungal strains to enhance the nutritional composition and *in vitro* ruminal degradability of grape pomace

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Agro-industrial by-products like red grape pomace (RGP), are generated in substantial quantities and are often underutilized in livestock feeding systems due to their high lignin content and poor fiber digestibility. This limits their nutritive value for ruminants despite their abundance, low cost, and potential as sustainable feed resources for smallholder farmers. Biotechnological interventions using white-rot fungi offer a promising strategy for selectively degrading lignin and enhancing the nutritional value of fibrous residues through fibrolytic enzymatic activity. The study evaluated the ability of four white-rot fungi, *Pleurotus ostreatus* (PO), *Hericium erinaceus* (HE), *Lentinus edodes* (LE), and *Pleurotus eryngii* (PE), to enhance chemical composition and *in vitro* dry matter degradability (IVDMD) of RGP. A total of 105 pots (5 control), each containing substrate (500 g), were inoculated with four white-rot strains at five inclusion levels (100, 200, 300, 400, and 500 g/kg), each with five replicates and incubated at room temperature for 35 days to allow for the development of fibrolytic enzymatic activity. Substrates were analysed for DM, ash, and total N according to AOAC (1999), with CP calculated as $N \times 6.25$ (Kjeldahl method) and OM determined by difference. NDF and ADF were measured using the Van Soest et al. (1991) method with an ANKOM Fiber Analyzer, and ADL was determined by treating ADF residue with 72% H₂SO₄. *In vitro* ruminal DM degradability was determined using ANKOM Technology Method 3 in a DaisyII incubator at 39 °C. Approximately 0.45–0.5 g samples were sealed in ANKOM F57 bags and incubated in jars containing buffer solution (A:B, 1:5; 1600 mL) and 400 mL rumen fluid collected from a slaughtered Bonsmara cow which was fed lucerne and blue buffalo grass. Bags were removed at 2, 4, 8, 12, 24, 36, 48, & 72 h, rinsed, and dried at 105 °C for 12 h to determine degradability. Ethical approval for the use of this animal was obtained from North-West University Animal Research Ethics Committee (NWU-00808-24-A5). All fungal treatments significantly reduced lignin content and only three (except for *Pleurotus ostreatus*) exhibited quadratic dose–response patterns for lignin degradation and IVDMD at 48 h. Optimal degradability values were achieved at 46.3% for HE ($Y = 306.153 + 5.653x - 0.061x^2$), 37.7% for LE ($Y = 292.410 + 6.328x - 0.084x^2$), and 32.9% for PE ($Y = 309.761 + 6.062x - 0.092x^2$). Overall, the cultivation of *H. erinaceus*, *L. edodes*, and *P. eryngii* on RGP effectively enhanced lignin degradation and digestibility. These findings highlight fungal bioprocessing as a viable strategy for upgrading red grape pomace, thereby adding nutraceutical potential and supporting its use as a sustainable and reliable feed ingredient for ruminant production systems.

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Functional and genomic characterization of *Pediococcus acidilactici* RTMP1 isolated from South African Cape Speckled goats

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The resistance of antibiotics in livestock production has intensified the need for safe and effective probiotic alternatives. Indigenous goat breeds represent underexplored reservoirs of host-adapted beneficial microorganisms that may enhance gut health, productivity, and antimicrobial control in small ruminant systems. This study aimed to evaluate the phenotypic and genomic probiotic potential of *Pediococcus acidilactici* RTMP1 isolated from South African Cape Speckled goats. The Agricultural Research Council–Animal Production Institute Ethics Committee (APIEC24/04) and Tshwane University of Technology Animal Research Ethics Committee (AREC-010411-009) approved ethics for fecal collection. Strain RTMP1 was phenotypically characterized by catalase activity and CO₂ production. Probiotic potential was evaluated through acid (pH 2.5–3.0) and bile (0.3% and 0.5%) tolerance assays. Antimicrobial activity was determined using agar well diffusion against selected pathogens, with inhibition zones measured after incubation. Antibiotic susceptibility was assessed by disk diffusion following CLSI guidelines. Whole-genome sequencing (Illumina) was performed, with assembly and annotation used to identify antimicrobial resistance genes, virulence factors, and probiotic-associated functional genes. The isolate was catalase-negative and non-gas-producing. RTMP1 survived at pH 3 for 24 h but showed no survival at pH 1–2 beyond 2–3 h. The strain tolerated bile salts, with viable counts recovering to 18–277 CFU after 24 h at 0.3–0.5% bile. RTMP1 exhibited antimicrobial activity against *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhimurium*, *Pseudomonas aeruginosa*, and *Enterococcus faecalis*, with inhibition zones ranging from 9–13 mm. Antibiotic susceptibility testing showed strong sensitivity to erythromycin and ampicillin, moderate response to cephalexin, and weak inhibition to tetracycline, while resistance was observed against Cefoxitin, trimethoprim-sulfamethoxazole, streptomycin, and gentamicin. RTMP1 was identified as *Pediococcus acidilactici* via GTDB-Tk v2.3.2. Genomic analysis confirmed the absence of transferable antimicrobial resistance and virulence genes, and identified functional genes (*dltD*, *clpB*, *groES*, *pyk*, *rplS*, and *tuf*) associated with stress tolerance, adhesion, and bacteriocin production. *P. acidilactici* RTMP1 exhibits characteristics consistent with probiotic potential; however, in vivo studies are required to validate its effects on gut health and animal performance.

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Differences in meat quality attributes between the *Bos indicus*, *Bos taurus*, and Sanga breeds

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The genetic make-up of cattle has been found to influence meat tenderness, and thus, there is major interest in genetic selection to decrease problems with meat tenderness variations. Several studies have reported that some breeds produce more tender meat than others. It has also been proven in some studies that tenderness decreases as the percentage of *Bos indicus* inheritance increases. The *Bos Indicus* breed has been characterised by its production of tougher meat when compared to other breeds. The breed has also been discriminated for producing meat with lower marbling than other beef breeds. Marbling is an important factor determining the tenderness and juiciness of meat. On the other hand, the *Bos taurus* breed is reported to be genetically predisposed to better marbling and tenderness. The Sanga breed is also often regarded as inferior in terms of meat quality, mostly because it is judged by its conformational similarity to the *Bos indicus*. The aim of the study was to compare the differences in meat colour, drip loss, water holding capacity and tenderness between the *Bos indicus*, *Bos taurus* and Sanga beef breeds raised under controlled feedlot conditions. The study was approved by the ARC Animal Ethics Committee (ARC AEC-I 2010 001). The following pure beef breeds were used: Brahman (*Bos indicus*), Nguni (Sanga type), Angus (British *Bos Taurus*), Charolais (European *Bos Taurus*) and Bonsmara (composite), with 10 steers per genotype. The animals were finished off on a feedlot diet and electrically stimulated after slaughter. Steaks were sampled from the *Longissimus lumborum* muscle and aged for 3, 14, and 20 days in vacuum bags. Meat colour, water holding capacity (WHC), drip loss, and meat tenderness were analysed. ANOVA was used for analysis of the results. Results showed breed differences ($P < 0.05$) in colour, WHC, drip loss, and shear force (tenderness). Drip loss was higher in steaks from Charolais and lower in steaks from Angus. The Bonsmara, Brahman and Nguni breeds had similar drip loss. The WHC was lower in Charolais and Angus steaks. However, the drip loss and WHC were within the recommended limit for good quality meat for all the breeds. Meat colour measured by Minolta meter showed differences between the breeds for all the measured colour characteristics, with Nguni producing the darkest meat with high discoloration rate (Hue angle), while the Charolais breed produced the lightest meat with the lowest discoloration rate. Meat tenderness characteristics showed that the Bonsmara and Charolais were more tender, Brahman was the least tender and Angus and Nguni were intermediate at 3 days *post mortem*. The lower meat tenderness in Brahman could be related to the presence of *Bos indicus* inheritance. However, all the breeds produced meat regarded as tender according to the literature. At extended ageing periods (20 days), there were no significant differences in meat tenderness between the breeds. This study has shown that breed effects can be reduced through proper management, nutrition, and standardizing pre-and post-slaughter procedures, which can substantially improve tenderness and other meat quality attributes even in breeds traditionally considered less tender.

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Complementary effects of probiotics and stimbiotics inclusion on growth performance and bone development in broiler chickens exposed to cyclic heat stress

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The poultry industry continues to face challenges associated with the overuse of antibiotics, which resulted in the global ban on antibiotic-growth promoters (AGPs), coupled with increasing prevalence of heat stress (HS) due to climate change, which heightens the need for sustainable strategies to maintain poultry health, welfare, and productivity. This study investigated the potential complementary effects of probiotics and stimbiotics as sustainable alternatives to AGPs in improving growth performance and bone development in broilers exposed to cyclic heat stress. A total of 600 broiler chicks were randomly allocated to 5 dietary treatments (each replicated 8 times): T1: Basal broiler diet, with no AGPs (NegControl); T2: Basal diet, with AGPs (PosControl); T3: Basal diet + 0.01% probiotics (Prob); T4: Basal diet + 0.01% stimbiotics (Stim) and T5: Basal diet + 0.01% (probiotics+ stimbiotics) (ProbStim). The experimental trial was conducted over three feeding phases: starter phase (day 1-14), grower phase (day 15- 8) and finisher phase (day 29-42). Birds were exposed to a 3-hr heat stress on days 27 and 41, with temperatures of 32- 35° C and RH of 40-60% inducing heat stress. Growth performance and bone quality characteristics were measured and analysed using one-way ANOVA in a Completely Randomised Design (CRD) with SAS (2010). Approved by the NWU-ANIMPROD REC (Ethic no. NWU-00802-24-A5). Of all the parameters measured in different feeding phases, diet significantly affected only the average daily gain (ADG) at the starter phase ($P < 0.05$). Broiler chickens fed Prob diet had the highest ADG ($P < 0.05$) while those fed Stim had the lowest ADG. Regarding bone quality characteristics, dietary treatments significantly affected tibia width, and boron and aluminium microminerals. Broiler chickens fed the PosControl had the highest tibia width. The highest boron level was observed in broilers fed Prob (9.80 mg/kg), and the lowest levels were in broilers fed ProbStim (7.10 mg/kg). Aluminium levels were higher in broilers fed the Stim diet (38.47 mg/kg), followed by ProbStim (31.89 mg/kg). In conclusion, this study's findings advocate that feed-based intervention of incorporating probiotics and stimbiotics in broiler diets enhanced growth performance, stress tolerance, bone development and resilience, deducing the beneficial effect of probiotics and stimbiotics inclusion in diets in broilers, partially ameliorating heat stress in broilers exposed to cyclic heat stress.

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Effects of local plants on internal parasites in different goat breeds of Botswana

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Internal parasites pose significant challenges to goat productivity with the impact negatively translating to substantial economic consequences for livelihoods and food security. The use of local plants as dewormers, although with a major gap on efficacy, has emerged as a promising alternative offering sustainable and affordable options in Botswana. The aim of the study was to evaluate the efficacy of the local plants; *Terminalia sericea* and *Gnidia capitata* on faecal egg counts of different goat breeds and sexes. The study was carried out in Botswana and complied with BUAN Animal Care and Ethics Committee (BUAN-AEC-2023-04). A total of 15 Tswana and 15 Boer goats, ageing 18-21 months were randomly allocated to three treatment groups comprising of 10 goats each. The leaves of *Gnidia capitata* and the roots of *Terminalia sericea* plants were collected in the veldt, sun dried and crushed into powder. Then 150g of each powdered sample was mixed with 2 liters of water and left to stand for 24 hours. Treatment 1 and 2 animals were given *Terminalia sericea* and *Gnidia capitata* mixture orally at a dose of 100ml, respectively, as recommended by farmers. Treatment 3 animals were given commercial drug, Ivermax 1% at 1ml per 50kg live mass, subcutaneously. The animals were treated once and had no anthelmintic treatment for at least 90 days prior to the commencement of the study. The body condition score and faecal egg counts based on McMaster technique were performed at the beginning of the trial (day 0) and on days 30, 60 and 90. The data were analysed using SAS. The results revealed an increase of 2 to 4 in the animal's body condition score in all treatments over the 90-day study period indicating reduced competition for nutrients between the animal and the gastrointestinal nematodes. The optimum efficacy against nematodes was on day 60 and *Gnidia capitata* had the highest efficacy of 76% followed by Ivermax with 71% and *Terminalia sericea* with 65%. However, *Terminalia sericea* plant extract was more efficient on reducing coccidia oocysts on goats with an efficacy of 80% and 89% on day 60 and 90, respectively. Tswana goats showed a very strong response to both local plants treatments probably due to genetic variations influencing drug or plant extract metabolism. At day 60, males treated with plant mixtures had lower faecal egg count than females with males treated with *Gnidia capitata* plant extract showing higher significant response. This could be due to the interaction of the sex hormone with the metabolic activity of the plant mixtures. The studied plants have potential of reducing internal parasitism in goats for at least 60 days. Further studies should be performed to determine active compounds and specific mechanisms of action.

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The effect of dietary peach pomace meal on growth performance, blood parameters and meat quality of broiler chickens

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The disposal of agro-industrial by-products, such as peach pomace (PP), presents environmental challenges, while the poultry industry is challenged by increasing feed costs. Peach pomace meal (PPM) contains fibre and bioactive compounds that may support sustainable poultry production. However, its nutritive value and physiological effects in broiler chickens remain largely unexplored. The aim of the study was to evaluate the effects of incremental dietary inclusion levels of PPM on growth performance, blood parameters, carcass traits, organ weights and meat quality of broiler chickens. Study procedures were approved by the Animal Production Research Ethics Committee of North-West University (NWU-0029-23-A5). Two hundred and eighty 7-day-old male Ross 308 broiler chicks (140 ± 0.07 g) were randomly allocated to four isoenergetic and isonitrogenous diets containing 0 (CON), 100 (PPM100), 150 (PPM150) and 200 g/kg (PPM200) PPM. Each treatment had seven replicate pens with 10 birds per pen. Birds were fed starter (7–14 d), grower (14–28 d) and finisher (28–35 d) diets. Growth performance parameters were recorded weekly. At day 35, blood samples were collected for hematological and biochemical analyses, and carcass traits, organ weights and meat quality parameters were evaluated. Data were tested for normality using the PROC UNIVARIATE procedure of SAS (2013) prior to analysis. Growth performance data were analyzed using one-way ANOVA with pen as the experimental unit, while individual birds served as the experimental units for blood parameters, carcass traits, organ weights, and meat quality. Repeated measures analysis within the General Linear Model was used for weekly performance data to assess diet $\times$ week interactions. Differences between means were separated using the LSMEANS procedure, and significance was declared at $P < 0.05$. Diet $\times$ week interactions affected feed intake (FI) and feed conversion ratio (FCR) ($P < 0.05$), but not body weight gain (BWG) ($P > 0.05$). Birds fed PPM200 had higher ($P < 0.05$) FI than CON during days 7–14 and 29–35, yet overall BWG and FCR were comparable across treatments ($P > 0.05$). Mortality remained low ($< 2\%$) and was not influenced by diet. Dietary PPM reduced ($P < 0.05$) lymphocyte counts and bilirubin concentrations compared to CON, while other blood parameters were unaffected, suggesting no adverse physiological impact. No significant dietary effects were observed for carcass traits or organ weights ($P > 0.05$). Meat colour parameters were influenced by PPM inclusion; PPM100 increased ($P < 0.05$) breast meat redness (a^*) compared to CON and PPM150, while higher inclusion levels increased lightness (L^*). The absence of negative effects on performance despite increased dietary fibre indicates that PPM did not compromise nutrient utilization under the conditions of this study. Dietary inclusion of PPM up to 200 g/kg did not impair growth performance, physiological status, carcass traits or overall meat quality of broiler chickens. Inclusion at 100 g/kg may enhance meat redness. PPM can therefore serve as a sustainable alternative feed ingredient in broiler production systems.

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Relationship between village chicken availability and dietary diversity along a rural-urban gradient

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Rearing village chickens is one of the sustainable strategies that can potentially improve households' access to diverse diets. Dietary diversity refers to different food groups that a household eats over a particular reference period. It is one of the fundamental factors of nutritional security and a proxy for measuring diet quality. The aim of the study was to investigate the relationship between village chicken availability and households' diet diversity along a rural-urban gradient. The relationship between village chicken flock sizes and dietary diversity was hypothesized to be linear. The study was performed according to protocol reference number: HSSREC/00005927/2023. Face-to-face interviews were conducted using the structured questionnaire on rural ($n = 100$), peri-urban ($n = 100$), and urban ($n = 100$) areas of Pietermaritzburg uMgungundlovu District, KwaZulu-Natal in South Africa. A positive linear relationship between distance from the city centre and village chicken flock sizes was observed. An increase of 1 km from the city centre increased village chicken flock size by 30.43 ($P < 0.01$). Village chicken flock sizes contributed positively to household dietary diversity through income from chicken sales and manure. There was a positive linear relationship between distance from the city centre and vegetable consumption. The number of consumed vegetables increased with an increase in distance from the city centre by 1.33 ($P < 0.01$). A positive linear relationship between village chicken flock sizes and consumed LDFs was observed. The number of consumed LDFs increased with an increase in village chicken flock sizes by 0.45 ($P < 0.05$). There was a positive linear relationship between village chicken flock sizes and consumed vegetables. The number of consumed vegetables increased with an increase in village chicken flock sizes by 0.68 ($P < 0.01$). A positive linear relationship was observed between distance from the city centre and dietary diversity score. The dietary diversity score increased with increasing distance from the city centre by 0.24 ($P < 0.05$). There was a positive linear relationship between village chicken flock sizes and dietary diversity. Dietary diversity score increased with an increase in village chicken flock sizes by 1.50 ($P < 0.05$). The availability of village chickens across a rural-urban gradient is a valuable opportunity to improve households' dietary diversity and alleviate poverty. It can be concluded that expanding village flock sizes could enhance household dietary diversity.

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Dietary effect of marula seed cake as soybean replacement on caecal microbial diversity and abundance in broiler chickens

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Due to its high nutritional profile, marula seed cake (MSC), a by-product of marula seed oil extraction, has potential as an alternative protein source to soybean meal (SBM). However, there is limited information on the influence of MSC on overall gut health, particularly on the gut microbial community (diversity and abundance) in broiler chickens. The fibrous fractions and phytochemicals present in MSC may selectively stimulate beneficial gut microbiota, while suppressing pathogenic gut microbes, thereby promoting microbial balance, improved gut integrity, and enhanced nutrient utilization. It is important to understand this because the gut microbiota plays a critical role in immune modulation, nutrient utilisation, and growth performance. The aim of the study was to evaluate the dietary effects of MSC as an alternative to SBM on the caecal microbial community in broiler chickens. The rearing and slaughter of broilers was conducted at North-West University Molelwane experimental farm (Ethics clearance #: NWU-00806-22-A5). Five iso-caloric and iso-nitrogenous diets were formulated such that they contained incremental levels (0, 5, 10, 15, and 20%) of MSC partially replacing SBM. In a completely randomised design, 400-day-old Ross 308 broiler chicks with an average initial weight of 45.61 ± 0.67 g were randomly allocated to the dietary treatments, each with 8 replicate pens of 10 birds. At day 42, all birds were humanely slaughtered, and visceral organs were removed by hand through an opening from the vent to the sternum. The caecum was cut, and the caecal content was transferred into a sterile tube. Immediately, the whole DNA was extracted and sent for sequencing at Inqaba Biotech. Post-sequencing, quality control, and all data were analysed using KBase platform. At the phylum level, the highest dietary inclusion of MSC (20%) increased the abundance of Bacteroidetes, whereas Firmicutes were most abundant in birds fed the control diet and those fed 5%, 10%, and 15% MSC. A similar pattern was observed at the order level, whereby higher MSC inclusion promoted greater abundance of Bacteroidales. Dietary inclusion of graded levels of MSC increased the number of operational taxonomic units (OTUs) compared with the control diet. However, there were no significant differences in Shannon alpha diversity or beta diversity among the treatment groups. The principal coordinate analysis (PCoA) based on Bray-Curtis distances showed a clear separation in caecal microbial clustering, with the control group positioned distinctly apart from the MSC-supplemented treatment groups. The relative abundances of the top 100 most dominant bacterial species were generally low in birds fed the control diet. Dietary inclusion of MSC increased the relative abundance of *Duncaniella* sp. B8 and *Limosilactobacillus vaginalis* in broilers fed diets containing 5% and 15% MSC, respectively. A higher dietary inclusion level of MSC (20%) also increased the relative abundance of *Phocaeicola salanitronis* and *Lactobacillus johnsonii*. Based on the principal coordinate analysis, dietary marula seed cake influenced caecal microbial community and increased the relative abundance of beneficial bacteria in broiler chickens. Further studies should explore the nutritional and metabolic pathways induced by these microbiotas.

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Livestock theft and retrieval constraints: Perspectives of Bizana livestock farmers of Alfred Nzo district, Eastern Cape province

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The South African livestock industry (cattle, sheep, goats, poultry, and pigs) contributes 42 to 50% of the gross agricultural value. Livestock theft undermines sustainable rural economic development, livelihoods, and food security across South African livestock farming communities, with annual losses exceeding R880 million. In the Eastern Cape, elevated cases persist, where unbranded livestock often results in permanent losses despite recoveries by the South African Police Services (SAPS), due to inadequate animal identification marks as required by the Animal Identification Act (Act No. 6 of 2002). Few studies, however, explore farmers perceptions of livestock theft and recovery challenges in the Bizana area of Alfred Nzo district, Eastern Cape Province. This study aimed to assess the perceptions of livestock farmers regarding livestock theft and the associated retrieval constraints among Bizana livestock farmers in Alfred Nzo District, Eastern Cape. A quantitative approach was employed, with primary data collected from a sample size of 327 Bizana livestock farmers, calculated using Cochran's sample size formula, selected through simple random sampling. Data was captured and analysed using the Statistical Package for the Social Science (SPSS) Version 27 software, employing descriptive statistics to identify farmers socio-economic characteristics, prevalent stolen livestock types, theft prevention and recovery practices, and key retrieval constraints. The findings reveal a farming demographic characterized by an average age of 63 years. A significant majority of participants (63%) reported rearing large stock, while 27% focused on small stock, with a notable proportion (10%) engaging in both. The results revealed that sheep (41%) were the prevalent stolen livestock types, followed by cattle (29%), goats (17%), poultry (9%) and pigs (4%). This results are consistent with broader South Africa literature, which affirms that the Alfred Nzo District is one of district in Eastern Cape that experiences some of the highest reported stock theft cases, accounting approximately 21.5% of the provinces total incidents with small stock like sheep and goats having a higher statistical livelihood of being stolen with significantly lower recovery rates due to its local demands. Key recovery constraints included absent branding (34%), insufficient rangers (26%), corruption (22%), and poor communal fencing (18%). Current practices rely heavily on SAPS Stock Theft Units, but efficacy remains limited by low legislative compliance rates. This study provides empirical evidence of the systematic vulnerabilities faced by Bizana livestock farmers regarding stock theft and clearly delineates the procedural and resource based barriers to effective livestock retrieval. The findings advocate for urgent interventions, including the strengthening of livestock identification systems and enforce farmers compliance with legislative requirements, particularly branding and record keeping. Furthermore, improved collaborative efforts among traditional authorities, community forums, Department of Agriculture, and law enforcement agencies are essential to streamline ownership verification processes and significantly enhance the efficacy of livestock retrieval operations. This research contributes to a better understanding of the on-the-ground realities of livestock theft and retrieval in the Eastern Cape, offering actionable insights for policy and practices.

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Comparing age at first calving between early and late born heifers among smallholder farmers in Mpumalanga province

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Cowherd fertility and efficiency cannot be separated from ultimate achievement of a profitable beef farming. Age at first calving (AFC) and inter-calving period (ICP) are the fundamental factors to ensure a financially healthy herd. Although late summer calving results in heavier calves, its effect on the reproductive efficiency of heifers has not been assessed. Such correlation would have significant positive impact of the profitability of the cow herd. The aim of the study was to compare AFC among smallholder beef farmers focusing on early and late born heifers with 21-day age difference. Data was collected from ten farmers, actively participating in Kaonafatso ya Dikgomo (KyD) in Mpumalanga province, and collectively recorded birth and calving data of 137 heifers born between 2009 and 2021. AFC data was extracted from the Integrated Registration and Genetic Information System (INTERGIS) to compute descriptive statistics for comparisons. Heifers were divided into two groups consisting of 68 that were born in early Summer and 69 born in late Summer. Descriptive statistics were used to summarise the data. The AFC over the eleven breeding years was 35 and 35.7 months for early born heifer and late born heifers, respectively, ranging from 26 to 48 months. Contrary to expectations, late born heifers had longer AFC than early births, in four breeding years (2009, 2014, 2018, 2019). AFC was either similar or just a fraction high towards late calving. The fluctuating results especially those showing prolonged AFC for late calving may be ascribed to varying quality of grazing due to seasonal changes. Based on this evidence, neither of the two practices may be regarded as superior to the other. Findings of this exploratory study are inconclusive and may not recommend either of the two practices. However, more data is required to replicate this type of assessments. By encouraging smallholder to keep animal records, more data can be generated to validate findings of this study.

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The effect of Ralgro® implant on the growth performance and carcass traits of Nguni and Merino sheep in a feedlot system

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The foot-and-mouth disease (FMD) outbreak in South Africa has had a significant impact on the wool industry, resulting in a total ban on wool exports. The prohibition on wool exports has severely affected profitability, production, and international trade. Furthermore, the outbreak has resulted in the loss of income for many farmers, since the wool industry is a major source of income for communal sheep farmers. The production of lamb and mutton is an alternative option for wool producers. The impact of a non-steroidal growth implant has been studied in some sheep breeds, such as Merino and Dorper, yet no study has investigated the impact of growth implant on growth performance and carcass traits of Nguni Sheep. The study aimed to evaluate the influence of non-steroidal growth implants on the growth performance and carcass traits of Nguni and Merino sheep breeds. The study was approved by the Departmental Research Committee, Project number AS 2021/01K. The study sites were Kokstad and Dundee Research Stations. Fourteen Merino and Nguni lambs were randomly allocated into two treatments. The treatments were: control and 12mg Zeranol (Ralgro®) implant per castrate. Lambs were provided with 14% CP commercial pellets, *Digitaria eriantha* hay, and water *ad libitum* for 120 days, following a 7-day adaptation period. Lambs were identified with ear tags, weighed, vaccinated with Multivax-P Plus (MSD Animal Health South Africa), and dewormed using Nem-a-rid® (MSD Animal Health South Africa). The initial weights were 29,00±0.02 kg and 21,57±0.021 kg for Merino and Nguni lambs, respectively. In each breed, seven lambs received 12mg Zeranol pellets at the start of the trial with a second administration on day 60. Weighing was done on weekly basis to calculate ADG. Lambs were slaughtered after 121 days of feeding. Warm and cold carcass weights were recorded to calculate chilling loss percentage. Growth performance and carcass traits data of lambs were analyzed using ANOVA on GENSTAT 23rd Edition, and any significant differences were tested using Tukey's LSD ($P < 0.05$). Significant differences in initial weight and weight gain ($P < 0.05$) between breeds were observed. This could be ascribed to phenotypic and genetic differences within breeds. Besides, no significant differences in weight ($P > 0.05$) were noted within treatments, and the interaction of breed × treatment. This could be attributed to low levels and short duration of feeding Zeranol®. There were no significant differences in carcass traits (warm mass, cold mass, dressing percentage, and chilling loss) ($P < 0.05$) within the breed, while significant differences were only seen between breeds. Some researchers also reported no improvement in carcass traits of lambs fed with Zilmax® with a combination of Ralgro® implant (Webb *et al.*, 2018). The use of Ralgro® implants in fattening lambs did not improve growth performance and carcass traits as expected. Similar research with an increased number of lambs and different levels of Zeranol® phase should be conducted.

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Synergistic influence of controlled LN₂ vapour exposure and *Moringa oleifera* leaf extract on epididymal bull sperm cryosurvival and functional parameters

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Cryopreservation of spermatozoa is widely used in animal reproduction; however, the process induces oxidative stress and cold shock, which collectively disrupt sperm membrane integrity, mitochondrial function, and DNA stability. These damages ultimately reduce post-thaw sperm quality ability. Natural antioxidants, such as *Moringa oleifera* leaf extract (MLE), have gained interest for their ability to mitigate oxidative damage during cryopreservation due to their high content of bioactive compounds, including flavonoids and phenolic. This study investigated the combined effects of controlled exposure to liquid nitrogen (LN₂) vapour at different heights and supplementation with *Moringa oleifera* leaf extract on the post-thaw quality of epididymal bull sperm. Ethical approval was obtained for the use of animal-derived materials. A total of 30 epididymides (n = 15 bulls) were collected from a local abattoir and transported to the laboratory at 5 °C. Spermatozoa were recovered and randomly allocated into a 4 × 2 factorial experimental design, consisting of four MLE concentrations (0, 4, 8, and 12%) and two LN₂ vapour heights (5 and 7 cm). Samples were diluted in a Tris-egg yolk (TE) extender containing the respective MLE concentrations (TE0, TE4, TE8, and TE12) and equilibrated for 120 minutes. Semen straws were frozen by suspending them at the designated heights above LN₂ vapour for 20 minutes prior to immersion in liquid nitrogen. Thawing involved air exposure for 10 seconds followed by immersion in a 37 °C water bath for 1 minute. The primary characteristic measured was sperm viability, defined as the proportion (%) of live spermatozoa, assessed alongside motility and morphology using a computer-assisted sperm analysis (CASA) system before and after cryopreservation. Data were analyzed using the General Linear Model procedure in Minitab (2019). The supplementation of MLE significantly improved post-thaw sperm viability (P < 0.01), with TE8 (57.94 ± 0.01%) and TE4 (54.06 ± 0.15%) outperforming TE0 (38.20 ± 2.31%) and TE12 (44.30 ± 3.10%). The improvement at moderate MLE levels (4-8%) is likely due to optimal antioxidant activity that reduces lipid peroxidation and preserves membrane integrity, whereas excessive concentration (12%) may exert pro-oxidant or osmotic effects that compromise cell stability. Freezing height also influenced viability (P < 0.05), with samples frozen at 5 cm (55.56 ± 0.11%) showing higher survival than those at 7 cm (52.41 ± 2.01%). This difference can be attributed to more controlled and gradual cooling rates at lower vapour distances, which reduce intracellular formation and thermal shock. The interaction between 8% MLE and 5 cm height indicates a synergistic effect, where antioxidant protection complements optimal cooling dynamics to enhance membrane stability and cellular resilience during freezing and thawing. The integration of phytogenic antioxidants with optimized cryopreservation conditions significantly enhances the post-thaw quality of epididymal bull sperm. An MLE concentration of 8% combined with a 5 cm LN₂ vapour height provides optimal protection, emphasizing the importance of balancing biochemical protection with physical freezing parameters to improve sperm cryosurvival.

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Methanogenic potential of selected agro-industrial by-products under simulated ruminal conditions

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Agro-industrial by-products (AIBPs) are generated in large quantities during food processing and are increasingly incorporated into ruminant diets. Their utilisation allows materials unsuitable for human consumption to be valorised while potentially reducing waste streams otherwise disposed of in landfill sites. However, fermentation of these substrates in the rumen may contribute to enteric methane production. Evaluating the methanogenic potential of individual AIBPs under controlled ruminal fermentation conditions is therefore important when assessing their suitability as ruminant feed ingredients. The aim of this study was to determine the methane production potential of selected agro-industrial by-products under simulated ruminal fermentation conditions. Ethical approval was granted by the Stellenbosch University Animal Care and Use Committee (ACU-30189-2026). Samples were collected across the Western Cape, South Africa and included: CPG - citrus pulp (orange, grapefruit and lime); CPN - citrus pulp (orange and mandarin); CPL - citrus pulp (lemon); CPP - pooled citrus pulp sample; WBR - wheat bran; SOC - soya oilcake; BGR - brewers' grains; and DGR - distillers' grains. Samples were frozen at -18 °C, thawed overnight, dried at 60 °C for 24 h and milled through a 1-mm screen prior to analysis. Methane production potential was determined using an in vitro ruminal fermentation system (AMPTS II). For each reactor, 2 g of substrate were incubated with 40 mL pooled rumen fluid and 160 mL buffer solution under anaerobic conditions. Rumen fluid was collected from two ruminally-cannulated Dexter cows three hours after feeding and maintained under anaerobic conditions prior to incubation. Fermentations were conducted in 250 mL reactors maintained at 40 °C in a shaking water bath. Carbon dioxide was removed using sodium hydroxide scrubbing to allow methane measurement. Seven experimental runs were conducted over seven weeks, resulting in seven replicates per treatment. Large differences in total gas ($P < 0.001$) and methane ($P < 0.01$) production were observed among substrates after 48 h of fermentation. Citrus pulp substrates produced the highest gas volumes, with CPN (232.037 mL g⁻¹ DM), CPL (257.911 mL g⁻¹ DM), CPP (257.491 mL g⁻¹ DM), and CPG (224.712 mL g⁻¹ DM). Considerably lower gas production was observed for WBR (198.978 mL g⁻¹ DM), BGR (134.979 mL g⁻¹ DM) and DGR (132.370 mL g⁻¹ DM), with SOC producing relatively low gas volumes (173.895 mL g⁻¹ DM). Methane production followed a similar trend. The highest methane volumes were recorded for CPP (111.792 mL CH₄ g⁻¹ DM), CPL (108.557 mL CH₄ g⁻¹ DM) and CPN (107.827 mL CH₄ g⁻¹ DM), whereas CPG produced lower methane volumes (90.059 mL CH₄ g⁻¹ DM). Wheat bran and soya oilcake produced intermediate methane volumes (100.643 and 93.642 mL CH₄ g⁻¹ DM respectively), while lower values were observed for brewers' grains (76,801 mL g⁻¹ DM) and distillers' grains (72,955 mL g⁻¹ DM). The methanogenic potential of the evaluated AIBPs differed substantially under simulated ruminal fermentation conditions. Citrus pulp substrates produced the highest total gas and methane volumes, indicating high fermentability, whereas soya oilcake and wheat bran produced lower gas volumes. These findings highlight the importance of considering methane production potential when evaluating agro-industrial by-products as ruminant feed ingredients.

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Effects of hempseed oil on haematological and parasitological responses in lambs challenged with *Haemonchus contortus*

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Given the significant economic & welfare challenges posed by *Haemonchus contortus* to sheep production, coupled with widespread anthelmintic resistance, alternative control strategies, including nutritionally based interventions such as hempseed oil (HSO) are important. Hempseed oil has emerged as a potential nutraceutical due to its phytochemical composition, including essential fatty acids (α -linolenic, linoleic acid), & polyphenols with reported antioxidant, antimicrobial, anthelmintic & anti-inflammatory properties (Fallahi *et al.*, 2022; Hassan *et al.*, 2023). The aim of the study was to evaluate the anthelmintic potential of HSO against *H. contortus* in lambs artificially infected with the parasite. Ethical approval (ACU-2025-32362) & section 20 permission were granted before the commencement of the study. For the *in vivo* trial, 60 Dohne Merino lambs (± 25 kg; 3-month-old) were allocated to six treatment groups in a 2 (infection vs. no infection) $\times$ 3 [control (no drug), 5% HSO, & chemical (ZolvixTM plus) completely randomised design (CRD; n=10/treatment). Diets were formulated to meet the nutritional requirements of growing lambs with HSO replacing maize at a 5% inclusion level. Lambs were adapted to the diets for 28 days. Following the adaptation period, animals were inoculated with 4000 *H. contortus* L3 larvae on day 0 & monitored for 42 days. Feed intake was recorded daily, while body weight, FAMACHA & body condition score (BCS) were recorded weekly. Blood samples were collected from the jugular vein on day 42 for packed cell volume (PCV) & total serum protein (TSP). After slaughter, the abomasum was collected, opened, & processed for worm enumeration. *In vitro*, larval counts were determined by culturing faecal samples from each lamb mixed with vermiculite & incubated at 27°C for 7 days. All data was analysed using PROC GLIMMIX of SAS v 9.4. In the model, diet & infection were added as a fixed factors, & animal as a random factor. Treatment means were compared using Tukey's post hoc test ($P \leq 0.05$). Anthelmintic treatment had no effect on body weight, BCS, & FAMACHA© scores, suggesting relatively low infection challenge. Infected lambs showed higher ($P < 0.05$) FAMACHA© scores than non-infected, indicating anaemia. A significant treatment $\times$ infection interaction was observed for PCV, with infected control & HSO lambs having lower values than the other interactions. Infected lambs had lower ($P < 0.05$) TSP than non-infected lambs, showing reduced protein status under infection. HSO had the highest TSP levels, outperforming control & chemical treatments, likely due to its bioactive compounds that promote bypass protein. Chemical treatment reduced ($P < 0.05$) larval counts than the other treatments. For worm counts, HSO performed better than control but was outperformed by the chemical treatment, demonstrating moderate anthelmintic activity. Though HSO moderately reduced adult worm counts, chemical treatment proved superior, achieving the largest reductions in both larval & adults worm counts. Overall, HSO showed nutraceutical potential to enhance physiological resilience, maintain lamb feedlot performance & support integrated parasite management.

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Effects of partial replacement of soybean meal with fermented water hyacinth on haematobiochemical indices, and gut microbiome in hy-line brown hens

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The poultry industry continues to seek sustainable and cost-effective alternatives to conventional protein sources like soybean meal, particularly in response to economic pressures and environmental concerns. Valorisation of water hyacinth, a problematic aquatic plant by harvesting and processing water hyacinth into a fermented meal, has the possibility to address both the protein shortage for poultry feed and the environmental challenges posed by this aquatic weed. The study evaluated the effects of partial replacement of soybean meal with fermented water hyacinth meal (FWHM) on blood and serum indices and the gut microbiome in Hy-Line laying hens. Ninety-six hens (16 weeks) were weighed and randomly assigned to one of three dietary treatments a control diet 0% FWHM, 2.5% FWHM and 5% FWHM in a completely randomised design. Following a 2-week dietary adaptation period and a subsequent 8-week feeding trial 3 birds per replicate were randomly selected for blood collection at day 63. Blood samples (2ml) were drawn from the wing median brachial vein of birds using a needle and a syringe and was immediately transferred into purple-coloured lid tubes with anti-coagulant for haematology and red coloured tubes with clot activator. Pure serum samples were aspirated and serum concentrations of albumin, total protein, urea and serum enzymes; alanine amino transferase and aspartate amino transferase were determined using the BS 220 chemical analyser. Haematology was analysed using Mindray auto haematology analyser model BC-5150. After slaughter at day 65 the caecum was dissected using sterile surgical scissors and caecal contents were pooled using medical cotton swabs, placed in swab tubes with buffered peptone gel immediately and analysed for *E. coli*, *Staphylococcus aureus*, *Bacillus subtilis*, Yeast and *Lactobacilli* species. All experimental procedures that were used in the research project were approved by the Zimbabwe Animal Act, Chapter 19:12, 1963, Licence number L729 (Scientific Experiments on Animal Act, 1963; 03 2025-18). Blood haematobiochemical parameters across dietary treatments, indicated that FWHM inclusion up to 5% will not impair bird health and nutritional status. White blood cell count was significantly low in 5% FWHM compared to other dietary treatments and can be an effect of high fibre. Serum creatine levels for dietary treatment 5% FWHM were low compared to other dietary treatments, and it can be attributed to high fibre in diet FWHM and its effect on oxidative stress. Inclusion of FWHM in layer diets significantly modulated the gut microbiota, reducing *Escherichia coli* in $1.35 \pm 0.05 \times 10^6$ CFU/mL in 5% FWHM, $P < 0.001$ and *Staphylococcus aureus* $1.40 \pm 1.7 \times 10^4$ CFU/mL in 2.5% FWHM population, yeast populations increased $2.5 \pm 5.0 \times 10^4$ CFU/mL in 2.5 % FWHM and $2.7 \pm 1.7 \times 10^4$ CFU/mL in 5% FWHM. The study concludes fermented water hyacinth meal (FWHM) as a potential protein source ingredient in poultry and has prebiotic and probiotic properties that influence gut microbiota while maintaining physiological homeostasis.

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Nutritive values and *in vitro* protein degradation of oil cakes from *Tylosema esculentum* (morama) and *Schinziophyton rautanenil* (mongongo) as feed supplements for ruminants

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Animal feeds under ruminant production are a challenge, and ruminants are mostly fed on fibrous with no protein supplementation. Protein supplements, such as oil cakes (e.g. soybean oilcake) are used mainly in animal diets but are considered a limiting factor under smallholder farming operations. As a results, alternative protein sources are needed to solve this problem. The production of oil from oil seeds results in the production of oil cakes which contain appreciable amounts of protein that can be used to feed ruminants. However, the quality of protein depends on its utilization by the rumen microbes. The aim of this study was to evaluate the nutritive values and in vitro degradability of protein from non-conventional oil cakes such as Morama and Mongongo in comparison with soybean oil cake. Batches of oilcakes (i.e. Morama and Mongongo) were obtained from small scale oil producers in Gaborone, Botswana and brought to the ARC-API for nutrient analysis and in vitro protein degradation at the Nutri-lab of the university of Pretoria under the Animal Ethics Clearance NAS113-2025. Samples of the oil cakes were analysed for dry matter (DM), organic matter (OM) gross energy (GE), crude protein (CP), neutral detergent fibre (NDF) and acid detergent fibre (ADF). The samples were then incubated in laboratory tubes that contained rumen liquor that was mixed with McDougall artificial saliva for a period of 48 hrs. This was done to determine the CP degradation rates, which were recorded at 0, 3, 6, 12, 24 and 48 hrs. Both the analysis of nutrient content and the CP degradation of these non-conventional oil cakes were done in comparison with soybean meal (SBM), which served as a control. Morama oil cake had higher ($P<0.05$) DM, OM and CP content compared to the other oil cakes. However, SBM had higher ($P<0.05$) IVOMD than the non-conventional oil cakes. The contents of fibre fraction (NDF and ADF), ether extract, ash and gross energy were higher ($P<0.05$) in mongongo than the other two oil cakes. This high energy in mongongo oil cake can be attributed to its high fat content. Morama oil cake had a lower CP degradability during the < 24hours of incubation but had a similar degradation rate at 48 hrs with SBM while mongongo oil cake had lower degradation rate after 48 hrs of incubation. The high fibre fraction and fat content in Mongongo oil cake might be the reason for its reduced CP degradability after 48 hrs of incubation. Morama oil cake has a potential to substitute SBM in the diet of ruminants compared to mongongo oil cake, which is higher in fat and fibre contents.

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Assessment of identity disequilibrium and inbreeding variation in Gauteng and Mpumalanga provinces of South Africa

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Understanding the extent and distribution of inbreeding within livestock populations is essential for effective genetic management and conservation. Identity disequilibrium, measured as covariance in heterozygosity across loci, provides insight into variation in realized inbreeding among individuals and the reliability of multilocus heterozygosity as a proxy for inbreeding. This metric enables evaluation of the effects of inbreeding on genetic diversity and trait expression within populations. The aim of this study was to quantify identity disequilibrium (ID) and evaluate the extent of inbreeding variation within two cattle populations from Gauteng (GP) and Mpumalanga (MP) provinces. Ethical clearance was obtained from the Agricultural Research Council-Animal Production (APIEC24/07). The study consisted of two cattle populations, GP (n=93, 52 911 SNPs) and MP (n= 96, 54 349 SNPs). Statistical analysis was performed using the base R 'stats' package. Identity disequilibrium was quantified using the g_2 estimator, and the reliability of the markers was evaluated through heterozygosity–heterozygosity correlations (HHC) and the expected correlation (r^2) between marker heterozygosity and true inbreeding (f) using inbreedR. Population inbreeding levels were determined using the “—het” function in PLINK v1.9. The Identity disequilibrium (g_2) analysis showed differences between the populations. Stronger identity disequilibrium signals were displayed in GP ($g_2 = 0.032$), with g_2 estimates nearly three times higher than MP ($g_2 = 0.013$, $P = 0.01$). This shows significantly higher variance in inbreeding and suggests a mixed population likely with differentiated breed lineages or more recent crossbreeding events. The weaker g_2 signal in MP shows a lower while significant variance in inbreeding coefficients indicating uniform individual heterozygosity, possibly due to a longer history of random mating. Both populations displayed high mean heterozygosity–heterozygosity correlation (HHC) values, indicating strong and significant correlations among heterozygosity estimates. In Mpumalanga (Mean = 0.97, 95% CI [0.959, 0.977], $r^2 = 1$), the HHC estimate demonstrated approximately 97% reliability, suggesting that the marker set is reliable for this population. Gauteng population (Mean = 0.987, 95% CI [0.983, 0.991], $r^2 = 0.99$) displayed a narrower confidence interval around the mean HHC estimate, indicating greater precision of the correlation measure. Additionally, GP showed a higher mean inbreeding coefficient (Mean = 0.438; SE = 0.0067), indicating evident levels of inbreeding within this population. In contrast, the mean inbreeding coefficient in MP was low (Mean = 0.005; SE = 0.0079), implying this population is minimally inbred. Gauteng cattle demonstrate a stronger signal of inbreeding variance compared to Mpumalanga based on the significantly higher g_2 value, reflecting stronger population structuring and heterogeneous breeding. In contrast, the lower but still significant g_2 in MP suggests a more genetically uniform population, reflecting a longer history of random mating and reduced variation in individual inbreeding levels. The high heterozygosity correlations observed in both populations confirm that the SNP panel accurately captures genome-wide inbreeding signals. The high marker–inbreeding correlation (r^2) provides a robust, high-resolution foundation for future monitoring of inbreeding depression and management of hybrid vigour in GP and MP cattle populations. GP may require stricter genetic management to mitigate inbreeding, whereas MP appears to retain a stable and genetically diverse structure.

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The relationship between staple strength, fibre diameter and coefficient of variation of fibre diameter in a dual-purpose sheep breed

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Wool has several quality and quantity characteristics, such as fibre diameter (FD), staple strength (SS) and staple length that are very important to wool producers, manufacturers and consumers. The second most important factor, after fibre diameter, that influences the processing of wool and consequently the price for wool is staple strength. It is a well-established fact that the strength of wool is largely a function of FD and the coefficient of variation of fibre diameter (CV). Tender wool with a staple strength of below 30 N/Ktex will obtain a much lower price due to its effect on the processing of wool. The fact that finer wool types tend to have a lower staple strength compared to stronger wool types is of major concern to wool producers. To determine the relationship among SS, FD and CV in a dual-purpose sheep breed, the Dohne Merino. Ethical clearance was obtained from the Grootfontein Animal Ethics Committee (number AP2/24). Data collected from 2001 to 2024 on 5552 Dohne Merino ram and ewe progeny from the Grootfontein Dohne Merino stud were used for this study. The traits analysed were SS, FD and CV at performance testing age. The fixed effects included in the analysis were year of birth, gender, rearing status and dam age (years), as well as animal age (days) as a covariate. Variance components and estimated breeding values were obtained through bivariate analysis with ASREML software. The heritability estimates for FD, SS and CV were 0.68 ± 0.02 , 0.32 ± 0.03 and 0.51 ± 0.03 , respectively. The genetic correlations between SS and FD, and SS and CV were 0.46 ± 0.05 and -0.69 ± 0.04 , respectively. It is evident from these correlations that fibre diameter and staple strength are unfavourably correlated, because selection for decreased fibre diameter would result in an unwanted decrease in strength. The correlation between SS and CV was negative, but favourable, with a decrease in CV leading to an increase in SS. Direct selection response in SS was calculated as 7.20 N/Ktex per generation, while the correlated selection response in SS for selection based on CV is 3.55 N/Ktex per generation, which is 49% of the direct response. The correlated response in SS for selection based on FD was 2.73 N/Ktex per generation. However, due to the additional cost in measuring SS, breeders do not typically do these analyses. It is therefore not a viable option to include SS in selection objectives. The inclusion of CV in the selection objectives is therefore a much more viable option to improve SS. Furthermore, no additional cost will be involved because CV values are obtained as part of the FD analysis. It can be concluded from the results of this study that selection pressure for decreased FD can have a detrimental effect on SS. The fact that these two traits are the main factors influencing wool price, further complicates selection strategies. It is therefore important that CV must be included in the selection objectives to improve SS when selection for decreased fibre diameter is practised.

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Effect of fruit fortification on vitamin and mineral composition of yoghurt

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Yoghurt is a nutrient-dense dairy product with recognized nutritional and probiotic benefits. Fruit fortification of dairy products is increasingly explored as a strategy to improve micronutrient intake and develop functional foods. The aim of the study was to evaluate the effect of fruit fortification on the vitamin and mineral composition of yoghurt. Yoghurt was produced from fresh cow milk, which was pasteurized, inoculated with starter culture, and supplemented with strawberry, soursop, kiwi, blueberry and beetroot extracts at inclusion levels of 5, 10, 15 and 20% (w/w) prior to fermentation, while plain yoghurt served as the control. The experiment followed a factorial arrangement (fruit type × inclusion level), and analyses were conducted in triplicate (n = 3). Vitamins A, D, E and K were selected to evaluate changes in fat-soluble vitamins within the dairy matrix, alongside selected minerals (calcium, phosphorus and potassium). All values were expressed per 100 g of final product, and formulation conditions were maintained consistently across treatments. Data were subjected to analysis of variance and means were separated using Tukey HSD test. Vitamin A values ranged from 248.70 to 326.40 µg/100 g, with yoghurt containing 15% blueberry extract recording the highest level relative to the control. Vitamin D ranged from 0.49 to 1.30 µg/100 g, while vitamin E varied between 0.75 and 1.61 µg/100 g across treatments. Vitamin K values ranged from 0.46 to 1.25 µg/100 g. Phosphorus and potassium contents ranged from 102.85 to 165.00 mg/100 g and 171.48 to 315.73 mg/100 g, respectively, while calcium ranged from 82.57 to 128.66 mg/100 g. Significant differences (p < 0.05) were observed among treatments for most vitamins and selected minerals. Yoghurt fortified with 15% blueberry extract showed the most consistent improvement in vitamin content, while variations in mineral content indicate that different fruit types contributed to higher levels of specific minerals. Fruit fortification influenced the micronutrient composition of yoghurt, with 15% blueberry inclusion identified as the most effective level for improving vitamin content. The findings support the potential application of fruit-fortified yoghurt as a value-added dairy product.

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Growth performance and prevalence of gastrointestinal nematodes in weaned goat kids foraging in grassland and forestland vegetation type

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In developing countries, gastrointestinal nematodes (GIN) are one of the major constraints to goat production. These parasites are strongly associated with great economic losses, as it reduces body condition, feed intake, anthelmintic resistance, fecundity and survival of goat kids. The prevalence of GIN in goats is highly influenced by vegetation, season, age, and sex. There is limited information on the effect of vegetation type on body weight changes, body condition and GIN infection in weaned goat kids. The study was conducted to assess the prevalence and loads of GIN and growth performance of weaned goat kids foraging in grassland and forestland vegetation types. Body condition scores (BCS), body weights (BW), and faecal egg counts (FEC) were assessed on clinically healthy weaned goat kids from January to May 2020 in both vegetation types on different farms. A total of 72 weaned goat kids were sampled from grassland (n = 32, 47% males and 53 % female) and forestland (n =40, 37% males and 63 females), with an average body weight of 18.2 ± 0.84 , were used in the study. Data were analyzed by linear mixed models with repeated measures statements (SAS, 2016). The chi-square test was also used to determine association between prevalence of GIN, vegetation types and months of sampling. The study complied with the standards required by the Animal Research Ethics Committee of the University of KwaZulu-Natal (Reference Number: 1434/018D). Weaned goat kids in the forestland had higher ($p < 0.05$) BCS, BW and lower FEC compared to those in grassland, due to a wide variety of evergreen and nutritious trees and shrubs in forestland compared in grassland. Generally, a higher ($p < 0.05$) prevalence of GIN were recorded between January and February. The prevalence and counts of *Strongyloides* and *Nematodirus* eggs were low in March and April on both vegetation types. Weaned goat kids aged from 5 to 12 months showed a higher FEC than 2–4 months. In conclusion, weaned goat kids in the grassland were more susceptible to GIN infestations than those in the forestland, suggesting the need to develop GIN control strategies that are unique to each vegetation type.

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Biosecurity measures and their impact on health performance -on small-scale broiler farms in Limpopo province

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Poultry disease management involves biosecurity practices, medication and mitigation strategies. Biosecurity measures consist of a combination of systems and practices designed to reduce the burden of disease-causing agents on farms and thereby prevent the adverse effects of diseases. Improving farm biosecurity is one of the most important ways the poultry industry can reduce disease incidence while enhancing productivity. However, it is equally important to determine whether these improvements translate into increased farm profitability. Although most biosecurity interventions are relatively inexpensive, farmers must understand the required management changes and be willing to implement them effectively. This study examined the use of biosecurity practices and their impact on health performance among small-scale broiler producers in Limpopo Province, South Africa. The study was conducted in all five districts of the Limpopo province namely Capricorn, Mopani, Sekhukhune, Vhembe and Waterberg. A simple random sampling method was used to select 124 small broiler farmers. The study was submitted and approved by the Tshwane University of Technology Ethics committee (Ref: AREC2021/10/007). Data were collected through face-to-face interviews using a structured questionnaire and analysed using Frequency procedures of SAS. The majority (86 %) of respondents vaccinated their flocks; however, inadequate quality control during vaccine storage and transportation was identified as a major cause of vaccine failure. Majority (69 %) of the respondents indicated that coccidiosis affected their broiler chickens at the age of 4 weeks old. While 33 % of the respondents reported that lameness, respiratory illnesses and diarrhoea affected their broiler chickens at 6 weeks old. Regarding biosecurity practices, 53.23 % of broiler farms provided antiseptic footbaths, and those without footbaths cited lack of resources and knowledge. The observed 53 % of the small-scale broiler farmers are implementing biosecurity measures, and over 80 % farmers are vaccinating their birds, which indicates that Limpopo Province small-scale broiler production is not at risk of frequent outbreaks of diseases. However, the farmers still lack knowledge on how to handle vaccines properly. With a noticeable surge in farmers lacking knowledge on vaccination handling, it is recommended that the farmers need to be trained to improve in their chickens' health, production efficiency: essential precursors for farm profitability.

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Flock composition, production and reproductive performance of indigenous village chickens of the Limpopo province

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Indigenous village chicken production is a low-input farming system characterized by small to medium flock sizes. Flock composition has a direct impact on the reproductive performance and overall productivity of the flock, therefore balancing chicken flock composition and performance against improvement strategies becomes a first and crucial step in effective flock management for optimized production. To determine indigenous village chicken flock composition in order to gain better understanding of their reproductive characteristics and performance. The study protocol was assessed and approved by Agricultural Research Council Ethics Committee (AEC-I 2010 002). The study employed multistage sampling technique whereby Sekhukhune and Capricorn District municipalities of the Limpopo Province were purposively selected. A structured questionnaire was used to acquire general household information, breeding and flock management information from 55 households randomly selected from Sekhukhune (n=33) and Capricorn (n=22) Districts. The study was based on farmer memory as there were no records kept, as a result farmers only shared the information they recalled. The data was analyzed using FREQ and GLM Procedures of Statistical Analysis Software (SAS). Indigenous village chicken flock comprised 14.14±16.07 hens, 3.42±3.31 cocks, 3.94±4.68 pullets, 4.00±5.48 cockerels, and 13.24±9.52 chicks, with an average flock size of 33.65±31.34 chickens. There was no significance difference ($P>0.05$) between the flock sizes of the two districts. The mating ratios were 1:3.2 and 1:5.6 for Sekhukhune and Capricorn District municipalities, respectively, with the average of the districts at 1:4.1. Village chicken farmers (100%) did not share cocks, however 3.64% of the respondents did not have their own cock. For the respondents that had cocks, 88.89% were of local breed, with 88.46% of the cocks hatched and grown from the household flock. These farmers did not caponize cocks, they slaughtered or donated when they did not need them for breeding. Indigenous village chickens started laying for the first time at 6.34±2.85 months of age, and produced a total of 61.33±27.60 eggs per hen per year, with frequent eggs laid recorded at 1.06±0.30. The hens had 3.81±1.80 clutches per hen per year, they produced 14.64±4.78 eggs per hen per clutch, with clutch length at 14.28±5.21 days. Females produced 46.10±26.67 chicks per hen per year and had reproductive life span of 4.35±2.17 years. Cockerels and pullets first mated at 7.03±4.83 and 5.93±2.09 months, respectively. This study reported bigger flock sizes and higher male to female ratios, whereas traits of egg laying performance, number of clutches, and clutch length were in agreement with reports from other studies. Hens dominated the flock structure, with uncastrated cocks higher than the 1:10 mating ratio that is reported to achieve optimal egg production and fertilization rate. This higher male to female ratio can affect production due to fighting cocks. Managing flock composition and optimizing mating ratio will improve productivity in these flocks. This knowledge of the age-sex distribution of local chicken flocks at village production level can serve as a guide for developing community-based improvement strategies.

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Whole-plant nutrient and tannin characterization of Bambara groundnut (*Vigna subterranea*) as a climate smart feed resource for sustainable livestock production

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Escalating feed costs, climate variability, and increasing competition between human food and animal feed systems demand innovative and sustainable alternatives for livestock nutrition. Climate-resilient, underutilized legumes such as Bambara groundnut (*Vigna subterranea*) offer potential to diversify feed resources while supporting circular and resource-efficient production systems. Although the seed fraction is relatively well studied, limited information exists on the nutritional value of other plant components, including leaves, stems, shell covers, and roots. Whole-plant characterization may enable improved biomass utilization and reduced feed food competition. This study evaluated the nutrient composition and tannin content of selected *Vigna subterranea* plant parts to determine their potential contribution to sustainable livestock feeding strategies. Seeds, leaves, stems, shell covers, and roots were harvested, oven-dried, milled, and analysed for crude protein, crude fibre, ether extract, gross energy, dry matter, ash, starch, and tannins using standard AOAC procedures. Data were analysed with SPSS software using one-way analysis of variance (ANOVA). The separation of means was done using Tukey's test. Significance was declared at $p \leq 0.05$. Nutrient composition differed significantly ($p \leq 0.05$) among plant parts, highlighting functional diversity within the crop. Seeds contained the highest crude protein ($21.4 \pm 0.08\%$) and starch ($40.9 \pm 0.16\%$), confirming their suitability as energy-protein feed ingredients. Leaves exhibited high dry matter ($96.1 \pm 0.14\%$) and gross energy (18.6 ± 0.42 MJ/kg), indicating potential as supplementary forage. Roots recorded the highest crude fibre ($35.0 \pm 0.28\%$) and ash ($12.7 \pm 0.41\%$), suggesting mineral contribution but possible digestibility constraints. The high fibre fractions in roots and shell covers indicate potential suitability for ruminants, while the higher protein and starch content of seeds supports their use in monogastric diets. Tannin concentrations were highest in leaves ($1.2 \pm 0.00\%$) and shell covers ($0.7 \pm 0.05\%$) and lowest in seeds ($0.1 \pm 0.00\%$), suggesting that processing may be required to optimize inclusion levels, particularly in monogastric. *Vigna subterranea* plant demonstrates potential as a climate-smart alternative feed resource. Strategic processing and targeted inclusion could enhance its value, contributing to resilient, diversified, and future-oriented livestock production systems.

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Impact of anti-tick vaccination on cattle and pasture tick loads in an extensive beef system

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Increasing resistance of ticks to acaricides poses a significant challenge to livestock health and sustainable parasite management. Vaccination of cattle using concealed tick antigens derived from tick organs represents a potential alternative strategy that may exert effects on both the host animal and the environmental reservoir of ticks. This study evaluated the efficacy of an anti-tick vaccine in reducing tick burdens on cattle and in associated pastures under extensive grazing conditions. The trial was conducted over a 28-month period at the Bathurst Experimental Station (33°30'14"S, 26°49'26"E) under Döhne Ethical Certification No. 14/2017. Twenty Bonsmara cows were randomly allocated to a vaccinated (n = 10) or control group (n = 10) and managed under identical conditions on separate 1-ha kikuyu (*Pennisetum clandestinum*) pastures. The vaccine comprised antigens derived from organs of multiple endemic tick species, combined with a nucleic acid-based adjuvant and an immune enhancer (Institute for Disease Control Africa). Animals received a 28 mg vaccine dose containing 10 µg adjuvant, followed by a booster at 21 days and annually thereafter. Whole-body in situ tick counts were conducted bi-weekly for the first 16 months and monthly thereafter. Acaricide treatment was applied when infestations exceeded 50 engorged adult ticks per animal. Pasture tick populations were assessed monthly using six 100-m flannel drag samples per camp, with collected ticks preserved in 70% ethanol for identification and enumeration. Tick species recorded on cattle included *Rhipicephalus decoloratus/microplus*, *R. appendiculatus*, *R. evertsi evertsi*, *Hyalomma* spp., *Amblyomma* spp. and *R. simus*, while *Hyalomma* spp. was not detected in pasture samples. Vaccinated cows had significantly lower ($p < 0.05$) mean tick counts for *R. appendiculatus* (3.69 ± 4.84 vs. 5.29 ± 5.07), *R. evertsi evertsi* (0.62 ± 1.16 vs. 1.10 ± 1.57), *Amblyomma* spp. (6.82 ± 7.04 vs. 10.86 ± 8.97) and *R. simus* (15.51 ± 7.47 vs. 16.81 ± 7.98) as compared to the control group. Lower counts were also observed for *R. decoloratus/microplus* (5.64 ± 10.07 vs. 6.73 ± 7.21) and *Hyalomma* spp. (0.02 ± 0.25 vs. 0.04 ± 0.41), although these differences were not statistically significant. Pastures grazed by vaccinated cattle consistently exhibited lower tick populations, with *R. evertsi evertsi* being significantly reduced (7.79 ± 4.45 vs. 11.11 ± 5.33). Positive but non-significant correlations ($r = 0.614\text{--}0.616$) were observed between animal and pasture tick populations. Anti-tick vaccination significantly reduced infestations of several economically important tick species on cattle and was associated with reduced pasture tick burdens. These findings support the potential of anti-tick vaccination as a sustainable, integrated alternative to chemical tick control in extensive beef production systems.

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The effect of climate patterns on prenatal reproductive performance and pre-weaning kid losses of Boer goats at the Adelaide Research Center, Eastern Cape, South Africa

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The potential influence of climate on livestock reproductive performance is undisputed, and adaptation will be essential under climate change scenarios. Increased ambient temperatures and erratic rainfall with subsequent humidity changes, may adversely affect the reproductive efficiency of Boer goats in South Africa through reduced conception rates and increasing pre-wean kid mortality. The objective of this study was to determine whether climatic conditions have influenced prenatal reproductive performance in does and the incidence of pre-wean kid losses at the Adelaide research station of Döhne ADI. The study utilised production and climatic data (Ethical certificate 01/2003) collected at the Adelaide research station (32°40'S, 26°17'E). Records of Boer goat prenatal and pre-weaning reproductive traits from 2010-2025 (excluding 2011 for prenatal data) together with climatic data for the same period, were analysed to identify historical trends. Four reproductive traits were evaluated in relation to climatic variables. Conception rate and kidding percentage were assessed as primary reproductive indicators. Prenatal reproduction was defined as a categorical trait comparing real-time ultrasound scan conception outcomes with the subsequent birth status (1270 observations). Pre-weaning kid losses (1116 observations) were expressed as the number of kids lost per doe prior to weaning. Climatic variables included annual total rainfall, annual mean maximum temperature, and annual mean maximum relative humidity, which were correlated with reproductive performance prenatal and pre-weaning. Over the 15-year study period, conception rate exhibited a slight increasing trend, whereas kidding percentage showed a marginal decline. Notably, during the most recent seven years, kidding percentage decreased steadily ($b = -1.18$; $R^2 = 0.89$). Year of measurement had a significant ($P < 0.05$) effect on both prenatal reproductive performance and the number of pre-weaning kid losses. Prenatal reproductive performance remained relatively constant, while the pre-wean kid losses increased slightly. During the same period, annual total rainfall declined, whereas annual maximum temperature and the annual relative maximum humidity showed slight increases. However, no significant correlations were detected between conception rate, kidding percentage, prenatal reproductive performance, pre-wean traits and the climate variables considered. Although no pronounced climatic shifts were evident during the study period, ongoing monitoring remains essential, as subtle long-term climatic changes may be difficult over relatively short timeframes. While kidding percentage declined and a slight negative trend was observed in the pre-weaning kid losses, conception rate, prenatal reproductive performance and pre-weaning kid losses were not significantly affected by the climatic conditions during the recording period. These findings suggest that the Boer goats at the Adelaide Research Centre are well adapted to their prevailing environment.

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Shifts in the distributional ranges of *Rhipicephalus (boophilus)* ticks in South Africa: Displacement of the native tick, *Rhipicephalus decoloratus* by the invasive cattle tick, *Rhipicephalus microplus* in communal areas of the Eastern Cape

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In addition to the threat of infestation by indigenous ticks and the diseases they transmit, cattle in several countries on the African continent are put at risk by the introduction and spread of the Pantropical blue tick (*Rhipicephalus microplus*). The to establish to what extent the native tick species *Rhipicephalus decoloratus* has been displaced by the invasive introduced tick, *Rhipicephalus microplus* at two communally grazed areas in the Eastern Cape Province, South Africa. Before data collection, ethical approval was obtained from the University of South Africa's Animal Research Ethics Committee (Ref #: 2025/CAES_AREC/7719). Ticks were collected quarterly from 20 cattle over a period of 12 months at each locality. During tick sampling, cattle were restrained in a crush pen. Ticks were collected mainly from one side of the animal, including half the head and one ear, but also from the whole of the upper perineum and tail brush. Forceps were used for collecting adult ticks from the cattle skin and after each collection, ticks were stored in 70% ethanol in a labelled glass vials for later identification and counting. A total number of 17 691 ticks were collected and from these about 17 393 was *R. microplus* (98.32%) followed by 298 *R. decoloratus* (1.68%). Significantly ($P < 0.01$) higher numbers of *R. microplus* were found throughout the four seasons at Wesley; during summer (144.70 ± 7.27), autumn (101.35 ± 10.31), winter (46.75 ± 4.23) and spring (143.45 ± 9.65). Furthermore, similar results were obtained from Gcinisa for summer (108.35 ± 4.27), autumn (117.75 ± 2.83), winter (67.20 ± 5.01) and spring (140.10 ± 4.77) between the two localities compared *R. decoloratus* which was only significant ($P < 0.05$) in Wesley. A study conducted in the Eastern Cape reported that it was possible that *R. microplus* being selected for resistance against amitraz, the acaricide in use at both localities and this eventuality would further enhance its potential as an invasive species. Therefore, this could mean that the displacement was fast in the communal grazing than commercial spaces because of uncontrolled movement of different animal species. These results support the phenomenon of displacement of indigenous ticks by the pantropical blue tick, *R. microplus*. It is evident that *R. microplus* was continuing to displace the native tick and this has implications for diseases transmission caused by its pathogen, *Babesia bovis* which was more virulent than the African counterpart. Thus, this study recommends that future study focuses on the acaricide resistance of the *R. microplus* ticks in the localities to find ways to reduce the abundance of these ticks.

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Daily manure production impact on anaerobic biogas digester design for small-scale pig farmers in Gauteng

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Piggery manure waste is considered as one of the most important causative agents of environmental pollution in the form of water, soil or air pollution. The benefits of installing biogas digesters at a pig farm include a localized and affordable way of waste and odor management, self-energy generation, a reduced energy bill and production of organic fertilizer. Pig slurry has been found to be a suitable substrate for biomethane production. The studies focused on biochemical methane potential, degradation kinetics, and process optimization. In this study, a biogas digester was designed based on pig herd dynamics data and manure samples collected over a period of a year from six smallholder pig farmers across three regions of Gauteng province. The digester design was guided by specifications in the Agriculture Research Council Digester Manual. The design steps involved calculations of: 1) amount of pig manure produced daily; 2) digester volume; 3) amount of biogas produced daily; 4) gas storage capacity, and 5) effluent storage requirements. The amount of pig manure generated daily at each farm was determined via four steps. Firstly, the daily dry matter output per pig was calculated using the daily feed intake and percentage dry matter digestibility. Secondly, pig manure samples were collected from each farm and the average total solid (TS) content for each sample was determined. Total solids values ranged between 28 to 51 percent. Thirdly the daily amount of wet manure produced per pig for each production stage was determined from the dry matter output and TS content. Lastly the total amount of pig manure generated at each farm per day was calculated by multiplying the daily wet manure generation rate per pig by the total number of pigs at that production stage and summing. The farm with the maximum biogas production capacity was Radali's farm with a biogas production potential of 2.12 m³/day. It also had the biggest digester size of 18 m³ while Diphoko farm pig manure produced could only sustain a 3.24 m³ digester volume. However, after monitoring production on the farms, Makoko farm consistently maintained pig production over the period under review whereas the other farmers reduced production, and consequently their manure production. Daily biogas production ranged from 3.24 m³/day to 13.04 m³/day. A comparison of daily biogas production capacity of the biogas plants to the average daily biogas energy demand showed that the biogas produced would not meet the demand necessitating a need to obtain additional manure from nearby farmers or using other feedstock types for co-digestion. Daily biogas production capacity is very low to meet basic energy demand or requirements for basic lighting or cooking, therefore there is a need to increase manure production or supplemental feeding from other feedstock types for co-digestion. The cost of biogas digester in combination with low manure production capacity can be barriers. However cooperative model and farmers pooling of manure to feed digesters.

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The impact of temperature and humidity on aflatoxigenic *Aspergillus* species in broiler feeds

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Aflatoxins, a toxic secondary metabolites produced predominantly by *Aspergillus flavus*, pose a significant threat to feed safety, animal health, and productivity. Under changing climatic conditions, fluctuations in temperature and moisture are increasingly influencing fungal proliferation and mycotoxin contamination in feed systems, thereby affecting the sustainability of poultry production and the broader agricultural value chain. This study aimed to evaluate the impact of temperature and humidity variations conditions on aflatoxin biosynthetic gene expression in aflatoxigenic *Aspergillus* species isolated from broiler feeds. Aflatoxigenic *Aspergillus* isolates were inoculated into starter, grower, and finisher broiler feed samples and incubated under controlled environmental conditions, including temperatures (12°C, 25°C, 35°C, and 41°C) and moisture levels (10%, 12%, and 15%) over 42 days. Gene expression of key aflatoxin biosynthetic genes (aflR, aflD (nor), aflP (omt), and aflM (ver)) was assessed using PCR and gel electrophoresis. Aflatoxin production was quantified and correlated with environmental conditions. Ethical clearance was obtained in accordance with institutional research guidelines. Environmental conditions significantly influenced gene expression and aflatoxin production, demonstrating the sensitivity of mycotoxin biosynthesis to climate variability. The regulatory gene aflR showed inconsistent expression, with reduced activity at 12% moisture and 25°C, corresponding to lower aflatoxin levels, particularly in starter feeds during early incubation (Days 4–8). The structural gene aflD was consistently expressed across all treatments, confirming its fundamental role in aflatoxin biosynthesis. Expression of aflP and aflM increased at higher moisture (15%) and moderate temperatures (25–30°C), corresponding with elevated aflatoxin accumulation, especially in grower and finisher feeds during Days 12–14. Higher temperatures ($\geq 35^\circ\text{C}$) suppressed aflR and aflM expression, suggesting thermal inhibition of toxin synthesis. Moisture was identified as the dominant factor influencing aflatoxin production. These findings highlight the importance of integrating environmental monitoring and molecular tools in managing feed safety under climate change conditions, supporting innovation in animal production systems. The study clearly demonstrates that environmental variability, particularly fluctuations in temperature and humidity, significantly influences aflatoxin biosynthesis in broiler feeds. Among these factors, moisture emerged as a critical regulatory determinant, strongly affecting fungal growth and toxin production. Elevated humidity levels create favourable conditions for *Aspergillus* proliferation, thereby increasing the risk of aflatoxin contamination in stored feed. The findings emphasize the importance of integrating improved feed storage practices with effective environmental control strategies to mitigate contamination risks. These results also contribute to the development of climate-resilient and sustainable poultry production systems. By addressing the impact of environmental variability on feed safety, the study reinforces the role of animal science in responding to emerging challenges across the agricultural value chain, particularly in the context of climate change, food storage and security.

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Dynamic systems interactions shaping indigenous chicken productivity in South Africa

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Productivity in indigenous chicken systems is shaped by interacting management practices, disease ecology, predation pressure, household resources, and environmental conditions. However, most studies examine these factors in isolation, limiting a system-level understanding of how they jointly structure production systems in smallholder contexts. The aim of this study was to characterize structural patterns in indigenous chicken production systems by integrating epidemiological, management, socio-economic, and spatial variables to identify underlying system structure. A cross-sectional survey of 967 households was conducted across five districts of KwaZulu-Natal, South Africa (uMkhanyakude, Zululand, eThekweni, Ugu, and uThukela). Data on socio-economic characteristics, production practices, and production constraints was collected. Statistical Package for the Social Sciences (SPSS) was used for the two-step cluster analysis and Multiple Correspondence Analysis (MCA). Model adequacy was assessed using Akaike's Information Criterion (AIC), Schwarz's Bayesian Information Criterion (BIC), and silhouette coefficients. The MCA was used to identify latent dimensions and describe system structure. Predation, disease, feed shortages, housing limitations, and theft were identified as the dominant production constraints. The uMkhanyakude district exhibited significantly higher ($P=0.001$) incidence of combined aerial predators, wild animals, and reptiles, reflecting spatial ecological heterogeneity. In contrast, disease profiles, predator categories, and market participation patterns were broadly similar across districts. Two-step cluster analysis suggested a two-cluster solution based on AIC and BIC values; however, the very low silhouette coefficient (0.025) indicated weak and poorly separated clusters, suggesting that production systems are not well represented by discrete typologies. In contrast, MCA revealed two reliable latent dimensions (Cronbach's $\alpha = 0.869$ and 0.847), jointly explaining 61.3% of total inertia. Dimension 1 captured socio-spatial context (district, gender, land occupation), while Dimension 2 represented a management and resource-use continuum characterized by feeding practices, housing, disease control, transport access, and income. Market participation contributed minimally to both dimensions, indicating that it is an emergent rather than a primary structuring system characteristic. Indigenous chicken production systems in KwaZulu-Natal are best understood as continuous, multi-dimensional systems structured by interacting socio-spatial and management gradients rather than discrete typologies. These findings highlight the need for integrated, context-specific interventions addressing nutrition, disease control, housing, and predator management to improve productivity in smallholder systems.

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Chemical composition of *Vachellia erioloba* pods silage treated with bacterial inoculant, molasses and Nano-ZnO for use as an antibiotic alternative in indigenous chickens

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Vachellia erioloba (VE) pods, a readily available agroforestry resource in Southern Africa, have been explored for their potential as a nutritious feed ingredient for indigenous chickens. The pods are rich in protein, fibre and bioactive compounds like tannins, which may confer antimicrobial properties. With the increasing demand for antibiotic-free poultry products and growing concerns about antimicrobial resistance, VE pod-based silage offers a promising alternative to conventional antibiotics growth promoters. Indigenous chickens are well-adapted to local conditions, and could benefit from this cost-effective, locally sourced feed additive, enhancing their overall productivity, while reducing reliance on conventional antibiotic. The aim of this study was to evaluate the effects of treating *Vachellia erioloba* pods silage with bacterial inoculant, molasses, and Nano-ZnO on its chemical composition and to assess its potential as a natural alternative to antibiotic growth promoters in indigenous chickens. The milled pods were ensiled with and without a bacterial inoculant (2 g/kg), molasses (0%, 3%, and 6%) and Nano-ZnO (0, 25, and 125 mg/kg) for 55 days, with each treatment replicated 3 times, in a 2 x 3 x 3 factorial experiment in a completely randomised design (CRD). Silage samples were then taken for chemical analysis. (Ethic no. NWU-01205-25-A5). Ensiling increased ($P < 0.05$) the dry matter (DM), crude protein (CP), phenol, calcium (Ca), and copper (Cu). whilst it decreased ($P < 0.05$) the condensed tannins content of the pods. The highest CP content (14.94%) was observed in ensiled pods treated with 0 g/kg bacterial inoculant, 3% molasses, and 0 mg/kg Nano-ZnO. Condensed tannins content decreased ($P < 0.05$) in pods treated with 2 g/kg bacterial inoculant, 0% molasses, and 125 mg/kg Nano-ZnO. Phenol content increased ($P < 0.05$) in pods treated with 0 g/kg bacterial inoculant, 6% molasses, and 125 mg/kg Nano-ZnO. Silage treated with various combinations of bacterial inoculant, molasses, and Nano-ZnO showed increased levels of calcium. VE pods treated with 2 g/kg bacterial inoculant, 6% molasses, and 0 mg/kg Nano-ZnO exhibited increased Cu content. The study demonstrated that silage produced from VE pods can be successfully enhanced through the application of bacterial inoculant, molasse, and Nano-ZnO. Chemical composition analysis indicated improvements in crude protein retention, reduced fibre fractions and enhanced mineral availability, particularly zinc content in Nano-ZnO- treated silage. Therefore, based on its proximate composition and inherent phytochemical potential, VE pod-based silage demonstrated efficacy as a natural feed additive that could contribute towards reducing reliance on conventional antibiotic in indigenous chicken production systems.

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Impact of varying levels of ascorbic acid on quality attributes and shelf life of beef and pork during simulated retail display

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Red meat is highly susceptible to deterioration during retail display due to lipid oxidation, myoglobin oxidation and microbial proliferation, resulting in colour loss and reduced consumer acceptance. Colour stability, particularly maintenance of oxymyoglobin, is a primary determinant of purchasing decisions. The increasing demand for clean-label meat products has intensified interest in natural antioxidants. Ascorbic acid (vitamin C) functions as a reducing agent that stabilises oxymyoglobin and delays lipid oxidation. However, limited dose-response studies comparing beef and pork under simulated retail conditions are available. The aim of the study was to evaluate the effect of varying concentrations of ascorbic acid on pH and instrumental colour attributes of beef and pork during refrigerated retail display and shelf-life extension. Fresh beef and pork samples were randomly allocated to three treatments: control (0%), 0.5% ascorbic acid (w/w), and 1.0% ascorbic acid (w/w). Samples were displayed aerobically in a commercial refrigerated display unit (HYC-410) maintained at $4 \pm 1^\circ\text{C}$ under continuous fluorescent lighting (~ 1000 lux). The pH was measured using a calibrated benchtop pH meter. Instrumental colour (L^* , a^* , b^*) was determined using a Tintometer Spectrocolorimeter (LC 100) following white-tile calibration. Chroma and hue angle were calculated from a^* and b^* values. The experiment followed a completely randomised design with repeated measures over 14 days of storage. Data were analysed using a linear mixed-effects model in IBM SPSS Statistics version 29. Species, treatment, storage time and their interactions were included as fixed effects, while the sample was treated as a random effect to account for biological variability. Mean separation was performed using Tukey's post hoc test, and significance was declared at $P < 0.05$. Ethical approval was applied for and granted by the University of Mpumalanga Research Ethics Committee (UMP/CHITIMA222510773/SAS/BScAgric/2025/01). Ascorbic acid significantly improved redness (a^*) retention and reduced discolouration compared to the control ($P < 0.05$). Treated samples exhibited lower hue angle shifts, indicating delayed metmyoglobin formation. The 0.5% treatment was most effective for pork, while beef showed greater oxidative stability at 1.0%, reflecting species-specific differences in myoglobin concentration and lipid composition. Untreated samples displayed rapid colour deterioration consistent with oxidative degradation patterns reported in retail meat systems. The antioxidant effect of ascorbic acid is attributed to its electron-donating capacity, which interrupts free radical propagation and regenerates oxymyoglobin. Ascorbic acid effectively enhanced colour stability and delayed oxidative deterioration in beef and pork during simulated retail display. Optimal concentrations differed between species, with 1.0% recommended for beef and 0.5% for pork under the conditions evaluated. These findings support the application of natural antioxidants as clean-label strategies to extend red meat shelf life and reduce post-harvest losses.

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Field evaluation of monitoring tools for dairy fly burden assessment

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Arthropods like flies, ticks, lice, and mites are common pests in livestock. Lachryphagous flies impact bovine ocular health and animal welfare, as well as the goals of cost-effective and sustainable agriculture and food security. Species of the subgenus *Eumusca* (*Musca autumnalis*, *M. xanthomelas*, *M. lusoria*, *M. nevillei*) are pasture-associated and show regional and seasonal variation. In contrast, *M. domestica* breeds in dung and organic waste near homesteads and feedlots. These species feed on ocular and nasal secretions of cattle and act as mechanical pathogen vectors. Single-modality fly control strategies, heavily reliant on pesticides, are unsustainable and ineffective due to resistance development, disruption of natural biological control, ecological impact, and potential negative influences on livestock health. Integrated pest management (IPM) of *Musca* species combines breeding substrate management and biological control with a threshold-based chemical intervention approach applied only as a last resort to preserve natural enemies. To be able to apply IPM, efficient fly monitoring is critical. The aim of the study was to develop and evaluate cost-effective, farm-applicable monitoring strategies for quantifying lachryphagous fly burden on dairy farms to support integrated pest management. A pilot study was conducted to evaluate fly-trap colour (yellow, blue, and white/pink), size, placement, and exposure duration. Traps made from Coroplast were constructed in various dimensions and deployed across livestock operational areas. Fly counts were performed using a mask counting grid to record fly bodies, heads, and wings. Sampled fly genera were identified using IdentiFly software in combination with wing venation patterns. During the test phase of nine months (April–January), fly burden was assessed across five commercial dairy farms in the Western Cape using sticky card traps and face counts. Optiroll Yellow (Insect Science) traps were used for their higher attraction, while Aptaor Fly Curtain C60 (DeLaval) white/pink traps were included for sustained adhesiveness. Face counts were obtained from digital photographs of both sides of each cow's face after a 30-second post-restraint settling period, with concurrent meteorological data considered. Farms were sampled at 30-day intervals to reduce operational disruption. Data from both methods were integrated into a Weighted Fly Burden Index (WFBI), using a 2:1 ratio of face-count to trap-based indices. Approved by University of Pretoria Veterinary Ethics Committee (REC113-23). WFBI values demonstrated clear and biologically expected seasonal trends across all farms, confirming that the integrated monitoring method functioned effectively. Fly burden declined from early winter peaks (Farm 1: 7.85 in May–June; Farm 2: 6.45; Farm 5: 5.48) to consistent mid-winter minima (all farms ~3.8–4.3 in June–August), followed by pronounced spring increases (Farm 3 rising to 7.85 in November–December; Farm 1 to 8.21 in December–January). Detection of these parallel seasonal patterns validates the method's reliability for field conditions. Face-count photography offers a fast, low-cost option for farmers, while sticky-trap genus identification supports consultants needing finer taxonomic resolution. These findings enable development of integrated fly-control programmes, combining chemical and non-chemical strategies for more sustainable pest management. Fly activity can be monitored reliably using simple counts on livestock and sticky traps. This supports a targeted, threshold-based integrated pest management principles, leading to sustainable fly management strategies, ultimately guiding farmers toward more sustainable, targeted, and effective fly control practices.

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The effect of *Berchemia discolor* (Muni tree) leaf meal on gastrointestinal nematode infections of South African non-descript goats

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Gastrointestinal parasites such as *Haemonchus contortus* reduce goat productivity by increasing mortality, lowering fertility, and resulting in poor health, particularly in resource limited-farming systems. Due to the high cost and limited access to commercial anthelmintics, alternative strategy such as *Berchemia discolor* is needed. This study aims to investigate the impact of *Berchemia discolor* leaf meal (Muni tree) on gastrointestinal nematode infections in South African non-descript goats. It was hypothesised that the *Berchemia discolor* leaf meal (Muni tree) has no effect on gastrointestinal nematode infections in non-descript goats. The study was conducted at the University of Limpopo's Animal. Sixteen yearling intact male goats were randomly assigned to four dietary treatments (BFL_0 , $BFL_{1.5}$, $BFL_{2.0}$, and $BFL_{3.0}$ kg inclusion levels) in a completely randomized design. Goats were housed individually and fed for 37 days. Faecal samples were collected at the end of the trial and analysed for parasite load. Data were analysed using ANOVA in Statistical Package for the Social Sciences (SPSS), version 29. Dietary supplementation significantly affected ($P < 0.05$) parasite prevalence. *Strongyloides* were absent in goats receiving $BFL_{2.0}$ kg and control diets but were highest in the and $BFL_{3.0}$ kg group. *Trichuris* sp. prevalence was highest in the control group and lowest in the $BFL_{1.5}$ kg group. Oocyst counts were lowest at the $BFL_{2.0}$ kg inclusion level, suggesting improved parasite control at moderate supplementation. *Berchemia discolor* leaf meal influenced gastrointestinal parasite dynamics, with the $BFL_{2.0}$ kg inclusion level showing the most consistent reduction in parasite indicators. However, responses varied among parasite species, indicating that its effectiveness depends on dosage and parasite type. Further research is required to confirm its practical application as a natural parasite control strategy.

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The effect of canola oil on intrinsic methane production and the performance of feedlot lambs

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Canola oil has been shown to contain bioactive compounds with potential anti-methanogenic properties in ruminants. The study investigated the effects of dietary canola oil inclusion on growth performance, feed efficiency, and enteric methane emissions in feedlot lambs. To assess the effect of canola oil supplementation on *in vivo* methane emissions from feedlot lambs and to examine the effect of canola oil supplementation on production parameters of feedlot lambs. Thirty-eight Merino ewes with an average initial body weight of 26 kg were randomly allocated to four dietary treatment groups: (1) 0 g canola oil per kg DM (T1; control), (2) 20 g canola oil per kg DM (T2), (3) 40 g canola oil per kg DM (T3), and (4) 60 g canola oil per kg DM (T4). The trial was conducted over seven weeks, with weekly measurements of dry matter intake (DMI) and body weight, and daily methane emissions measured using laser methane detection technology. Ethical clearance for this study was obtained from Stellenbosch University Research Ethics Committee: Animal Care and Use (ACU-2024-29331). Canola oil inclusion significantly affected animal performance parameters. Final body weight was highest ($P = 0.002$) for T3 (43.7 kg) and lowest for T4 (38.9 kg), while T3 did not differ from T1 and T2. Average daily gain (ADG) followed a similar pattern ($P = 0.019$), with T3 recording the highest ADG (0.26 kg/d) and T4 the lowest (0.20 kg/d). A higher ($P = 0.006$) feed intake was observed for T3 (1.53 kg/d) compared to 1.38 kg/d, and 1.29 kg/d for treatments T1, T2 and T4, respectively. No differences among treatments were observed for feed conversion ratio (FCR). Regarding methane emissions, no differences were observed among treatments for methane production, in either grams per day, grams per kilogram bodyweight per day or grams per kilogram DMI per day. This could be related to the type of methane measurement that was used and that the laser instrument might not have been sensitive enough. Initial hourly observations showed some reduction in methane emissions across treatment groups within individual weeks, but overall, no consistent response to canola oil addition was found. This was likely due to changes in enteric fermentation that were insufficient to reduce methane production significantly. This study concluded that canola oil can successfully be included in lamb feedlot diets at rates up to 40 g/kg DM without compromising growth performance or feed efficiency but would be more expensive than the control feed. Under the conditions of this study, canola oil supplementation was unsuccessful in reducing methane emissions when included at levels of up to 60 g/kg DM in feedlot lamb diets. Therefore, further research is needed to understand how oil supplementation can be used to maintain animal performance and reduce methane emissions under feedlot conditions.

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The effect of canola oil on *in vitro* ruminal gas production kinetics

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Dietary lipid supplementation, particularly with oils rich in unsaturated fatty acids, has shown potential for mitigating enteric methane emissions from ruminants. This study evaluated the effects of incremental levels of crude canola oil inclusion on *in vitro* total gas and methane production kinetics. To determine the effect of canola oil supplementation on total *in vitro* gas production kinetics and to evaluate the effect of canola oil supplementation on *in vitro* methane production kinetics. Four experimental substrates were prepared by replacing maize with crude canola oil at 0 g/kg dry matter (DM), (T1; control), 20 g/kg dry matter (T2), 40 g/kg dry matter (T3), and 60 (T4) g/kg dry matter in a mixed sheep feed. Substrates were incubated with bovine rumen fluid as inoculum using an automated methane potential test system (AMPTS III) in a completely randomized design with six replicates. Total gas and CO₂ production were measured directly, and methane production was estimated by difference. Cumulative gas production data were fitted to modified Gompertz and Ørskov-McDonald models to derive kinetic parameters. Ethical approval for this study was granted by the Animal Care and Use Committee of the Stellenbosch University (ACU-2024-29931). Maximum total gas production (b) decreased significantly ($P < 0.05$) with increasing canola oil inclusion, with T4 producing 18-19 % less total gas than T1. The maximum rate of total gas production (kmax) decreased ($P < 0.001$) progressively from T1 (0.300 Nml/g DM per minute) to T4 (0.187 Nml/g DM per minute). Similarly, the maximum rate of methane production declined ($P = 0.011$) from T1 (0.181 Nml/g DM per minute) to T2 - T4 (0.131-0.149 Nml/g DM per minute), but canola oil treatment did not decrease absolute methane volumes. The ratio of methane to total gas also did not differ significantly across treatments. The parallel reductions in total gas production and methane production rate (kmax), combined with the constant methane:total gas ratio, indicate that the primary effect of canola oil was a general inhibition of ruminal fermentation rather than specific anti-methanogenic activity. The observed reductions in fermentation rate and total gas production, particularly at 60 g/kg DM inclusion, likely result from inhibitory effects of unsaturated fatty acids on ruminal microorganisms and potential coating of feed particles, reducing substrate accessibility. This may ultimately negatively impact nutrient availability and animal performance. Based on the current *in vitro* findings the viability of crude canola oil as an effective methane mitigation strategy remains questionable and requires careful *in vivo* validation before practical recommendations can be made for its use in ruminant production systems. Therefore, further studies are needed to understand the implications of using oil supplementation as a way of combating methane emissions from ruminants.

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Quantifying the relationship between fleece colour and objective and subjective wool characteristics

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Subjective fleece colour refers to the visual assessment of wool brightness, whiteness, or yellowness in the fleece. It is an important quality attribute because it affects the dyeing performance, and overall market value. Wool contains natural secretions collectively known as yolk, consisting mainly of wool grease (lanolin) and suint, which can influence the subjective appearance of fleece colour. Because of the economic importance of wool colour, the trait is often included in sheep breeding and selection programs. To quantify the relationship between fleece colour and important objective and subjective wool characteristics in the Grootfontein Merino stud. Ethical clearance was obtained from the Grootfontein Animal Ethics Committee (number AP10/1/3). Data recorded from 2015 to 2023 on 1253 Merino ram and ewe progeny from the Grootfontein Merino stud were used for this study. The animals were run under natural veld conditions at Grootfontein Agricultural Development Institute near Middelburg (Eastern Cape). The traits included in the analysis were fibre diameter (FD), clean yield (CY), fleece weight (FW), wool quality (WQ), wool yolk (WY), staple formation (SF) and fleece colour (FC). The WQ, WY, SF and FC were subjectively assessed on a scale from 1 to 50, where a high score was given to an animal with good WQ and SF, more WY and whiter FC. The descriptive data and variance components were obtained with the ASREML software. Fixed effects included in the analysis were year of birth, gender, rearing status and age of the dam (years), as well as animal age (days) as a covariable. The average FC score was 30.18 ± 3.25 and the scores ranged from 5 (yellow colour) to 45 (white colour). The heritability estimated for FC was 0.23 ± 0.07 . The genetic correlations estimated between FC and FD, FW, CY, WQ, WY and SF were 0.30 ± 0.22 , 0.40 ± 0.34 , 0.12 ± 0.28 , 0.38 ± 0.25 , -0.21 ± 0.43 and 0.46 ± 0.32 respectively. From these results it is evident that animals in this stud with higher FD, more (FW) and cleaner wool (CY), better WQ and SF tend to have a whiter fleece. The relationship between FC and WY was also favourable, meaning that less WY will lead to a whiter fleece. The positive relationship between FC and FD in this study is contrary to the general idea from the literature that animals with finer wool tend to have whiter fleeces. This contradiction might be explained by the relatively large average FD reported in this study ($16.71 \mu\text{m}$; range: $12.30\text{--}21.50 \mu\text{m}$). Our results suggest that fleece colour would be improved through either direct or indirect selection. By including the subjective FC as a culling fault will therefore increase the proportion of more white fleeces in a clip. However, further research needs to be conducted to quantify the effect of subjectively assessed FC on wool processing and price.

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Repeatability and between-animal correlation between rumen and rectal temperature in South African sheep recorded during summer

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It is of interest to monitor sheep during variable heat stress conditions. Rectal temperature is a common method to assess core body temperature (CBT), but the manual measurement is marginally invasive, time-consuming, and labour-intensive. Rumen thermologgers provide an automated and continuous method of monitoring and would be an attractive proxy for rectal temperature as an indicator of heat stress response. However, the relationship between these traits needs to be validated on the animal level. The aim of the study was to investigate the between-animal (co)variance components and correlation between automatically recorded rumen temperature and manually measured rectal temperature. Data for this study were collected across two summer seasons (November to March) at Langgewens research farm located in the Swartland region of the Western Cape. The dataset included records from a total of 181 ram lambs, comprising 97 lambs in the first season (of which 64 were fitted with loggers) and 85 lambs in the second season (65 with loggers) [ACU-2023-26750]. Each animal had between 8 to 10 repeated measurements recorded for rectal temperature (T_{REC}) for both morning (A.M., low heat load) and afternoon (P.M., high heat load) periods. Rumen temperature (T_{RUM}) was recorded continuously, but the hourly means nearest to the time of recording the A.M and P.M. T_{REC} were extracted to align with the structure of the repeated measures data. Data were analysed using linear mixed models in ASREML V4.2 software, treating A.M. and P.M. observations as separate traits. Breed and sampling day were fitted as fixed factors and animal weight and coat depth as fixed covariates, where appropriate. Subsequently, animal, animal.month and sampling batch were fitted as random identity terms. The animal variance to phenotypic variance ratio was used to estimate repeatability, and a two-trait analysis was used to obtain the between-animal covariance ratio between T_{REC} and T_{RUM} . Both T_{REC} (0.20 ± 0.029) and T_{RUM} (0.17 ± 0.037) were moderately repeatable during the A.M. session. In the P.M. session, the repeatability estimates were slightly lower at 0.16 ± 0.027 for T_{REC} and 0.09 ± 0.031 for T_{RUM} . It is expected that measurements would fluctuate owing to random, short-term disturbances between sampling points, especially in the case of T_{RUM} where the effects of drinking would not have been perfectly screened from the data. However, a strong and statistically significant between-animal correlation was derived between T_{REC} and T_{RUM} for both the A.M. (0.86 ± 0.057) and P.M. (0.87 ± 0.063) sessions. This indicates that animals with relatively lower T_{RUM} also tend to display lower T_{REC} under both high and low heat load. Automatically recorded rumen temperature is repeatable and has potential for being a reliable proxy for rectal temperature in sheep heat stress studies. In addition to enabling long-term and continuous monitoring, sheep could be monitored under natural circumstances with no need for handling. Addition of new records to the dataset will allow for more precise estimates in future.

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