Sheep reproduction RD&A alert

This sheep reproduction RD&A alert is an initiative of the Sheep Reproduction Strategic Partnership (SRSP).

Papers relating to various aspects of genetics in sheep reproduction presented during the 24th AAABG Conference in early November are featured in this month's RD&A Alert. Invited papers were published in a Special Issue of Animal Production Science (Volume 61, Issue 18) and contributed papers are available from the AAABG website.

If you missed the SRSP November webinar on **breeding ewe fitness and maternal ewe mortality**, recordings of both presentations (*Reducing maternal ewe mortality* by Mary McQuillan and *Ewe fitness to join, what have we learnt from case studies* by Andrew Whale both from Livestock Logic) will soon be available to view from the SRSP website.

The SRSP aims to help sheep producers to profitability and sustainably increase lamb production through increasing lamb survival and weaning rates and will coordinate a national approach to improving sheep reproductive performance.

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Scientific papers

Ewe vaginal microbiota: associations with pregnancy outcome and changes during gestation

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Abstract

Reproductive performance is paramount to the success of livestock production enterprises focused on lamb meat production. Reproductive success is influenced by various factors, possibly including the reproductive tract microbial communities present at the time of copulation and throughout pregnancy. There are few publications that identify the vaginal microbial communities of livestock, and even fewer exist for sheep. To compare ewe vaginal microbial communities, vaginal swabs were taken from 67 Hampshire and Hampshire X Suffolk crossbred ewes from the Iowa State University sheep farm at a pre-breeding time point (S1) and after pregnancy testing (S2). Animals that were determined pregnant were sampled again within a few days of expected parturition (S3). DNA was extracted from these swabs, and 16S rRNA gene Illumina MiSeq amplicon sequencing was conducted to fingerprint the bacterial communities found within this system. Pre-breeding time point samples showed no differences in community structure between animals later found to be pregnant or non-pregnant, but significant changes were detected in species richness (Chao; $P < 0.001$) and species diversity (Shannon; $P < 0.001$) at the second sampling time point. A higher microbial diversity within the S2 time point samples may suggest a more stable environment driven by pregnancy, as this increased diversity is maintained in pregnant animals from the S2 to the S3 time point. Additionally, several bacterial

phylotypes, such as Mannheimia, Oscillospiraceae-like OTUs and Alistipes, were more abundant at either the S1 or S2 time points in animals that established pregnancy, suggesting a beneficial effect on pregnancy outcome. This study identifies changes within the microbial communities of the ewe vagina before and during gestation and offers inferences on how these changes may impact pregnancy outcome. Information presented herein offers new knowledge about sheep vaginal microbial communities and serves as a starting point to help guide researchers to improve sheep reproductive performance in the future.

Growth, body composition and body wrinkle are favourably correlated with reproductive performance in 2-8-year-old Merino sheep

Jackie Chapman (jackie.chapman@dpi.nsw.gov.au), Michelle Hebart and Forbes Brien

Abstract

Context: Despite the increased economic importance of reproductive rate in Australian Merinos, there have been low genetic improvements in reproductive performance over the past several decades. Genetically improving reproductive traits through direct selection is restricted by low heritability, low selection intensity directly on reproductive traits, high recording costs and lack of accurate maternal pedigrees in the majority of industry breeding programs. However, indirect selection via correlated traits may be useful as a supplement to direct selection or even on its own where reproduction records are not collected.

Aims: The aims of the present study were to determine whether various production and quality traits have the potential to be used as indirect selection criteria for genetically improving lifetime reproductive rate, but also whether their selection could be detrimental to reproduction via unfavourable correlations.

Methods: Reproductive traits studied included pregnancy rate (ewes scanned pregnant per ewe joined), fetal number (number of fetuses scanned per ewe joined), number of lambs born (per ewe joined), number of lambs weaned (per ewe joined) and ewe rearing ability (number of lambs weaned per fetuses scanned). Using data from the SA Selection Demonstration Flocks project (1997–2005), reproductive traits were modelled against various visual and production traits to estimate correlations.

Key results: Favourable genetic correlations with reproductive traits were estimated with adult ewe bodyweight (0.37–0.50), hogget eye muscle depth (HEMD, 0.40–0.57), fat depth (HFAT, 0.27–0.48) and hogget body (HBWS) and neck wrinkle scores (–0.13 to –0.50). However, the estimates for genetic correlations with hogget eye muscle depth and fat depth were lower when bodyweight was fitted as a covariate, being 0.11–0.35 and 0.17–0.32 respectively. Genetic correlations with ewe rearing ability were generally unfavourable (except those with hogget body and neck wrinkle scores, which were –0.24 and –0.15 respectively), but were either negligible (adult ewe bodyweight, hogget eye muscle depth, fibre diameter and fleece weight) or low in magnitude (fat depth). Unfavourable genetic correlations were observed between fibre diameter and reproductive traits (0.13–0.33). Fleece weight had negligible genetic correlations with all reproductive traits studied (–0.08 to 0.10). Predictions of response to index selection using indirect criteria of one or more of yearling weight, HBWS, HEMD and HFAT measurements projected substantial genetic gains in the number of lambs weaned per ewe joined (NLW). Without reproduction records on the dams of candidates for selection, indirect selection using all four indirect criteria (yearling weight, HBWS, HEMD and HFAT) was predicted to achieve 112–168% of the genetic gains of direct selection for NLW. When all indirect and direct criteria for NLW are combined as part of index selection, even larger gains for NLW are predicted (from 164–215% of direct NLW genetic gains).

Conclusions: Findings from the present study suggest that bodyweight, HEMD and HFAT and HBWS could be potentially beneficial as indirect selection criteria for lifetime reproductive rate. Selection for reduced fibre

diameter is potentially detrimental to reproductive performance; however, selection for improved fleece weight is unlikely to have any effect on genetic gain for reproductive traits.

Implications: Use of indirect selection for lifetime reproductive could allow for genetic gain when either used with or without the direct selection criteria of reproduction records.

Proximity sensors provide an accurate alternative for measuring maternal pedigree of lambs in Australian sheep flocks under commercial conditions

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Abstract

Context: Proximity sensors were used recently to determine the maternal pedigree of lambs on a small plot with high accuracy. If this accuracy is maintained under commercial grazing conditions, this method could be a useful alternative to improving genetic gain in sheep, including reproduction traits.

Aims: To investigate using proximity sensors to determine the maternal pedigree of lambs and to define the level of interactions required to determine maternal pedigree confidently irrespective of differences in ewe age, lamb age, birth type, paddock size, flock size or stocking rate under commercial grazing conditions.

Methods: We compared maternal pedigree determined using the proximity sensors to DNA profiling (n = 10 flocks) and lambing rounds (n = 16 flocks). Ewes (n = 7315) and lambs (n = 8058) were fitted with proximity sensors under normal grazing conditions for each property for 1–3 days. Flocks varied in ewe age (adults, hoggets and ewe lambs), lamb age (up to 100 days old, except for 1 flock), birth type (singles, multiples), paddock size (0.25–320 ha), flock size (37–420 lambs) and stocking rate (2–100 dry sheep equivalents/ha, except for 1 flock).

Key results: An interaction ratio of >2 was required for a confident ewe–lamb match (ewe with the most interactions compared with the ewe with the second-most interactions for each lamb). Using this criterion, the average success of proximity sensors at matching a lamb to a ewe was 95% and the sensors were 97% accurate when compared with the pedigree results from lambing rounds or DNA. For lambs matched successfully, over 90% of this success was achieved in the first 7 h and over 99% in the first 20 h. While the success rate of matching a lamb to a ewe was not influenced significantly by ewe age, birth type, paddock size, flock size or stocking rate, the time to achieve sensor success was significantly quicker for singles than for twins and sensor accuracy was significantly higher for smaller paddocks with higher stocking rates.

Conclusions: Our results showed that proximity sensors can establish maternal pedigree effectively and accurately across a range of conditions experienced on commercial properties.

Implications: Private industry can now develop more cost-effective sensor technologies with greater confidence that will enhance recording of maternal pedigree and, hence, the rate of genetic gain across the sheep industry.

Genetic parameters and trends for lamb survival following long-term divergent selection for number of lambs weaned in the Elsenburg Merino flock

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Abstract

Context: Mortality of new-born lambs is well known to have important implications for both animal production and welfare. Improving survival rates by genetic selection is very desirable, but the low heritability of survival traits challenges the prospect of useful genetic gain.

Aim: This study aimed to derive genetic and environmental parameters for lamb survival in the Elsenburg Merino resource flock. It also investigated correlations to possible indicator traits birthweight and birth coat score and reported genetic progress in breeding values for lamb survival following 33 years of divergent selection.

Methods: The flock was divergently selected for number of lambs weaned and was separated by the High (positive) and Low (negative) selection groups. The pedigree file identified 8138 lambs as the progeny of 273 sires and 2062 dams. The study considered total survival from birth to weaning (Tsv) that was also partitioned into perinatal survival to 3 days of age, and the remaining period. Variance components were derived by linear mixed models by using the ASREML® program. Genetic trends were derived by predicting mean breeding values for selection groups within each year and evaluated by fitting linear and broken-stick regression models.

Results: Predicted Tsv of H-line lambs (0.81 ± 0.01) was higher (P < 0.01) than that of L-line lambs (0.68 ± 0.01). Heritability was significant but low for survival traits (0.03–0.07), moderate for birthweight (0.16) and high for birth coat score (0.54). Genetic trends of the H-line trended divergently (P < 0.01) to the L-line for survival traits, but a changepoint (P < 0.01) in trend suggested that the H-line reached a selection plateau following 19–22 years of selection. Preceding this period, the rate of genetic change equalled ~1% of the mean for Tsv.

Conclusions: Despite the low heritability of survival, the genetic trends reported in this study contradicted the premise that genetic selection is not a worthwhile method to reduce incidences of lamb mortality.

Implications: It is recommended that lamb survival phenotypes should be recorded and incorporated into indices individually where possible, but composite traits are a viable alternative.

Single-step genomic evaluation of lambing ease in Australian terminal sire breed sheep

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Abstract

Context: Australian sheep breeding values (ASBVs) for the categorical trait of lambing ease are routinely estimated by Sheep Genetics via a threshold model. This has been pedigree-only, and has not utilised genomic information.

Aim: The present study aimed to update the genetic evaluation model and parameters for lambing ease for terminal sire sheep (dominated by White Suffolk and Poll Dorset breeds). The model includes correlations with birthweight and gestation length. Cross-validation was used to determine the value of the improved models and the inclusion of genomic information.

Methods: New data-preparation pipelines were developed to accommodate improved data-filtering methods and contemporary group construction. Genetic parameters, including correlations among traits, were estimated using continuous and threshold models, with various combinations of effects in mixed animal models. Cross-validation of breeding values was performed against progeny performance, by using forward prediction.

Key results: The increased volume of data, improved data preparation steps and enhanced evaluation software now allow a more complex model to be fitted, including maternal, sire by flock-year and genetic group effects, which were significant for all traits, along with the inclusion of multiple sire groups in the pedigree. However, the inclusion of the direct-maternal covariance and sire by flock-year terms resulted in unrealistically inflated estimates of some components, and thus the final covariance matrices required some adjustments. Cross-validation of breeding values was performed against progeny performance using forward prediction. For all traits, the phenotype accuracies and estimated breeding value correlations were higher from the new model without genomics than were those from the current routine evaluation. The benefit from including genomic information based on cross-validation is minimal currently but is expected to improve as the size of the reference population grows. Further work is required to define acceptable data-quality thresholds for the construction of datasets for routine breeding value estimation.

Conclusions: The new model and parameters resulted in ASBVs with an improved predictive ability, with increased accuracy and reduced bias compared with the current analysis. Furthermore, a small increase in accuracy was observed for all traits from utilising genomic information in the model.

Implications: The new genetic evaluation procedures and models will be used to update those being applied in the routine Sheep Genetics evaluation system and also support further index development for the terminal sire breeds in Australia.

Phenotypic trade-offs between lambs and wool reflect weak antagonistic genetic correlations between reproductive and wool traits

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Available from AAABG 24th Proceedings

Summary

Rearing lambs while producing wool is an annual source of competition for available nutritional resources supplied to breeding ewes. Genetic correlations between wool and reproductive traits were estimated from industry data, comparing models that did or did not account for the effects of reproductive level on wool traits recorded at different wool age stages (yearling, hogget, adult). Small to moderate antagonistic correlations between wool and reproductive traits tended to decrease in magnitude when birth-rear type of the individual (yearling and hogget stages) or reproductive output (adult ewes) were accounted for in models for wool traits. Increased recording of reproductive performance would make it possible to more accurately compare young animals for wool traits as well as genetically improve both trait sets (ewe reproduction and wool traits) for Merinos.

Split paternity is high in twines born from syndicate-mated Merino ewes

Bronwyn Clarke (bronwyn.clarke@murdoch.edu.au), Kathryn Egerton-Warburton, Jen Smith, Beth Paganoni, Graeme Martin and Andrew Thompson

Available from AAABG 24th Proceedings

Summary

Split paternity rates in multiple born lambs of syndicate-mated Merino flocks have previously not been reported, primarily due to the cost of genotyping. Pedigree data from litters born to genetically diverse

syndicate mated ewes in three Merino Lifetime Productivity flocks across Australia were analysed to examine rates of split paternity, or heteropaternal superfecundation. Over three joinings at three sites, 1082 twin or triplet litters were marked, of which 577 were heteropaternal (53.3%). There was no effect of age of dam, year of birth, sire or maternal grandsire on heteropaternity rates. These high rates of heteropaternity confirm the need to genotype all progeny from multiple births in syndicate mated flocks to ensure accurate genetic evaluation.

Visual classing grades are heritable and visually classed Merino sheep born and reared as twins are graded lower than singles

Brodie Metcalfe, Johan Greeff, Andrew Thompson and Bronwyn Clarke (bronwyn.clarke@murdoch.edu.au)

Summary

Selection of Merino sheep for use in breeding programs includes the combination of visual assessment and measurement of production traits. Genetic evaluation of these assessments and traits takes into account non-genetic effects to improve the accuracy of breeding value predictions. The hypothesis tested in this paper was that visual classing assessment of sheep on a traditional threepoint and a novel five-point visual scoring system are heritable and both are also affected by nongenetic effects such as birth and rearing type. Using data from the first two years of classing ewes in the Merino Lifetime Productivity project at Pingelly, WA, moderate heritability estimates were observed for both scoring systems (0.24±0.08 for three-point and 0.17±0.07 for five-point). Both traits were moderately repeatable (0.31-0.36+0.03). Birth and rear type impacted visual scoring grades significantly, indicating that they should be accounted for when visually classing Merino sheep.

Genetic parameters for reproduction in intensively and extensively managed Dohne Merino flocks in South Africa

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Summary

The study used 61,974 ewe-year records of 26,254 ewes aged 20 months and older for number of lambs born per ewe lambed (NLB), number of lambs weaned per ewe lambed (NLW) and ewe rearing ability (ERA) obtained from intensively managed South African Dohne Merino flocks. Corresponding numbers for extensively managed flocks numbered respectively 14,067 and 5,181. Reproductive output of intensively managed flocks was higher at respectively 1.49 vs. 1.28 NLB and 1.32 vs. 1.19 NLW when compared to extensively managed flocks. In contrast, ERA was slightly lower at 0.894 vs. 0.932 in intensively managed flocks. Estimates of heritability in intensively manage flocks were 0.028 for NLB, 0.016 for NLW and 0.002 for ERA. Corresponding values in extensively managed flocks were respectively 0.066, 0.040 and 0.008. Genetic correlations of NLB with NLW and of NLW with ERA were positive, while genetic correlations of NLB with ERA were not significant. Genetic correlations between performance in intensive and extensive flocks, as derived from pedigree information, amounted to 0.999 for NLB, 0.840 for NLW and 0.595 for ERA. However, large

SEs for the latter two correlations made it impossible to make firm recommendations. Further research is indicated.

The effect of GDF9 on litter size in Australian sheep

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Available from AAABG 24th Proceedings

Summary

Growth differentiation factor 9 (GDF9) is a known autosomal gene which regulates ovulation rate in mammals. In sheep, numerous polymorphisms have been reported in coding regions of GDF9 with a significant impact on ovulation rate and hence litter size. To study the effect of GDF9 on litter size in Australian sheep breeds, an association analysis was performed between 1,600,633 imputed sequence single nucleotide polymorphisms (SNPs) on OAR5 and litter size phenotypes in 8,850 Merino and 7,613 maternal sheep breed ewes (predominantly Border Leicester, Coopworth, Corriedale and composite maternal lines) respectively. Results showed a significant association between litter size and SNPs in the GDF9 region in maternal breeds. After filtering for high linkage disequilibrium, a highly significant SNP (p_value = 9.09E-09) was found in an intron of the GDF9 gene at OAR5:41841588, which accounted for a 0.22 increase in litter size and explained 4.75% of the total genetic variance. This SNP and the surrounding SNPs in the region of GDF9 were not significantly associated with litter size in Merinos. Information on this SNP genotype could be useful for obtaining a more accurate estimate of genetic merit for reproduction traits in some breeds of sheep.

Ewe reproduction status and its impact on greasy fleece weight breeding values

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Available from AAABG 24th Proceedings

Summary

Using industry records (n=12,912), the effect of ewe reproductive status (defined as combined lambing outcomes during previous and current production cycles) on adult greasy fleece weight (AGFW) was estimated for pre-joining and pre-lambing shearing systems. Increasing ewe reproductive output significantly decreased AGFW, by up to 26% over 2 cycles of shearing. Differences in adjustments between shearing systems reflected that AGFW was most affected by the reproductive cycle completed before shearing. Estimated breeding values for AGFW of sires and ewes were little affected by bias due to reproductive status (< 1% for the highly reproductive ewes comprising 36% of the data) and re-ranking of animals was limited. Nevertheless, adjusting AGFW for reproductive status is proposed, but this would be difficult under the current low recording levels.

An evaluation of the effect of the Booroola gene, Fec B, on productivity in a Border Leicester x Merino prime lamb production system

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Summary

The direct effect of the Booroola gene, Fec B, on ewe reproduction rates and ewe productivity traits has been evaluated in a typical Border Leicester x Merino prime lamb production system. The ovulation rate and prolificacy of the Border Leicester x Booroola Fec Bb+ ewes were significantly higher than those of traditional Border Leicester x Merino ewes. This advantage was offset by significantly lower lamb rearing ability with the result that there was no advantage in terms of lambs weaned/ewe joined or in $ returned/ewe joined. Targeted supplementary management strategies (ultra-sound scanning, supplementary feeding) appear to show promise in realising the gains from the increased prolificacy.

Defining longevity and estimating genetic parameters in Australian Merino ewes

MD Rahman (mrahma47@myune.edu.au), Daniel Brown and Sam Walkom

Summary

Currently, there are no measures of ewe longevity recorded by Australian sheep breeders for utilisation as part of their breeding objective. In the absence of disposal codes, this study explored the potential to use production records to define ewe longevity in Merino sheep and estimate genetic parameters for the resulting trait. The longevity trait was defined as the ewe's total life (TL) in the flock from birth to their last available production record. To identify suitable non-censored data, cohorts were selected based on the amount of pedigree and consistent annual production recording. Under these assumptions, the MERINOSELECT database provided 267,517 longevity records from 143 flocks. The heritability of TL was 0.22 ± 01. Adjusting TL for the ewe's lifetime reproductive performance, accounted for 94% of the variation in TL, reduced the heritability to 0.11 ± 01. The results herein indicate that it is possible to describe longevity in the Merino ewes using production records from the MERINOLSELECT database. TL was found to be heritable but further exploration is required before incorporation in industry breeding objectives.

Economic analysis of Merino ewe performance from diverse industry sires using GrassGro™

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Summary

Differences in profitability between genetically different sire groups at the Macquarie site of the Merino Lifetime Productivity Project (MLP) were compared using GrassGro™ to simulate animal performance based on the interactions between animal production and pasture growth determined by historical climate data. Mean gross margin (GM) differences of $13/Dry Sheep Equivalent (DSE) and $42/head (hd) were found between sire groups for wool and meat median prices. In median to high markets wool income had a higher influence on GM/DSE than meat income, with fibre diameter being the trait of most influence. In low markets meat income had a greater influence on GM/DSE with weaning rate the most influential single trait. Utilising a combination of traits, through either of three different selection indexes, showed the strongest correlations with GM/DSE.

Deriving breeding values for net reportion rate from component traits in sheep

Andrew Swan (andrew.swan@une,edu,au) and Kim Bunter

Summary

Genetic analyses for sheep reproduction traits in LAMBPLAN and MERINOSELECT have recently been upgraded to separate number of lambs weaned per ewe joined (NLW) into the component traits of conception (CON), litter size (LS) and ewe rearing ability (ERA). Methodology was developed to combine breeding values for component traits post-analysis into the net reproduction traits: reproduction rate (RR, lambs born per ewe joined) and weaning rate (WR, lambs weaned per ewe joined). Comparisons from the LAMPLAN maternal analysis show that RR and WR breeding values were closely aligned to single trait number of lambs born per ewe joined (NLB) and number of lambs weaned per ewe joined breeding values, ≈0.93 for RR with NLB, and ≈0.85 for WR with NLW. The derived net reproduction breeding values are useful as a tool for transition from old to new upgraded analyses.

Ewes for the future: a commercial comparison of ewe breeds for reproduction, wool and lamb growth

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Summary

The Elmore Field Days Inc ran a comparison to determine the merit of six ewe genotypes in common commercial use for prime lamb and wool production from 2014 to 2019. Each of the six genotypes were represented by 42 ewes randomly selected from three properties. They were three crossbred types and three Merino types; Border Leicester x Merino cross, Multimeat x Merino cross carrying the Booroola high fecundity gene, Composites with genes from many meat breeds, local Merinos from northern Victoria and two specialist dual-purpose Merinos, Centre Plus and Leahcim Merinos. The ewes were joined annually to terminal sires for prime lamb production and run together as one mob except at lambing; there were five opportunities to lamb, the first as ewe lambs. The specialist dual purpose Merino team had the highest gross lamb and wool returns per ewe due to good reproduction, lamb growth and wool value. This is a similar result to a previous field study and subsequent financial analyses that highlighted gross margin increases of 20 to 30 percent from high performance dual purpose Merinos.

Lactobacillus fermented plant extracts provided to yearling ewes improves their lambs' antioxidant status at weaning

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Highlights

- The number of lambs raised by yearling ewes increases weight loss.

- As weight loss increases plasma total antioxidant status decreases.
- Yearling ewes appear to effectively manage oxidative stress.
- Providing fermented products to dams increases lambs' antioxidant status at weaning.

Abstract

The objective of this experiment was to determine if supplementation with Lactobacillus fermented plant extracts will affect the livestock performance (BW change and reproduction) and antioxidant status of ewe lambs managed to lamb as yearlings (EWES). A further objective of this experiment was to determine how providing the Lactobacillus fermented plant extracts may influence their lambs' (LAMBS) performance, rumen fermentation patterns, and antioxidant status following weaning. The EWES [n = 60; initial body weight (BW) = 29.6 ± 2.4] were provided a concentrate supplement (100 g/ewe/d) with either no extract (CON), a seaweed based extract (SWO; 10 mL/ewe/d), or a seaweed plus terrestrial plant extract (SWP; 10 mL/ewe/d), from their weaning through to the weaning of their lambs. Treatment did not influence EWES plasma total antioxidant status (TAS), whole blood glutathione peroxidase activity (GPx), or EWES or LAMBS body weight change. However, one day after weaning, the LAMBS born to SWO and SWP EWES had 13–14% greater (P = 0.02) TAS and had lower (P = 0.03) GPx activity than LAMBS born to CON EWES indicating greater antioxidant transmission to their offspring in SWO and SWP EWES. Overall, it was concluded BW changes did not appear to be great enough to elicit oxidative stress in EWES. Supplying SWO and SWP to sheep increased the maternal transmission of antioxidants to their offspring.

Multiple matings modify the estrous length, the moment of ovulation, and the estradiol and LH patterns in ewes

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Abstract

In several species, mating reduces the estrous length and advances ovulation. The aim of this study was to determine if multiple matings reduces the estrous length and modifies the moment of ovulation, as well as the estradiol and LH patterns in ewes. The estrous cycle of Corriedale ewes was synchronized, and the onset of receptivity was monitored every 3 h with rams, avoiding mating. At the estrous onset, ewes were assigned to two experimental groups (n=10 each): 1) estrous was monitored every 3 h with a ram avoiding mating (group CON), and 2) a ram was allowed to mate and ejaculate once every 3 h (group MAT). The ovaries were scanned with transrectal ultrasonography and blood samples were collected for measuring 17β-estradiol and LH concentrations every 3 h until ovulation. Estrus was shorter in MAT than CON ewes (24.7 ± 1.5 h vs. 30.4 ± 1.5 h, respectively; P=0.02); the proportion of animals that ovulated before the end of estrus was greater in CON ewes: (9/10 vs. 3/10, P=0.009). The area under the LH curve (AUC) was greater in MAT than CON ewes (36.1 ± 3.5 ng.h-1.mL-1 vs 24.9 ± 3.5 ng.h-1.mL-1 P=0.03). However, MAT ewes had a lower 17β-estradiol AUC than CON ewes (41.0 ± 4.9 pg.h-1.mL-1 vs 59.4 ± 4.9 pg.h-1.mL-1 P=0.01). Mating reduced the estrous length, induced a greater secretion of LH but less total 17β-estradiol secreted and, additionally, ovulation occurred more frequently after the end of estrus in mated ewes.

Effects of maternal nutrition and rumen-protected arginine supplementation on maternal carotid artery hemodynamics and circulating amino acids of ewes and offspring

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Abstract

Multiparous Rambouillet ewes (n = 32) were allocated in a completely randomized design to determine if rumen-protected L-arginine (RP-Arg) supplementation during mid- and late gestation would 1) alter maternal carotid artery hemodynamics and 2) affect circulating amino acids associated with arginine metabolism in dams from day 54 of gestation to parturition and in their offspring from birth to 54 d of age. Ewes were assigned to one of three treatments from day 54 ± 3.9 to parturition: control (CON; 100% nutrient requirements), restricted (RES; 60% of CON), and RES plus 180 mg RP-Arg•kg BW-1•d1 (RES-ARG). Ewes were penned individually in a temperature-controlled facility. Carotid artery hemodynamics was measured via Doppler ultrasound at day 50 and 130 of gestation. Maternal serum was collected at day 54 and 138 of gestation and at parturition. At parturition, lambs were immediately removed from their dams and reared independently. Lamb serum samples were collected at birth and 1, 3, 7, 33, and 54 d of age. Pulsatility index was the only hemodynamic measurement altered by dietary treatment, where day 130 measurements were greater ($P \leq 0.04$) for RES and RES-ARG compared with CON. The change in pulsatility index was greater ($P < 0.01$) for RES compared with CON but tended to be intermediate ($P \geq 0.12$) for RES-ARG. Maternal serum Arg, Cit, and Asp at day 138 were greater ($P < 0.01$) for CON compared with RES and RES-ARG; serum Orn at day 138 was greater ($P = 0.04$) for CON compared with RES. Maternal serum Cit at parturition was greater ($P \leq 0.03$) for CON and RES-ARG compared with RES. Offspring serum Arg was affected by a maternal treatment by day of age interaction ($P = 0.03$), where at day 3, CON and RES-ARG had greater ($P \leq 0.03$) serum Arg concentrations than RES, and at day 54, RES-ARG was greater than ($P = 0.002$) CON and RES was intermediate and did not differ from ($P \geq 0.09$) CON and RES-ARG. Offspring serum Orn and Cit were less ($P \leq 0.03$) for RES and RES-ARG compared with CON. Results indicate that distal tissue blood perfusion decreased due to maternal RES, and RES-ARG was able to improve perfusion but not to the level of CON ewes. Further, maternal RP-Arg altered offspring Arg and related amino acid concentrations during the postnatal period.

Upcoming events

Date	Event	Location