The RBST
Progress in livestock conservation science

This monthly, scientific newsletter serves to highlight recent advances in the science of biological conservation. Species are treated individually, with more general article summaries grouped further on. This acts as a resource for members, breeders and general interest, and a structured platform to share pertinent progress in the field.

Sheep

Revealing new tick-borne encephalitis virus foci by screening antibodies in sheep milk

Wallenhammar, A., Lindqvist, R., Asghar, N. et al. Revealing new tick-borne encephalitis virus foci by screening antibodies in sheep milk. Parasites Vectors ***13,*** *185 (2020)*

Tick distribution in Sweden has increased in recent years, with the prevalence of ticks predicted to spread towards the northern parts of the country, thus increasing the risk of tick-borne zoonoses in new regions. Tick-borne encephalitis (TBE) is the most significant viral tick-borne zoonotic disease in Europe. The disease is caused by TBE virus (TBEV) infection which often leads to severe encephalitis and myelitis in humans. TBEV is usually transmitted to humans *via* tick bites; however, the virus can also be excreted in the milk of goats, sheep and cattle and infection may then occur *via* consumption of unpasteurised dairy products. Virus prevalence in questing ticks is an unreliable indicator of TBE infection risk as viral RNA is rarely detected even in large sample sizes collected at TBE-endemic areas. Hence, there is a need for robust surveillance techniques to identify emerging TBEV risk areas at early stages.

Goats

Genetic diversity, Population Genetic Structure and Conservation Management of Spanish Verata Goat Breed

Martínez-Trancón, M., Parejo, J.C., Rabasco, A., Padilla, P. and Padilla, J.A., 2020. Genetic diversity, Population Genetic Structure and Conservation Management of Spanish Verata Goat Breed. Small Ruminant Research, p.106106.

Verata goat is an endangered autochthonous breed from Extremadura (Spain). Genetic diversity, genetic Bottleneck hypothesis and population genetic structure were analysed for conservation management purposes. Twenty-two microsatellite markers were used to genotype 570 animals belonging eight different sampling regions. Average number of alleles per locus (9.09 ± 0.71) and the expected gene diversity ($H_e = 0.694 \pm 0.025$) revealed substantial genetic variation in the breed, greater than other Spanish and European breeds not threatened. The decrease of heterozygotes in the total population is a consequence of the population's subdivision instead of inbreeding in subpopulations. The F_{ST} value was similar to those obtained in other Spanish goat breeds. Clustering analysis performed by structure software and by the modal value of the distribution of the ΔK showed clear membership of individuals in four clusters. Clear genetic drift of Verata goat population has been observed, as it was demonstrated by the assignment of individuals to pre-defined sampling regions. It was detected a certain degree of genetic flow (immigrant and admixed animals) among the sample herds located in these regions. Verata goat population had not undergone a genetic bottleneck in the recent past; however, a recent population expansion without immigration or introduction of some unique or rare alleles by immigrants has been detected. Based on the above results, we have designed a conservation program based on maintaining of live animals in a conservation nucleus with minimum coancestry mating system and constant family sizes and on the cryopreservation of germplasm. Development of this program will allow us the maintenance and sustainable use of the breed in its geographical and socio-economic environment, preserving racial purity of animals and the variability of the breed.

Caprine semen cryopreservation and the factors affecting it: An overview

Sharma, A. and Sood, P., 2020. Caprine semen cryopreservation and the factors affecting it: An overview. Veterinary Sciences: Research and Reviews, 6(1), pp.46-57.

Semen cryopreservation is a complex process that which involves balancing many factors in order to obtain satisfactory results. It causes ultrastructural, biochemical and functional damage to the spermatozoa leading to reduced motility, viability, impaired transport and fertility. Caprine sperms are extremely sensitive to cryopreservation compared to other species which is mainly attributed to the compositional variation of the sperm plasma membrane. Different factors affect affects the semen cryopreservation viz. species, breed, semen collection technique, collection season, extender composition, type of cryoprotectant used, cooling rate, equilibration time, freezing and thawing rate. All these factors should be given due credit for achieving better post-thaw post thaw quality of semen to be utilized in different advanced reproductive techniques.

Cattle

Understanding breeding preferences among small-scale cattle producers: implications for livestock improvement programmes

Mutenje, M., Chipfupa, U., Mupangwa, W., Nyagumbo, I., Manyawu, G., Chakoma, I. and Gwiriri, L., 2020. Understanding breeding preferences among small-scale cattle producers: implications for livestock improvement programmes. animal, pp.1-11.

Livestock production provides a pathway for improving livelihoods and reducing poverty in semi-arid tropical regions. However, this contribution has been affected by low livestock productivity. Most livestock programmes have also failed due to, among other things, the inability to understand the dynamics in smallholder breeding preferences. Using data from the sub-humid region in Zimbabwe, this paper sought to provide evidence on smallholder cattle breeding preferences and the implication on livestock improvement programmes. It applies the choice experiment approach to model farmer preferences for selected cattle breeding attributes. The results show three attributes that significantly affect breeding preferences. The attributes ‘cow body condition score’ and the ‘useful life of a bull/semen’ have a positive influence while ‘artificial insemination/bull maintenance cost’ negatively affects farmer preferences. This means farmers prefer breeding strategies which improve the nutrition of their cows, have a longer lifespan for the bull/semen and whose cost of breeding services is low. However, access to education and income affected these preferences. Education made farmers to make informed choices while higher incomes increased the propensity of investing in livestock breeding technologies. The findings also show that existing institutional arrangements in animal management and community grazing do not promote investment in livestock improvement. Thus, more attention should be given to improving animal nutritional management which includes promoting sustainable grazing schemes. There is also a need to provide affordable livestock breeding services through recruiting and training more artificial insemination service providers. Strong and effective institutions that provide incentives for collective participation are integral to any community-based livestock breeding programme. There is also a need to promote access to information and enhance farmers’ knowledge and capacity in improved livestock management practices.

Effect of cattle breed, Holstein or Angus, and basal diet, grain or forage, on diet digestibility, rumen bacterial communities, and eating and rumination activity

Carvalho, P.H., Pinto, A.C., Millen, D.D. and Felix, T.L., 2020. Effect of cattle breed, Holstein or Angus, and basal diet, grain or forage, on diet digestibility, rumen bacterial communities, and eating and rumination activity. Journal of Animal Science.

Objectives were to compare ruminal total tract digestibility, bacterial communities, and eating and rumination activity between Holstein and Angus steers fed grain- or forage-based diets. Six Holstein steers (average BW = 483 ± 23 kg) and 6 Angus steers (average BW = 507 ± 29 kg), previously fitted with rumen cannulae, were fed in a crossover design with a 2 × 2 factorial arrangement of 4 treatments: 1) Holsteins fed a grain-based diet, 2) Holsteins fed a forage-based diet, 3) Angus fed a grain-based diet, and 4) Angus fed a forage-based diet. Each period was 35 d with 26 d of diet adaptation and 9 d of sample collection. On d 1 and 2 of collection, feeding activity was recorded for 48 h. On d 3, rumen contents were sampled to measure ruminal pH at 0, 3, 6, 12, and 18 h after feeding. A portion of the strained ruminal fluid was subsampled at 0, 3, and 6 h for VFA analysis. Rumen contents were subsampled at 3 h for analysis of bacterial communities. From d 4 to 8, total fecal excretion, feed, and refusals samples were collected and analyzed for DM, NDF, and starch. On d 8 and 9 (0 and 3 h post-feeding, respectively), total reticulorumen evacuation was conducted and contents were weighed. Data were analyzed using the MIXED procedures in SAS (v9.4 SAS Inst. Inc., Cary, NC). Repeated measures were used to analyze changes in ruminal pH and VFA over time. There were no interactions of diet × breed ($P \geq 0.07$). While main effects of diet were expected, unique to these data are the fact that bacterial diversity and richness were reduced ($P < 0.01$) in cattle fed grain-based diets. There was no main effect ($P > 0.34$) of breed on total tract DM, OM, and starch digestibility; but, Angus cattle had greater ($P = 0.01$) NDF digestibility than Holsteins. The increased NDF digestibility may be associated with a numerical ($P = 0.08$) increased numbers of bacterial species in Angus steers compared to Holstein steers. Holstein steers also spent more time ($P \leq 0.05$) ruminating than Angus steers. There was no effect ($P > 0.80$) of breed on reticulorumen content at feeding time; however, Holstein steers had greater ($P = 0.04$) reticulorumen content on wet basis 3 h post-feeding. Although Holstein steers spent more time ruminating, Angus steers were better able to digest NDF when compared to Holsteins, regardless of basal diet, and this improvement may be related to changes in bacterial communities in the rumen or to rumination activity.

Poultry

Molecular Characteristics of MC1R Gene in Tile-grey Plumage of Domestic Chicken

Shi, X.W., Zhang, L.Y., Huang, M.Y., Li, Y., Yang, X.D. and Luo, Y.S., 2020. Molecular Characteristics of MC1R Gene in Tile-grey Plumage of Domestic Chicken. British Poultry Science, (just-accepted).

Tile-grey plumage is a unique and rare feather type of local chicken breeds in China, but its genetic mechanism and corresponding genes remain unknown. In order to identify the genetic basis and molecular characteristics of tile-grey plumage, this experiment investigated variations of melanocortin 1 receptor (*MC1R*) gene in Yunnan Piao chickens with typical tile-grey plumage characteristics in contrast with three Yunnan local breeds as well as two standard breeds with different plumage colour, and analysed the association between genic variation and tile-grey plumage.Through sequencing and comparison of the entire coding region of the *MC1R* gene, a total of 10 SNP loci were detected, of which eight were non-synonymous mutations that cause amino acid changes. The gene frequency and genotype frequency of the *MC1R* mutation sites in different breeds and different plumage colour groups revealed that C69T, T212C and A274G were significantly associated with tile-grey plumage. Eighteen haplotypes of the *MC1R* gene were constructed based on 10 nucleotide variations and eight amino acid variations. Haplotype distribution and the median joining network in breeds and plumage colour groups revealed a main haplotype (*hap2*) for tile-grey plumage. *Hap2* is unique to the tile-grey feather of Piao chicken, and the individuals carrying this haplotype account for 62.96% of the whole tile-grey chicken. The results of this study are of significance for further analysis of the molecular basis of tile-grey plumage and the selective breeding of tile-grey plumage.

Estimating genetic diversity and population structure of 22 chicken breeds in Asia using microsatellite markers

Roh, H.J., Kim, S.C., Cho, C.Y., Lee, J., Jeon, D., Kim, D.K., Kim, K.W., Afrin, F., Ko, Y.G., Lee, J.H. and Batsaikhan, S., 2020. Estimating genetic diversity and population structure of 22 chicken breeds in Asia using microsatellite markers. Asian-Australasian Journal of Animal Sciences.

Estimating the genetic diversity and structures, both within and among chicken breeds, is critical for the identification and conservation of valuable genetic resources. In chickens, microsatellite (MS) marker polymorphisms have previously been widely used to evaluate these distinctions. Our objective was to analyze the genetic diversity and relationships among 22 chicken breeds in Asia based on allelic frequencies.

We used 469 genomic DNA samples from 22 chicken breeds from eight Asian countries (South Korea: KNG, KNB, KNR, KNW, KNY, KNO, Laos: LYO, LCH, LBB, LOU, Indonesia: INK, INS, ING, Vietnam: VTN, VNH, Mongolia: MGN, Kyrgyzstan: KGPS, Nepal: NPS, Sri Lanka: SBC) and three imported breeds (RIR: Rhode Island Red, WLG: White Leghorn, CON: Cornish). Their genetic diversity and phylogenetic relationships were analyzed using 20 MS markers.
In total, 193 alleles were observed across all 20 MS markers, and the number of alleles ranged from 3 (MCW0103) to 20 (LEI0192) with a mean of 9.7 overall. The NPS breed had the highest expected heterozygosity (Hexp, 0.718 ± 0.027) and polymorphism information content (PIC, 0.663 ± 0.030). Additionally, the observed heterozygosity (Hobs) was highest in LCH (0.690 ± 0.039), whereas WLG showed the lowest Hexp (0.372 ± 0.055), Hobs (0.384 ± 0.019), and PIC (0.325 ± 0.049). Nei's DA genetic distance was the closest between VTN and VNH (0.086), and farthest between KNG and MGN (0.503). Principal coordinate analysis showed similar results to the phylogenetic analysis, and three axes explained 56.2 % of the variance (axis 1: 19.17 %; 2: 18.92 %; 3: 18.11 %). STRUCTURE analysis revealed that the 22 chicken breeds should be divided into 20 clusters, based on the highest △K value (46.92).This study provides a basis for future genetic variation studies and the development of conservation strategies for 22 chicken breeds in Asia.

Parallel genetic origin of foot feathering in birds

Bortoluzzi, C., MegenS, H.J., Bosse, M., Derks, M.F., Dibbits, B., Laport, K., Weigend, S., Groenen, M.A. and Crooijmans, R.P., 2020. Parallel genetic origin of foot feathering in birds. Molecular Biology and Evolution.

Understanding the genetic basis of similar phenotypes shared between lineages is a long-lasting research interest. Even though animal evolution offers many examples of parallelism, for many phenotypes little is known about the underlying genes and mutations. We here use a combination of whole-genome sequencing, expression analyses, and comparative genomics to study the parallel genetic origin of ptilopody (Pti) in chicken. Ptilopody (or foot feathering) is a polygenic trait that can be observed in domesticated and wild avian species and is characterized by the partial or complete development of feathers on the ankle and feet. In domesticated birds, ptilopody is easily selected to fixation, though extensive variation in the type and level of feather development is often observed. By means of a genome-wide association analysis, we identified two genomic regions associated with ptilopody. At one of the loci, we identified a 17 kb deletion affecting PITX1 expression, a gene known to encode a transcription regulator of hindlimb identity and development. Similarly to pigeon, at the second loci we observed ectopic expression of TBX5, a gene involved in forelimb identity and a key determinant of foot feather development. We also observed that the trait evolved only once as foot feathered birds share the same haplotype upstream TBX5. Our findings indicate that in chicken and pigeon ptilopody is determined by the same set of genes that affect similar molecular pathways. Our study confirms that ptilopody has evolved through parallel evolution in chicken and pigeon.

Pigs

Maternal behaviour in gilts–The effect of genotype, social rearing environment and mixing after weaning

Bolhuis, S.D.L. and Wallenbeck, A., Maternal behaviour in gilts–The effect of genotype, social rearing environment and mixing after weaning.

Maternal behaviour in pigs is influenced negatively by stress, and may therefore be linked to social behaviour of gilts (first litter) and sows that are kept in group housing during gestation. Gilts and sows in group housing are often aggressive towards each other, which causes stress and possibly injuries or even death. Measures to improve their social skills could lead to more positive social behaviour, which would reduce stress and could therefore lead to better maternal behaviour. Swedish Yorkshire gilts may have better social skills than Dutch Yorkshire gilts, because the Swedish genotype has been kept in and selected for group housing for a longer period of time. Furthermore, additional opportunities to practice social behaviour may improve later social skills. We studied three factors in a 2x2x2 factorial design, being genotype (Swedish versus Dutch Yorkshire), rearing environment (access farrowing pen allowing socialization with another litter versus control in standard farrowing pen) and group mixing (grouping after weaning with unfamiliar gilts or control grouped with sisters only). Sixty gilts were exposed to the treatments from birth and video recorded when their first litter of piglets was separated from them and after their piglets were returned. We analysed the first three minutes the gilt spent alone and the first three minutes after reunion with the piglets using the 'Qualitative Behaviour Assessment' (QBA) from the Welfare Quality® Assessment Protocol. Furthermore we recorded the occurrence of nursing during the first three minutes after reunion, the gilt's responsiveness towards the piglets during these three minutes and piglet growth until weaning. We analysed the QBA scores by Principle Component Analysis (PCA), which yielded two components for alone time and two for reunion time. None of the component scores were significantly affected by any of the three treatment factors or their interactions. Treatment factors also did not significantly affect piglet growth, responsiveness or the occurrence of nursing. However, low responsiveness did associate with a high likelihood of nursing during the first three minutes after reunion in a Chi-square test (χ2=11.2, P=0.001, df=1). Furthermore, an association between responsiveness and the first PCA component of the behaviour during reunion time indicated a more positive emotional state in low responsive gilts (independent samples t-test, equal variances assumed; P

Determining pig holding type from British movement data using analytical and machine learning approaches

Smith, R.P., Gavin, C., Gilson, D., Simons, R.R.L. and Williamson, S., 2020. Determining pig holding type from British movement data using analytical and machine learning approaches. Preventive Veterinary Medicine, p.104984.

Determining the size, location and structure of a livestock population is an essential aspect of surveillance and research as it provides understanding of the representativeness and coverage of any project or scheme. It is an important input for a variety of epidemiological analyses, for example, allowing generation of more accurate sample size calculations for estimating prevalence or freedom from disease, cost-benefit analyses for control measures to reduce or eradicate livestock disease, or development of between-herd network models to estimate the impact of movement of animals between farms on the spread of livestock diseases.

The work described here provides information on how British pig movement data was compared against other datasets related to the British pig population to define its appropriateness for defining pig holding demographics. The data were then used to identify the location of pig holdings and the estimated herd size (split into five categories). Two methods are described that were used to classify the holding type of the identified pig holdings. The first method was an epidemiological method that used expert opinion to determine a set of rules based on movement characteristics to classify each holding. The second method was a machine learning approach that used k means cluster analysis to automatically estimate the holding type based on a set of proxy indicators.

Each method had a good accuracy rate, when compared to matched holdings present in data provided by the Annual June Agricultural Survey, but all misclassified some holdings. While both of the methods on their own provided a reasonable estimate, it was concluded that a consensus model, considering the results of both models and the Survey, provided the most accurate result. However, the machine learning approach was beneficial, as although some technical expertise was needed to set up the model, it was considerably faster to implement than the other method, as well as being quicker and easier to adapt and re-run with updated information.

Equine

The effects of inbreeding on covering success, gestation length and foal sex ratio in Australian thoroughbred horses

Todd, E.T., Hamilton, N.A., Velie, B.D. et al. The effects of inbreeding on covering success, gestation length and foal sex ratio in Australian thoroughbred horses. BMC Genet ***21,*** *41 (2020). https://doi.org/10.1186/s12863-020-00847-1*

Horses produce only one foal from an eleven-month gestation period, making the maintenance of high reproductive rates essential. Genetic bottlenecks and inbreeding can increase the frequency of deleterious variants, resulting in reduced reproductive levels in a population. In this study we examined the influence of inbreeding levels on foaling rate, gestation length and secondary sex ratio in Australian Thoroughbred mares. We also investigated the genetic change in these traits throughout the history of the breed. Phenotypic data were obtained from 27,262 breeding records of Thoroughbred mares provided by three Australian stud farms. Inbreeding was estimated using the pedigree of each individual dating back to the foundation of the breed in the eighteenth century. While both gestation length and foaling rate were heritable, no measurable effect of inbreeding on either trait was found. However, we did find that the genetic value for both traits had decreased within recent generations. A number of environmental factors also had significant effects on foaling rate and gestation length. Secondary sex ratio had only an extremely small paternal heritable effect and was not susceptible to environmental influences. In contrast to racing performance, inbreeding had no measurable effect on foaling rate or gestation length in Australian Thoroughbred horses. This could be because the level of inbreeding in the population examined is not high enough to show a discernible effect on reproductive traits. Populations that experience higher levels of inbreeding due to use of artificial reproductive technologies or extremely small population sizes may show a more pronounced reduction in natural foaling rate or gestation length. It is also possible that the intensive management techniques used in the Thoroughbred population masks any negative effects of inbreeding. The decrease in the genetic value of foaling rate is likely to be because horses with unfavourable genetic potential have not yet been selected out of the population. The change in genetic value of gestation length may be due to selective breeding favouring horses with shorter pregnancies. We also found that prioritising the mating of older mares, and avoiding out of season mating could lead to an increased breeding success.

Determining a Welfare Prioritization for Horses Using a Delphi Method

Rioja-Lang, F.C., Connor, M., Bacon, H. and Dwyer, C.M., 2020. Determining a Welfare Prioritization for Horses Using a Delphi Method. Animals, 10(4), p.647.

Equine welfare issues are receiving increasing attention in the UK, but welfare problems can arise from a wide range of causes. In order to identify the most important welfare concerns for horses, we used a Delphi method with 19 equine welfare experts. An initial list of 84 equine welfare issues was generated using an online discussion board and NVivo thematic analysis. Subsequently, experts ranked these welfare issues for perceived prevalence, severity and duration of suffering associated with each issue on a 6-point Likert scale. All issues with a mean score of 3 or above (*n* = 37) were included in subsequent rounds. Finally, a subset of experts attended a two-day workshop to determine the final priority list of welfare issues. The welfare issues perceived to be most prevalent were lack of biosecurity, delayed euthanasia, lack of owner knowledge of equine welfare needs, fear and stress from use, and obesity. The issues considered to cause greatest suffering for individual horses were delayed euthanasia, lack of recognition by owners of pain behaviour, large worm burdens, obesity and being fed unsuitable diets for equine feeding behaviour. These outcomes can help to focus research and education interventions on the most pressing welfare issues for horses.

Veterinary Science

Animal domestication in the era of ancient genomics

Frantz, L.A.F., Bradley, D.G., Larson, G. et al. Animal domestication in the era of ancient genomics. Nat Rev Genet (2020).

The domestication of animals led to a major shift in human subsistence patterns, from a hunter–gatherer to a sedentary agricultural lifestyle, which ultimately resulted in the development of complex societies. Over the past 15,000 years, the phenotype and genotype of multiple animal species, such as dogs, pigs, sheep, goats, cattle and horses, have been substantially altered during their adaptation to the human niche. Recent methodological innovations, such as improved ancient DNA extraction methods and next-generation sequencing, have enabled the sequencing of whole ancient genomes. These genomes have helped reconstruct the process by which animals entered into domestic relationships with humans and were subjected to novel selection pressures. Here, we discuss and update key concepts in animal domestication in light of recent contributions from ancient genomics.

An alternative model for fetal loss disorders associated with mare reproductive loss syndrome

Swerczek, T.W., 2020. An alternative model for fetal loss disorders associated with mare reproductive loss syndrome. Animal Nutrition.

Fertile chicken eggs were used as an alternative model for large animals to evaluate suspect toxic dietary ingredients for fetal loss disorders associated with mare reproductive loss syndrome (MRLS) and fetal losses in other livestock. Nitrate, ammonia, and sulfate may react with proteinaceous compounds to enable the formation of abiotic pathogenic nanoparticles which were constant findings in pathognomonic placental lesions associated with non-infectious fetal losses of previously unknown etiology in mares, chickens and other livestock. The pathogenic nanoparticles may be produced naturally by toxic elements associated with air pollution that affect pasture forages or crops, unintentionally by reactions of these elements in protein-mineral mixes in dietary rations, or endogenously within tissues of fetuses and adult animals. The nanoparticles may form niduses in small vessels and predispose animals to a host of secondary opportunistic diseases affecting the reproductive, respiratory and gastrointestinal tracts of animals. The newly recognized abiotic pathogenic micro and nanoparticles are associated with MRLS. The discovery of the pathogenic nanoparticles led to the identification of nitrate, ammonium, and sulfur, in the form of sulfate, that seemingly enable the formation of the pathogenic nanoparticles in embryonic and fetal tissues.

Long-term production effects of clinical cryptosporidiosis in neonatal calves

Shaw, H.J., Innes, E.A., Morrison, L.J., Katzer, F. and Wells, B., 2020. Long-term production effects of clinical cryptosporidiosis in neonatal calves. International Journal for Parasitology.

Cryptosporidiosis can have a devastating effect in neonatal calves, resulting in diarrhoea, dehydration and, in severe cases, death of the animal. The disease is caused by *Cryptosporidium* spp. and is one of the most common causes of calf enteritis in the UK. The parasite is very difficult to remove from the farm, as the oocysts have a tough outer wall which enables the parasite to survive for several months in moist temperate environmental conditions and it is difficult to kill oocysts with common disinfectants used on a farm. If appropriate management practises are applied, the disease is usually self-limiting and most calves will recover. It has been shown, in studies with children and in lambs, that severe clinical cryptosporidiosis can result in long-term growth and cognitive impairment compared with individuals with no obvious signs of the disease. This study measured the long-term growth rate of beef calves on farm by comparing groups of animals that had suffered differing degrees of clinical severity of cryptosporidiosis as neonates. A group of 27 beef calves were enrolled in the study and monitored from birth to 6 months of age. The calves were scored for severity of cryptosporidiosis and weighed at regular intervals. The average difference in weight gain, at 6 months, between a group of calves that had severe cryptosporidiosis as neonates and a group of calves with no clinical signs of infection was 34 kg. Those calves that had experienced severe cryptosporidiosis as neonates showed a significantly reduced live weight gain compared with those calves showing no clinical signs of infection ($P = 0.034$). Therefore, the impact of severe cryptosporidiosis in neonatal calves has longer term effects on weight gain and production efficiency, resulting in the parasite having a greater impact on cattle production than previously thought.

A Tool for Prioritizing Livestock Disease Threats to Scotland

Bessell, P.R., Auty, H.K., Roberts, H., McKendrick, I.J., Bronsvoort, B. and Boden, L.A., 2020. A Tool for Prioritizing Livestock Disease Threats to Scotland. Frontiers in Veterinary Science, 7, p.223.

There are a number of disease threats to the livestock of Scotland that are not presently believed to be circulating in the UK. Here, we present the development of a tool for prioritizing resources for livestock disease threats to Scotland by combining a semi-quantitative model of the chance of introduction of different diseases with a semi-quantitative model of disease impact. Eighteen key diseases were identified and then input into a model framework to produce a semi-quantitative estimate of disease priorities. We estimate this through a model of the potential impacts of the infectious diseases in Scotland that is interpreted alongside a pre-existing generic risk assessment model of the risks of incursion of the diseases. The impact estimates are based on key metrics which influence the practical impact of disease. Metrics included are the rate of spread, the disease mitigation factors, impacts on animal welfare and production, the human health risks and the impacts on wider society. These quantities were adjusted for the size of the Scottish livestock population and were weighted using published scores. Of the 18 livestock diseases included, the model identifies highly pathogenic avian influenza, foot and mouth disease in cattle and bluetongue virus in sheep as having the greatest priority in terms of the combination of chance of introduction and disease impact. Disregarding the weighting for livestock populations and comparing equally between industry sectors, the results demonstrate that Newcastle disease and highly pathogenic avian influenza generally have the greatest potential impact. This model provides valuable information for the veterinary and livestock industries in prioritizing resources in the face of many disease threats. The system can easily be adjusted as disease situations evolve.

Farming and Habitat management

Refuges for biodiversity conservation: A review of the evidence

Selwood, K.E. and Zimmer, H.C., 2020. Refuges for biodiversity conservation: A review of the evidence. Biological Conservation, 245, p.108502.

Refuges and refugia are important to conservation management because of their potential to protect species from difficult-to-manage threats such as changing climate, extreme events (e.g., drought, fire) and biotic threats (e.g., disease, invasive species). To provide conservation managers with an evidence-based approach to identifying refuges and refugia, we ask: which places have been observed to function as refuges/refugia, with results reported in the scientific literature? We systematically reviewed the past 20 years of research into refuges/refugia. To provide an objective picture of the evidence for different refuges/refugia, we analysed each study using the framework of: (a) the place providing protection and its environmental characteristics; (b) the threat; and (c) the biota being protected. We identified 16 categories of places which functioned as refuges/refugia. These places occurred at spatial scales varying from within-habitat elements (e.g., crevices and burrows) to regions, and functioned at temporal scales from minutes to millennia. Most studies focused on large-scale, geographically specific places (mainly glacial refugia) or small-scale within-habitat refuges; relatively few studies described environmental characteristics of the refuges/refugia. However, three landscape elements: rocky environments, montane environments and riparian areas (and other terrestrial wet-spots), were identified as refuges/refugia for multiple species and threats. Conservation managers seeking to increase the resistance of local biodiversity can act now to protect these places within their sphere of influence. Clearly describing of refuges/refugia in terms of place (and environmental characteristics), threat and biota protected, enables application of research findings beyond individual study sites, and provides direction for evidence-based conservation management.

Evaluation of the factors influencing the treatment performance of a livestock constructed wetland

Reyes, N.J., Geronimo, F.K. and Kim, L.H., 2020. Evaluation of the factors influencing the treatment performance of a livestock constructed wetland. Ecological Engineering, 149, p.105811.

The expansion of livestock industry resulted to larger waste production and pollutant deposition in the natural environment. Advanced treatment systems for treating wastewater and discharges from livestock areas are necessary to reduce the pollutant loads in receiving water bodies. This study mainly focused on evaluating the effectiveness of a livestock constructed wetland in treating composite wastewater discharge and stormwater runoff. Water and sediment samples were collected and analyzed to determine the factors that can potentially affect the performance of the facility. Positive pollutant removal performances for turbidity (52% to 81%), TSS (61 to 82%), organics (34% to 50%), and nutrients (10% to 48%) were noted in the CW for storm events and dry days due to the continuity of flow and adequate HRT conducive to pollutant removal. SLR models for pollutant removal efficiency yielded low r^2 values (0.26 to 0.53) and high errors (6.85% to 31.45%) implied that the predictive removal efficiencies were not precise. Despite the significant decrease ($p < .05$) in pollutant concentrations after the treatment, water quality standards were still exceeded by the effluent from the CW. Further improvements in the design of CWs can be incorporated to achieve the desired water quality standards. The findings of this inquiry can be used to establish the factors affecting the treatment performance of CWs and formulate design guidelines to improve the treatment process.

Achieving win-win outcomes for pastoral farming and biodiversity conservation in New Zealand

Norton, D.A., Suryaningrum, F., Buckley, H.L., Case, B.S., Cochrane, C.H., Forbes, A.S. and Harcombe, M., Achieving win-win outcomes for pastoral farming and biodiversity conservation in New Zealand.

Pastoral farming is the dominant land use in New Zealand today and is under considerable domestic social and political pressure to reduce its environmental footprint. In this article, we explore options to enhance native biodiversity conservation within New Zealand pastoral systems. We argue that there is strong synergistic interdependence between biodiversity conservation and pastoral farming and suggest that it is possible to have win-win outcomes for both. Landowners need to be incentivised and rewarded for good biodiversity management, rather than relying on a strict rules-based approach. To bring integrity and objective support to this incentive-based approach, farmers need to adopt environmental management planning that is supported by good biodiversity extension resources. Alongside this, a verification system is required that shows farmers are doing what they say they are doing and reflects agreed management targets for biodiversity. This approach requires trust and partnership among all players in agroecosystems – farmers, government, food and fibre processors, scientists, conservationists, NGOs, and the wider New Zealand population. We suggest that if we change the way we think about how farming and biodiversity interact, then we will achieve substantial biodiversity gains across the 50% of New Zealand under pastoral farming. This then brings integrity to the existing and expanding market story for pastoral farming and creates a stronger connection between all New Zealanders and the farming sector. Advancing our thinking in this way will enable New Zealand to maintain a premium for our farming products internationally while supporting conservation of our native biodiversity.

In the wider world

Molecular genetics of maternally-controlled cell divisions

Abrams, E.W., Fuentes, R., Marlow, F.L., Kobayashi, M., Zhang, H., Lu, S., Kapp, L., Joseph, S.R., Kugath, A., Gupta, T. and Lemon, V., 2020. Molecular genetics of maternally-controlled cell divisions. PLoS genetics, 16(4), p.e1008652.

Forward genetic screens remain at the forefront of biology as an unbiased approach for discovering and elucidating gene function at the organismal and molecular level. Past mutagenesis screens targeting maternal-effect genes identified a broad spectrum of phenotypes ranging from defects in oocyte development to embryonic patterning. However, earlier vertebrate screens did not reach saturation, anticipated classes of phenotypes were not uncovered, and technological limitations made it difficult to pinpoint the causal gene. In this study, we performed a chemically-induced maternal-effect mutagenesis screen in zebrafish and identified eight distinct mutants specifically affecting the cleavage stage of development and one cleavage stage mutant that is also male sterile. The cleavage-stage phenotypes fell into three separate classes: developmental arrest proximal to the mid blastula transition (MBT), irregular cleavage, and cytokinesis mutants. We mapped each mutation to narrow genetic intervals and determined the molecular basis for two of the developmental arrest mutants, and a mutation causing male sterility and a maternal-effect mutant phenotype. One developmental arrest mutant gene encodes a maternal specific Stem Loop Binding Protein, which is required to maintain maternal histone levels. The other developmental arrest mutant encodes a maternal-specific subunit of the Minichromosome Maintenance Protein Complex, which is essential for maintaining normal chromosome integrity in the early blastomeres. Finally, we identify a hypomorphic allele of Polo-like kinase-1 (Plk-1), which results in a male sterile and maternal-effect phenotype. Collectively, these mutants expand our molecular-genetic understanding of the maternal regulation of early embryonic development in vertebrates.

How Natural Genetic Variation Shapes Behaviour

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Nervous systems allow animals to acutely respond and behaviorally adapt to changes and recurring patterns in their environment at multiple timescales—from milliseconds to years. Behavior is further shaped at intergenerational timescales by genetic variation, drift, and selection. This sophistication and flexibility of behavior makes it challenging to measure behavior consistently in individual subjects and to compare it across individuals. In spite of these challenges, careful behavioral observations in nature and controlled measurements in the laboratory, combined with modern technologies and powerful genetic approaches, have led to important discoveries about the way genetic variation shapes behavior. A critical mass of genes whose variation is known to modulate behavior in nature is finally accumulating, allowing us to recognize emerging patterns. In this review, we first discuss genetic mapping approaches useful for studying behavior. We then survey how variation acts at different levels—in environmental sensation, in internal neuronal circuits, and outside the nervous system altogether—and then discuss the sources and types of molecular variation linked to behavior and the mechanisms that shape such variation. We end by discussing remaining questions in the field.