Sheep

Identification of Ancestry Informative Marker (AIM) Panels to Assess Hybridisation between Feral and Domestic Sheep

Once present in the entirety of Europe, mouflon (wild sheep) became extinct due to intense hunting, but remnant populations survived and became feral on the Mediterranean islands of Corsica and Sardinia. Although now protected by regional laws, Sardinian mouflon is threatened by crossbreeding with domestic sheep causing genetic hybridisation. The spread of domestic genes can be detrimental for wild populations as it dilutes the genetic features that characterise them. This work aimed to identify diagnostic tools that could be applied to monitor the level of hybridisation between mouflon and domestic sheep. Tens of thousands of genetic markers known as single nucleotide polymorphisms (SNPs) were screened and we identified the smallest number of SNPs necessary to discriminate between pure mouflon and sheep. We produced four SNP panels of different sizes which were able to assess the hybridisation level of a mouflon and we verified that the SNP panels efficacy is independent of the domestic sheep breed involved in the hybrid. The implementation of these results into actual diagnostic tools will help the conservation of this unique and irreplaceable mouflon population, and the methodology applied can easily be transferred to other case studies of interest.

Abstract: Hybridisation of wild populations with their domestic counterparts can lead to the loss of wildtype genetic integrity, outbreeding depression, and loss of adaptive features. The Mediterranean island of Sardinia hosts one of the last extant autochthonous European mouflon (Ovis aries musimon) populations. Although conservation policies, including reintroduction plans, have been enforced to preserve Sardinian mouflon, crossbreeding with domestic sheep has been documented. We identified panels of single nucleotide polymorphisms (SNPs) that could act as ancestry informative markers able to assess admixture in feral x domestic sheep hybrids. We applied a two-step selection algorithm to this data consisting of preselection via Principal Component Analysis followed by a supervised machine learning classification method based on random forest to develop SNP panels of various sizes. We generated ancestry informative marker (AIM) panels and tested their ability to assess admixture in mouflon x domestic sheep hybrids both in simulated and real populations of known ancestry proportions. All the AIM panels recorded high correlations with the ancestry proportion computed using the full medium-density

SNP array. The AIM panels proposed here may be used by conservation practitioners as diagnostic tools to exclude hybrids from reintroduction plans and improve conservation strategies for mouflon populations

A sheep's eye view: Land division, livestock and people in later prehistoric Somerset, UK

Authors: Randall, C. **Editors:** Arnoldssen, S., Lovschal, M., Johnston, B. and McOmish, D. http://eprints.bournemouth.ac.uk/33723/ **Publisher:** European Association of Archaeologists' (EAA)

Fields and field systems in later prehistoric British archaeology have generally been discussed in relation to territory or land tenure. They are also frequently assumed to relate purely to arable agriculture. Alongside this, we also tend not to situate livestock animals within landscapes. Increasingly, morphological features of fields can be identified as having use in animal handling. Consequently field system morphology, and changes to layouts over time, enable their re-examination in relation to pastoral and arable husbandry (and the interplay between them), and consideration as to why differing approaches may have been adopted within the same landscape at different times. This provides models which, focussing on pastoral husbandry, are potentially applicable to a range of places and periods. The second and first millennium BC bounded landscapes surrounding the hillfort at Cadbury, Castle, Somerset, UK, reveal an intimate relationship between the occupiers of the hillfort, sites in its environs, livestock, and the landscape. A series of different forms of land division and organisation from the earlier Bronze Age onwards can be compared with both faunal and plant macro-fossil data from within that landscape. Different forms of layout appear to reflect different types of strategy and approach in later prehistoric farming. During the second and first millennium BC changes can be observed between different forms of highly extensive pastoral farming and closely integrated and intensive systems. The explanation would seem to be more social than practical in origin, but discerning this is reliant on large scale field survey, and integration of multiple strands of information.

Molecular genetic analyses for adaptive conservation management of the Cyprus on (Ovis gmelini ophion, Caprinae)

The mouflon (Ovis gmelini ophion, Caprinae) is the largest terrestrial mammal and an endemic taxon of the island of Cyprus, which has remained separated for about 10,500 years. Nowadays, the Cyprus mouflon is threatened by poaching, habitat loss and fragmentation, and infection from pathogens. The Cyprus mouflon is included in the Appendix I of CITES, and based on a recent survey (2016), about 3,000 heads inhabit the Paphos forest and adjacent forested areas of the island. In this thesis, we attempted at carrying out the first in-depth genetic study of the mouflon of Cyprus to gain useful information and offer cogent management recommendations for its long-term protection. The Cyprus Veterinary Services in collaboration with the Game and Fauna Service (Ministry of Interior) collected (2007 to 2018) 92 GPS-referenced samples of wild mouflons from 39 localities across the entire island distribution range and 14 samples of captive mouflons from seven ex situ facilities. An interesting finding that pointed further to the genetic uniqueness of the Cyprus population. Based on genetic results, it is recommended that the conservation management of the Cyprus mouflon take place within a strict adaptive conservation framework, thus avoiding any contact with any allopatric Ovis resources. The Cyprus mouflon population would also certainly benefit from a

constant genetic monitoring and the application of genetically controlled breeding techniques in order to sustain or even increase its genetic variability.

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Cattle

Estimation of Chronological Age of Cattle using Spatially Resolved Diffuse Reflectance Measurements of Hide

Palendeng, M.E., Alvarenga, T.I., Fowler, S., Hopkins, D.L., McGilchrist, P. and Thennadil, S.N., 2020. Estimation of Chronological Age of Cattle using Spatially Resolved Diffuse Reflectance Measurements of Hide. *IEEE Sensors Journal*.

Determining the age of the cattle is important in the cattle industry especially for trading purposes. Dentition and ossification scores are currently used to estimate the age of cattle. Both these methods have limitations which can create significant differences in carcass value. In this study, a fibre-optic probe-based spatially resolved diffuse reflectance spectroscopy system was used to investigate the possibility of using visible-near-infrared spectra for predicting the chronological age of beef cattle. This investigation was carried out on hide samples taken from 80 cattle with accurate date of birth and of the same breed. Spectra of hide samples taken from the neck area were used to build partial least squares models to estimate the age of the cattle. Various empirical pre-processing methods and wavelength selection using genetic algorithm (GA) were used to investigate whether these approaches could enhance model performance. Model performance was evaluated using the repeated learning-training (RLT) method. A model with the lowest average root mean square error of prediction (ARMSEP) of 2.0 years was obtained when reflected intensity spectra collected from a source-detector distance of 1.0 mm was used after pre-processing with automatic Whittaker filter and applying wavelength selection using GA indicating the feasibility of this method for estimating the age of cattle. Two approaches for utilising measurements from all the source-detector distances collected by the spatially resolved measurement system were also considered. Both these approaches, co-adding and data fusion through augmentation, led to poorer model performance compared to using measurements from only one source-to-detector distance

Designing Cattle: The Social Practice of Constructing Breeds

Eriksson, C. and Petitt, A., 2020. Designing Cattle: The Social Practice of Constructing Breeds. *Anthrozoös*, *33*(2), pp.175-190.

This paper explores how cattle breeds are constructed through social practice—which we conceptually develop as "designing" cattle. We show how breed varieties are designed, informed by the social, material and moral embeddedness of cattle breeding associations' visions of the future and how they draw on science and technology in their breeding strategies. Based on an analysis of the trade magazines of three different breeding associations, we illustrate how breeding associations are working to establish four different varieties of Swedish Mountain Cattle (SMC). We conclude that the concept of designing cattle enables us to unpack how breeds are socially constructed and institutionally stabilized through sociotechnical imaginaries.

Novel haplotypes responsible for prenatal death in Nordic Red and Danish Jersey cattle

Wu, X., Mesbah-Uddin, M., Guldbrandtsen, B., Lund, M.S. and Sahana, G., 2020. Novel haplotypes responsible for prenatal death in Nordic Red and Danish Jersey cattle. *Journal of Dairy Science.*

Haplotypes that are common in a population but not observed as homotypes in living animals may harbor lethal alleles that compromise embryo survival. In this study, we searched for homozygous-deficient haplotypes in the genomes of 19,309 Nordic Red Dairy (RDC) and 4,291 Danish Jersey (JER) cattle genotyped using the Illumina BovineSNP50 BeadChip (Illumina Inc., San Diego, CA). For statistically significant deficient haplotypes, we evaluated the effect on nonreturn rate in at-risk matings (mating between carrier bull and daughter of carrier sire) versus not-at-risk matings (mating between noncarrier bull and daughter of noncarrier sire). Next, we analyzed whole-genome sequence variants from the 1000 Bull Genomes Project to identify putative causal variants underlying these haplotypes. In RDC, we identified 3 homozygous-deficient regions (HDR) that overlapped with known recessive lethal mutations: a 662-kb deletion on chromosome 12 in RDC [Online Mendelian Inheritance in Animals (OMIA) 001901-9913), a missense mutation in *TUBD1*, g.11063520T>C, in Braunvieh cattle (OMIA 001939-9913), and a 525-kb deletion on chromosome 23 in RDC (OMIA 001991-9913)]. In addition, we identified 15 novel HDR and their tag haplotypes for the underlying causative variants. The tag haplotype located between 39.2 and 40.3 Mbp on chromosome 18 had a negative effect on nonreturn rate in at-risk mating, confirming embryonic lethality. In Danish Jersey, we identified 12 novel HDR and their tag haplotypes for underlying causative variants. For 3 of these 12 tag haplotypes, insemination records of at-risk mating showed a negative effect on nonreturn rate, confirming the association with early embryonic mortality. Cattle that had both genotype and whole-genome sequence data were analyzed to detect the causative variants underlying each tag haplotype. However, none of the functional variants or deletions showed concordance with carrier status of the novel tag haplotypes. Carrier status of these detected haplotypes can be used to select bulls to reduce the frequencies of lethal alleles in the population and to avoid at-risk matings.

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Poultry

Assessing MHC-B diversity in Silkie chickens

Tarrant, K.J., Lopez, R., Loper, M. and Fulton, J.E., 2020. Assessing MHC-B diversity in Silkie chickens. *Poultry Science.*

The major histocompatibility complex (**MHC**) is a highly polymorphic region on chromosome 16, which contains numerous immune response genes, and is known to influence disease susceptibility and resistance in chickens. Variability of MHC-*B* haplotypes in various well-known and commercially utilized breeds has previously been identified. This study aims to understand MHC-*B* diversity in the Silkie breed using a high-density SNP panel that encompasses the chicken MHC-*B* region. DNA was obtained from 74 females and 27 males from a commercial Silkie breeder colony that is maintained through minimal genetic selection practices. A previously described panel of 90 SNPs, all located within the MHC-*B* region, was used to evaluate MHC-*B* variability in the commercial Silkie breeder colony. MHC-*B* haplotypes identified from the individual SNP information in the Silkie colony were compared to published haplotypes from the same region. Of the 27 haplotypes identified in the

Silkie population, 8 have been previously described. Nineteen haplotypes are unique to the Silkie population and include one novel recombinant and 2 additional possible novel recombinants. Six haplotypes were found at a frequency greater than 5% of the population, of which 4 are novel. Finally, Hardy Weinberg Equilibrium (**HWE**) was calculated for the observed haplotypes, which were found to be in HWE. This study shows considerable MHC-*B* diversity in the Silkie breed and adds further information on variability of the MHC-*B* region in the chicken.

Genome-Wide Analyses Identifies Known and New Markers Responsible of Chicken Plumage Color

Through the development of the high-throughput genotyping arrays, molecular markers and genes related to phenotypic traits have been identified in livestock species. In poultry, plumage color is an important qualitative trait that can be used as phenotypic marker for breed identification. In order to assess sources of genetic variation related to the Polverara chicken breed plumage colour (black vs. white), we carried out a genome-wide association study (GWAS) and a genome-wide fixation index (FST) scan to uncover the genomic regions involved. A total of 37 animals (17 white and 20 black) were genotyped with the Affymetrix 600 K Chicken single nucleotide polymorphism (SNP) Array. The combination of results from GWAS and FST revealed a total of 40 significant markers distributed on GGA 01, 03, 08, 12 and 21, and located within or near known genes. In addition to the well-known TYR, other candidate genes have been identified in this study, such as GRM5, RAB38 and NOTCH2. All these genes could explain the difference between the two Polverara breeds. Therefore, this study provides the basis for further investigation of the genetic mechanisms involved in plumage color in chicken. K

Performance, Behavior, and Welfare Status of Six Different Organically Reared Poultry Genotypes

In alterative rearing systems, the use of outdoor space has a crucial role. It is well known that only some commercial poultry genotypes are suitable to be reared in these systems. It is necessary to find a balance between productive performance and adaptability. The aim of this study was to evaluate the productive performance, behaviour, and welfare status of six poultry genotypes reared in an organic system. One hundred males/genotype (Hubbard RedJA (A), CY5XJA87 (CY), M22XJA87 (M), Ranger Classic (R1), Ranger Gold (R2), and Rowan Ranger (R3)) were reared from 1 to 81 days of age. The number of culled birds was recorded daily, whereas live weight and feed consumption were recorded weekly. Behaviour evaluation was undertaken through a computerized system one week before slaughtering; the breast yield and muscle/bone ratio of the drumstick was also evaluated in refrigerated carcasses. The results showed that A and R3 had good adaptability, showing active behaviours and satisfactory productive performance 3083.6 g and 3022.1 g, respectively. Although CY and M achieved the best productive performance, they did not appear adapted to the organic system due to a higher frequency of static behaviours (rest and roost), mortality, footpad dermatitis, breast blisters, and poor feather condition.

Pigs

Genome-wide association analyses for coat colour patterns in the autochthonous Nero Siciliano pig breed

Nero Siciliano (or Sicilian Black) is an Italian autochthonous pig breed reared in the Sicily island, mainly under extensive management systems. Nero Siciliano pigs are black (with black skin and black hair), but animals with white face or partially white face ("suino facciolo") can be registered to the breed herd book. Sometimes, other white patterns on extreme portions of legs could appear in this population. This study took advantage from the rare occurrence of pigs with white patterns in the Nero Siciliano population to carry out a genome-wide association study and comparative genome-wide Fixation index (F_{ST}) analysis to identify genomic regions that could affect coat colour variability (solid black *vs* white patterns over black) in this autochthonous pig breed. Analyses have been conducted on 66 Nero Siciliano pigs: 30 completely black and 36 black with white patterns. All samples have been genotyped for the *KIT* gene duplication and *MC1R* mutations, two genes well known to affect coat colours in pigs. Only pigs that did not carry any duplication of the *KIT* gene and were homozygous for the E^{D2} black dominant *MC1R* gene allele (n. = 26 completely black and n. 22 with white patterns) were genotyped with the Illumina PorcineSNP60 BeadChip. The genome-wide analyses identified on chromosome 2 a significant marker (rs81329493) associated with the coat colour white patterns in this breed. The homologous chromosome region in felids contains the gene responsible for the blotched tabby and striped coat colour patterns. Further studies, including a larger number of pigs, are needed to confirm this result and identify the causative mutation(s) affecting this coat colour diversity, which might be used to design a conservation programme in this breed aiming to maintain phenotypic homogeneity (i.e. solid black) that is typically associated with Nero Siciliano pigs. This study demonstrated how genetic diversity segregating in an autochthonous genetic resource can be explored to understand the genetic mechanisms affecting phenotypic traits in a livestock species.

Effects of Transport and Lairage on the Skin Damage of Pig Carcasses

Transport and associated handling can have adverse effects on pig welfare. The transport of fattening pigs can cause economic losses by virtue of mortality, skin damage, and the general deterioration of meat quality. A total of 4507 fattening pigs were transported from a farm to a commercial slaughterhouse (distance 110 km) in 128 transports. Skin damage was visually assessed in the slaughter line in different parts of the carcass, i.e., shoulder, middle, and ham, using a 4-point scale. The incidence of skin damage was most prevalent (31%) in the shoulder region of the pig carcass. Sex, wind velocity, regrouping, transport combination, transport compartment, lairage time,

and ham angle affected the skin damage incidence. In conclusion, scoring the incidence of skin damage is an indicator of the level of welfare exercised during transport and the slaughterhouse conditions. Furthermore, skin damage monitoring can be used to determine critical control points in the transport procedure. Given the importance from both a commercial and welfare perspective, it should be a powerful incentive to handle fattening pigs with care during the transport process and the lairage period.

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Equine

Genetic Differentiation of the Two Types of Polish Cold-blooded Horses Included in the National Conservation Program

Gurgul, A., Jasielczuk, I., Semik-Gurgul, E., Pawlina-Tyszko, K., Szmatoła, T., Polak, G. and Bugno-Poniewierska, M., 2020. Genetic Differentiation of the Two Types of Polish Cold-blooded Horses Included in the National Conservation Program. *Animals*, *10*(3), p.542.

The current role of the horse as a companion animal resulted in a decrease of interest in breeding and usage of draft horses. This meant that the population of cold-blooded horses in Poland has been dramatically reduced during the last decades. To avoid impoverishment of the gene pool of the local horse population, a conservation program was established which involves draft horses and other local horse breeds. The draft horses bred in Poland can be subdivided in a few horse types of which the most widespread and consolidated are Sztumski and Sokólski horses. These two subpopulations are phenotypically diversified, however, the overall level of their genetic differentiation seems to be relatively low and not precisely determined, especially with the use of molecular markers. In reference to this, in this study we used Illumina genotyping arrays to describe in detail the genetic differentiation of these two cold-blooded horse populations. We describe the genetic distance between them, as well as within-population variation, admixture patterns, and level of relatedness within populations. We also made an attempt to detect genome regions divergently selected between those horses by the detection of diversifying selection signals. The results of this study provide initial evidence supporting breeding decisions that were made during conservation breeding program design and answer questions raised by the breeders of Sokólski and Sztumski horses concerning the level of their genetic variation and differentiation.

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Veterinary Science

Molecular Epidemiology of Infectious Zoonotic and Livestock Diseases.

Gebreyes, W.A., Jackwood, D., de Oliveira, C.J.B., Lee, C.W., Hoet, A.E. and Thakur, S., 2020. Molecular Epidemiology of Infectious Zoonotic and Livestock Diseases. *Microbiology Spectrum*, *8*(2).

Zoonotic and livestock diseases are very important globally both in terms of direct impact on human and animal health and in terms of their relationship to the livelihood of farming communities, as

they affect income generation and food security and have other, indirect consequences on human lives. More than two-thirds of emerging infectious diseases in humans today are known to be of animal origin. Bacterial, viral, and parasitic infections that originate from animals, including hypervirulent and multidrug-resistant (MDR) bacterial pathogens, such as livestock-associated methicillin-resistant *Staphylococcus aureus* (LA-MRSA), invasive nontyphoidal *Salmonella* of animal origin, hyperviruent *Clostridium difficile*, and others, are of major significance to public health. Understanding the origin, risk factors, transmission, prevention, and control of such strains has been a challenge for various reasons, particularly due to the transdisciplinary partnership between and among human, environment, and animal health sectors. MDR bacteria greatly complicate the clinical management of human infections. Food animal farms, pets in communities, and veterinary hospital environments are major sources of such infections. However, attributing such infections and pinpointing sources requires highly discriminatory molecular methods as outlined in other parts of this curated series. Genotyping methods, such as multilocus sequence typing, pulsed-field gel electrophoresis, restriction fragment length polymorphism, and several others, have been used to decipher sources of foodborne and other zoonotic infectious diseases. In recent years, whole-genome-sequence-based approaches have been increasingly used for molecular epidemiology of diseases at the interface of humans, animals, and the environment. This part of the series highlights the major zoonotic and foodborne disease issues. *This article is part of a curated collection.

Whole-Genome Analysis of Livestock-Associated Methicillin-Resistant Staphylococcus aureus Sequence Type 398 Strains Isolated From Patients With Bacteremia in …

Sequence type (ST) 398 is the most prevalent clone of livestock-associated methicillin-resistant *Staphylococcus aureus* (MRSA). To evaluate the molecular characteristics and phylogeny of Chinese ST398 isolates, 4 MRSA ST398 strains and 4 methicillin-susceptible *S. aureus* (MSSA) ST398 strains were collected from patients with bacteremia at 6 teaching hospitals in China between 1999 and 2016. Moreover, 689 ST398 genome sequences were downloaded from the GenBank database for comparison. The 4 MRSA ST398 strains were resistant to β-lactam antibiotics, and 2 strains were also resistant to erythromycin. Among the 4 MSSA ST398 strains, 2 strains displayed multidrug resistance (MDR) and were resistant to penicillin, erythromycin, tetracycline, and gentamicin. The accessory genome of MSSA ST398 was more diverse than that of MRSA ST398. All 4 MRSA ST398 strains carried type V staphylococcal cassette chromosome *mec* elements; however, MSSA ST398 carried more resistance genes than MRSA ST398. These 4 MRSA ST398 strains carried hemolysin, along with virulence genes associated with immune invasion and protease. Phylogenic analysis showed that the 4 MRSA ST398 strains clustered in 1 clade. The global ST398 phylogeny showed that ST398 was divided into an animal clade and a human clade, and the ST398 strains of this study clustered in the human clade. A small number of human strains were also present in the animal clade and vice versa, suggesting transmission of ST398 between animals and humans. In conclusion, livestock-associated MRSA ST398 has caused severe infections in Chinese hospitals, and it should therefore be paid more attention to and monitored

Watery mouth disease in neonatal lambs: a systematic literature review

Watery mouth disease is considered to be a significant cause of neonatal mortality in lambs. The clinical signs are strongly associated with an endotoxaemia produced as a result of the lysis of Gram-negative bacteria. It has been associated with mass antibiosis to neonatal lambs at birth, a practice which is now untenable. It can be prevented in many cases through the timely administration of good quality colostrum and a hygienic birth environment. However, despite this, much remains unknown about the specific aetiopathogenesis. Alternative strategies for prevention, treatment and control are required, particularly when colostrum quality is poor, or delivery is absent, and where unhygienic conditions predominate

Mitochondrial diversity of Yoruba and Fulani chickens: A biodiversity reservoir in Nigeria

Poultry are the most widely distributed type of livestock in Nigeria. Indigenous chickens are extremely common throughout the country. Indeed, approximately 83 million chickens are raised in extensive systems and 60 million in semi-intensive systems. To provide the first comprehensive overview of the maternal lineages in Southwest Nigeria, we analyzed 96 mitochondrial DNA control region sequences from 2 indigenous chicken ecotypes: Fulani and Yoruba. All samples belonged to the most frequent haplogroup (E) in Africa and Europe and showed noticeably low haplotype diversity. Although only 11 different haplotypes were detected, with 2 of them never found before in Nigeria, the presence of unique sequences among our indigenous samples testified to their status as an important genetic resource to be preserved. Furthermore, a total of 7,868 published sequences were included in the comparative analysis, which revealed an east-west geographic pattern of haplogroup distribution and led to the conclusion that the gene flow from Southeastern Asia mainly involved one mitochondrial clade. Moreover, owing to the extensive genetic intermixing among Nigerian chickens, conservation efforts are required to safeguard the extant mitochondrial variability in these indigenous ecotypes and establish future improvement and selection programs.

Experimental Evidence Reveals Both Cross-Infection and Cross-Contamination Risk of Embryo Storage in Liquid Nitrogen Biobanks

In recent decades, gamete and embryo cryopreservation have become routine procedures in livestock and human assisted reproduction. However, the safe storage of germplasm and the prevention of disease transmission continue to be potential hazards of disease transmission through embryo transfer. This study aimed to demonstrate the potential risk of cross-infection of embryos from contaminated liquid nitrogen, and cross-contamination of sterile liquid nitrogen from infected embryos in naked and closed devices. Additionally, we examined the effects of antibiotic-free media on culture development of infected embryos. The study was a laboratory-based analysis using rabbit as a model. Two experiments were performed to evaluate both cross-infection (liquid nitrogen to embryos) and cross-contamination (embryos to liquid nitrogen) of artificially

inoculated *Salmonella* Typhimurium, *Staphylococcus aureus*, *Enterobacter aerogenes*, and *Aspergillus brasiliensis*. Rapid cooling through vitrification was conducted on rabbit embryos, stored for a year, thawed, and cultured. In vivo produced late morulae–early blastocyst stages (72 h) embryos were used (n = 480). Embryos were cultured for 1 h in solutions with and without pathogens. Then, the embryos were vitrified and stored in naked and closed devices for one year in two liquid nitrogen biobanks (one pathogen-free and the other artificially contaminated). Embryos were warmed and cultured for a further 48 h, assessing the development and the presence of microorganism (chromogenic media, scanning electron microscopy). Embryos stored in naked devices in artificially contaminated liquid nitrogen became infected (12.5%), while none of the embryos stored in closed devices were infected. Meanwhile, storage of artificially infected embryos incurred liquid nitrogen biobank contamination (100%). Observations by scanning electron microscopy revealed that all the microorganisms were caught in the surface of embryos after the vitrification-thawed procedure. Nevertheless, embryos cultured in antibiotics and antimycotic medium developed to the hatched blastocyst stage, while artificially infected embryos cultured in antibiotic-free medium failed to develop. In conclusion, our findings support that both cross-contamination and cross-infection during embryo storage in liquid nitrogen biobanks are plausible. So, to ensure biosafety for the cryogenic storage, closed systems that avoid direct contact with liquid nitrogen must be used. Moreover, it seems essential to provide best practice guidelines for the cryogenic preservation and storage of gametes and embryos, to define appropriate quality and risk management procedures.

Veterinary science on the conservation frontline

Greenwood, A., 2020. Veterinary science on the conservation frontline. *The Veterinary Nurse*, *11*(2), pp.104-104.

Experienced veterinary professionals use their specialist expertise gained from working with various taxa in captive situations such as zoos, falconry and exotic pets, to assist with all stages of wildlife conservation projects from initial stabilisation of critically-endangered populations through captive management, reintroduction/translocation and long-term monitoring.

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Farming and Habitat management

Potential of multi-species livestock farming to improve the sustainability of livestock farms: A review

Martin, G., Barth, K., Benoit, M., Brock, C., Destruel, M., Dumont, B., Grillot, M., Hübner, S., Magne, M.A., Moerman, M. and Mosnier, C., 2020. Potential of multi-species livestock farming to improve the sustainability of livestock farms: A review. *Agricultural Systems*, *181*, p.102821.

Diversified farming systems are proposed as a major mechanism to address the many sustainability issues of today's agriculture. Multi-species livestock farming, i.e. keeping two or more animal species simultaneously on the same farm, is an option that has received little attention to date. Moreover, most studies of multi-species livestock farming are limited, usually focusing on selected dimensions of farm sustainability and addressing lower organizational levels (i.e. within the farm) and rather limited time horizons (e.g. a few weeks in a grazing season). Thus, a comprehensive assessment of multi-species livestock farming in terms of farm sustainability is lacking. In this context, we outline

and discuss potential benefits and limitations of multi-species livestock farming for livestock farm sustainability from existing literature and list issues on multi-species livestock farming requiring further research. We show that multi-species livestock farming has the potential to improve the three dimensions of sustainability reviewed - economic viability for farmers, environmental soundness and social acceptability by being respectful of animals and humans - as long as locally relevant farming practices are implemented, especially an appropriate stocking rate during grazing. If relevant practices are not observed, multi-species livestock farming may produce undesirable effects, such as competition for resource acquisition during grazing, parasitic cross-infection and more intense work peaks. Therefore, we identify four focal research areas for multi-species livestock farming. First, characterizing the management of multi-species livestock farms. To do this, we suggest considering the integration of production enterprises (e.g. cattle and sheep enterprises) within the farm from three perspectives: farming practices (e.g. grazing management), work organization and sales. Second, exploring the complementarity of livestock species on multi-species livestock farms. This is especially true for species combinations that have been largely ignored (e.g. ruminants and monogastrics), even though they may have potential due to complementary diet compositions and resource-acquisition strategies. Third, assessing the sustainability of multi-species livestock farm scenarios (current or alternative) according to the management practices and production conditions, which requires adapting existing methods/models or developing new ones. Fourth, characterizing conditions for success and obstacles for multi-species livestock farming along the value chain from production to consumption, considering stakeholders' objectives, work habits and constraints. Increasing understanding should help prioritize actions and organize them to scale up multi-species livestock farming.

Grazing **and productivity alter individual grass size dynamics in semi-arid woodlands**

Travers, S.K. and Berdugo, M., Grazing and productivity alter individual grass size dynamics in semi-arid woodlands. *Ecography*.

The spatial arrangement of perennial vegetation is critical for ecosystem function in drylands. While much is known about how vegetation patches respond to grazing and abiotic conditions, the size dynamics of individual plants is mostly limited to theoretical studies. We measured the size distribution (mean, variance, skewness) and density of individual grasses, and grass species composition at 451 sites spanning a range of grazing intensities across three broad vegetation communities in semi-arid eastern Australia. We assessed the relative role of grazing by livestock (cattle and sheep), native (kangaroos) and introduced (rabbits) free ranging herbivores, and several environmental measures (productivity, diversity, composition and groundstorey plant cover) on the size distribution and density of individual grasses. We found mean grass size and density were more sensitive to shifts in grazing intensity and environmental conditions than size variance or the frequency of the smallest individuals (skewness), and shifts were mostly driven by site productivity and cattle and kangaroo grazing. Sheep grazing only reduced mean grass size, and rabbit grazing had no consistent effects. Importantly, we found that site productivity and species composition altered the impacts of grazing on grass density and size distribution. For example, increasing cattle grazing led to larger grasses in low productivity sites. It also led to larger, denser, more variable-sized grasses among grass species from sites with finer soil texture. Increasing kangaroo grazing led to smaller, denser individuals among grass species from sites with coarse soil texture. At high diversity sites kangaroo grazing led to denser, more homogenised grass sizes with a lower frequency of small individuals. Understanding the in situ response of individual plant sizes gives us insights into the

processes driving shifts in perennial vegetation patchiness, improving our ability to predict how the spatial arrangement of ecosystems might change under global change scenarios.

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Conservation in the wider world

Global conservation of species' niches

Environmental change is rapidly accelerating, and many species will need to adapt to survive[1]. Ensuring that protected areas cover populations across a broad range of environmental conditions could safeguard the processes that lead to such adaptations[1,2,3]. However, international conservation policies have largely neglected these considerations when setting targets for the expansion of protected areas[4]. Here we show that—of 19,937 vertebrate species globally[5,6,7,8]—the representation of environmental conditions across their habitats in protected areas (hereafter, niche representation) is inadequate for 4,836 (93.1%) amphibian, 8,653 (89.5%) bird and 4,608 (90.9%) terrestrial mammal species. Expanding existing protected areas to cover these gaps would encompass 33.8% of the total land surface—exceeding the current target of 17% that has been adopted by governments. Priority locations for expanding the system of protected areas to improve niche representation occur in global biodiversity hotspots[9], including Colombia, Papua New Guinea, South Africa and southwest China, as well as across most of the major land masses of the Earth. Conversely, we also show that planning for the expansion of protected areas without explicitly considering environmental conditions would marginally reduce the land area required to 30.7%, but that this would lead to inadequate niche representation for 7,798 (39.1%) species. As the governments of the world prepare to renegotiate global conservation targets, policymakers have the opportunity to help to maintain the adaptive potential of species by considering niche representation within protected areas[1,2].

Triad hybridization via a conduit species

Introgressive hybridization can affect the evolution of populations in several important ways. It may retard or reverse divergence of species, enable the development of novel traits, enhance the potential for future evolution by elevating levels of standing variation, create new species, and alleviate inbreeding depression in small populations. Most of what is known of contemporary hybridization in nature comes from the study of pairs of species, either coexisting in the same habitat or distributed parapatrically and separated by a hybrid zone. More rarely, three species form an interbreeding complex (triad), reported in vertebrates, insects, and plants. Often, one species acts as a genetic link or conduit for the passage of genes (alleles) between two others that rarely, if ever, hybridize. Demographic and genetic consequences are unknown. Here we report results of a

long-term study of interbreeding Darwin's finches on Daphne Major island, Galápagos. *Geospiza fortis* acted as a conduit for the passage of genes between two others that have never been observed to interbreed on Daphne: *Geospiza fuliginosa*, a rare immigrant, and *Geospiza scandens*, a resident. Microsatellite gene flow from *G. fortis* into *G. scandens* increased in frequency during 30 y of favorable ecological conditions, resulting in genetic and morphological convergence. *G. fortis*, *G. scandens*, and the derived dihybrids and trihybrids experienced approximately equal fitness. Especially relevant to young adaptive radiations, where species differ principally in ecology and behavior, these findings illustrate how new combinations of genes created by hybridization among three species can enhance the potential for evolutionary change.

[“Animals are designed for breeding”: captive population management needs a new perspective](#)

Kaumanns, W., Begum, N. and Hofer, H., 2020. "Animals are designed for breeding": captive population management needs a new perspective. *Journal of Zoo and Aquarium Research*, *8*(2), p.1.

A key purpose of the management of captive populations of birds and mammals is their long-term viability (sustainability). This paper considers why many captive populations of birds and mammals face serious challenges and links their lack of sustainability directly to the management and diagnosis of breeding problems. Two well-known population management paradigms are the "small population paradigm" and the "declining population paradigm". The paper argues that under the latter, better management options can be developed, as they emphasise an analysis of the reasons for the decline and the role of the individual's breeding performance, compared to traditional captive management which follows recommendations derived from the small population paradigm. This paper suggests that it will be helpful to manage a population predominantly as a "breeding device" and to view its individual members as its constituents that are "designed for breeding". Following life history theory, individuals are best regarded as phenotypes that combine traits which contribute to individual variation in survival and reproductive success (fitness). Regarding individuals as the units of management with all their fitness-related properties allows the establishment of an integrated management approach that considers their various properties (genotype, ethotype, demotype, etc.) at the same level of importance. Management should then focus on key traits-those traits that are primary determinants of fitness in terms of breeding conditions in a given environment. With reference to the altered conditions of captivity, the paper emphasises the preservation of the breeding potential of a population. This means, in practice, to enable patterns of reproduction and corresponding life histories of natural populations in captivity as much possible, with the implication that this can generate larger population sizes, in turn creating a surplus of individuals needing to be dealt with appropriately. Genetic management, including the use of molecular DNA information, should be part of such an integrated management approach, be compatible with "natural" population dynamics and concentrate on breeding units.

[Genotyping on the ark: A synthesis of genetic resources available for species in zoos](#)

Jensen, E.L., McClenaghan, B., Ford, B., Lentini, A., Kerr, K.C. and Russello, M.A., 2020. Genotyping on the ark: A synthesis of genetic resources available for species in zoos. *Zoo Biology*.

Using molecular genetic information to guide population management can improve the sustainability of species in captivity. However, empirical population genetics has not been commonly applied to species management programs in zoos. One limitation may be the availability of genetic resources (e.g., markers, primers, etc.) for species held in zoos. To assess the extent to which species

held in zoos have been studied using population genetics in the wild, we conducted a systematic literature review of close to 8,000 papers. We synthesized information on the availability and scale of population genetics studies across amphibian, bird, mammal, and reptile species held in zoos, and discussed their potential for informing ex situ management. We found that more than half of the species in zoos (52%) already have some genetic markers described in the literature specific for them, or a congeneric species, that could be further developed to aid the management of zoo populations, and the accumulation of these resources has been steady over the past decades. Furthermore, the proportion of species with genetic resources is even higher (62%) for species that are being managed through a formal breeding program in zoos. Our study provides encouraging results for captive program managers interested in integrating population genetics into ex situ management strategies.

Sentiment Analysis of Conservation Studies Captures Successes of Species Reintroductions

Learning from the rapidly growing body of scientific articles is constrained by human bandwidth. Existing methods in machine learning have been developed to extract knowledge from human language and may automate this process. Here, we apply sentiment analysis, a type of natural language processing, to facilitate a literature review in reintroduction biology. We analyzed 1,030,558 words from 4,313 scientific abstracts published over four decades using four previously trained lexicon-based models and one recursive neural tensor network model. We find frequently used terms share both a general and a domain-specific value, with either positive (success, protect, growth) or negative (threaten, loss, risk) sentiment. Sentiment trends suggest that reintroduction studies have become less variable and increasingly successful over time and seem to capture known successes and challenges for conservation biology. This approach offers promise for rapidly extracting explicit and latent information from a large corpus of scientific texts.