
Plenary talk 1 *Tuesday***Comparative life history trajectories between lagomorphs and larger herbivores: a pace and shape analysis**

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Schedules of growth, survival, and reproduction define life history trajectories, which display a tremendous diversity across the tree of life. In most taxonomic groups studied so far, the main axis of variation in life history trajectories across species corresponds to the slow-fast continuum, a time scale ranking species that grow fast and allocate lot of energy to each of their few reproductive attempts during their short lifespan to species that grow slowly and only allocate little energy to each of their numerous reproductive attempts during their long lifespan. For a given pace of life, species strongly differ in terms of trajectory shape. We analysed variation in life history trajectories in lagomorphs and large herbivores by comparing demographic data across herbivore species from the MALDDABA database. We first retrieved the slow-fast continuum as the main structuring axis of life history variation among herbivore species. As expected from their smaller body size, lagomorphs displayed faster life history trajectories than large herbivores. The shape analysis revealed that for a given pace of life lagomorphs have more variable life history trajectories than large herbivores, making predicted life history trajectory for species with unknown demography to be less reliable for that group.

Plenary talk 2 *Tuesday***Hybridization and adaptive evolution in pikas**

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Pikas represent one of the most successful taxa of lagomorphs that showed rapid speciation since the middle Miocene, but now are suffering dramatical extinction and range contraction with most species confined to Qinghai-Tibet Plateau and its vicinity. Based on the newly generated genome data of pikas (*Ochotona* sp.), we identified extreme mito-nuclear conflicts in the phylogenomic reconstruction, including ghost introgression, lineage replacement, and recent bidirectional introgression, pervasive mitochondria genome introgression (MTGI) occurred among six morphologically distinct but phylogenetically closely related species within the youngest subgenus *Ochotona*. Multiple algorithms identified extensive gene flow between these species' pairs. Local ancestry inference of mitochondrial admixed individuals evidenced recurrence of genomic introgression. Moreover, we identified clear genomic signal of reinforcement, the strengthening of reproductive isolation, between the *O. dauurica* and *O. cansus*. GO enrichment analyses identified selectively fixed genes are mainly related to mitotic cytokinesis and sensory, while subsequent reinforcement was mainly related to the intracellular environment balance and reproductive capacity. These evidences demonstrated MTGI and hybridization as stimulators in the adaptive radiation of pikas.

Plenary talk 3 *Wednesday*

Chemosensory interaction and mother-young relationships in the European rabbit

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In the European rabbit (*Oryctolagus cuniculus*), the mother visits her nest only once per day, to nurse for a very limited period of time (< 5 min). In this context, altricial neonates display a remarkable nipple-search and sucking behavior triggered by odors emitted by the mother. We will present here the pheromonal but also non-pheromonal nature of these odors, and describe some of the processes allowing for these stimuli to carry a predisposed or acquired signal value, and for young animals to adapt to the challenges required within the nest, and more generally within the environment.

Plenary talk 4 *Wednesday***The biological basis for the cultural importance of hares**

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Hares (genus *Lepus*) are an integrative part of human culture across the globe. They have been attributes to antique gods and goddesses due to their famous superconception. Moreover, hares were also linked to Maria, mother of Christ, as they were believed to be capable of immaculate conception. These reproductive patterns and phenomenon have a biological basis, as studies from the last century revealed. Superfetation was already described by the Greek philosopher Aristotle in the 4th century BCE and allows females to get fertilized again while pregnant, beginning with day 34 of pregnancy, and thus to bear two litters of different age in the uterus at the same time. Consequently, interbirth intervals are shorter than gestation length itself (around 42 days). Interbirth intervals can even be as short as 24 days. Although superfetation enables females to produce more young per time, this phenomenon seems to be rather rare in the wild. The knowledge about it, however, was observed in captive hare populations in enclosures (Latin: leporarium). While discussing superfetation it is worth notifying that males produce a substance that reduces the sperm motility, thus enabling them to survive for a longer time (at least 36 days). This would allow females to get pregnant in the absence of a male. However, also this phenomenon is presumably rather rare in the wild as hares are known to have an induced ovulation. Despite their reproductive performance, hare populations are declining in numerous countries due to high juvenile mortality thwarting the extraordinary reproductive output in this lagomorph taxon.

Plenary talk 5 *Thursday***Phylogenetic and taxonomic structure of modern pikas *Ochotona***

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Pikas that are small lagomorphs inhabiting a wide range of habitats with extreme natural conditions include 31–36 extant species. Taxonomy of pikas in both subgeneric and species level was rather controversial up to this century, when molecular approaches helped to build consistent phylogenetic and taxonomic schemes. Phylogenetic studies include almost all species of pikas now. Various approaches agree in existence of 5 lineages / subgenera. Species taxonomic composition is more problematic, since some taxa live in regions difficult of access. Nevertheless, taxonomic allocation of the absolute majority of the nominal taxa of the species group looks stable now. About 20 species of pikas have wide distribution ranges, which allow supposing existence of intra species variation. Nevertheless, such variation as well as details of species distribution was described for several pika species only. Recent studies on comparison of variation in existing cranial material with available genetic data allow reconstructing subspecific structure in the majority of pika species. Species distribution modelling is very helpful for the process of looking for intra species variation, since it allows discovering gaps in distribution in unavailable regions. New genomic data allows evaluation of the interspecies hybridisation that also helps in stabilisation of taxonomy on the species level.

O1 *Open session*

Recurrent evolution of winter coat colour polymorphism in mountain hares

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Understanding the emergence of phenotypic polymorphism that impacts the adaptive potential of species is a major endeavour of evolutionary biology. Several boreal mammals are adapted to snow seasonality by changing the colour of their coat from summer-brown to winter-white to remain camouflaged year-round. However, winter coat colour is often polymorphic in these species, with specimens in some populations showing alternative winter colour, such as grey or brown, presumably reflecting local adaptation to milder snow conditions. Here we study the evolution of winter coat colour polymorphism in the mountain hare (*Lepus timidus*). While in most of the species range mountain hares moult to winter-white coats, in Ireland mountain hares remain brown year-round and in the Faroe Islands hares display a winter-grey morph. Through whole-genome scans of differentiation and selection we mapped this polymorphism to a few genomic regions and confirmed the identified associations with SNP genotyping. Most of these regions have signatures of selective sweeps, in keeping with the hypothesis of local adaptation for winter coat colour. In both Faroese and Irish hares, the same gene, ASIP, is associated with non-white winter morphs, but with distinct underlying variants, suggesting independent evolution of the alternative adaptive phenotypes. We further reveal that diverse evolutionary pathways, including introgression and adaptation from standing variation, underlie winter colour variation in the species. These results show how replicated evolutionary responses to repeated environmental pressures trigger local adaptations in mountain hares.

O2 Open session**The evolution of seasonal camouflage in white-tailed jackrabbits in response to past and future climates**

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Adaptation from standing genetic variation is a critical component of evolutionary responses to rapid environmental change. However, the difficulty of identifying the genetic basis of fitness-relevant traits in natural populations has limited the direct incorporation of genotype-to-phenotype information into conservation efforts. We studied the evolution of adaptive winter color variation in the white-tailed jackrabbit (*Lepus townsendii*), a North American species undergoing population declines. Using extensive museum records, we show that winter pelage color closely tracks dynamics of snow cover across the range of white-tailed jackrabbits, suggesting that geographic variation for the trait is maintained by strong selection. Using whole genomes of specimens collected during winter, we show that seasonal camouflage variation was primarily determined by additive genetic variation at three pigmentation genes. With a phylogenetic analysis of whole genomes from 10 hare species, we further show that color variation is associated with highly divergent alleles at all three genes and link their origin to a mixture of long-term maintenance of ancestral polymorphisms and introgression from another species. Using ecological and genetic modeling and forecasted environmental parameters, we predict that future declines in snow cover will strongly favor darker winter phenotypes across much of the white-tailed jackrabbit distribution. We also predict that low levels of standing adaptive variation should enable severely mismatched populations to adapt to this shift in snow cover conditions. However, adaptation to future snow cover may be impeded by ongoing population declines that appear to differentially threaten adaptive standing genetic variation. Our study illustrates how evolutionary genomics can be used to identify functional genetic variation of critical importance for climate change adaptation.

O3 *Open session***What hares can tell us about fostering climate resilience for biodiversity**

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In two decades of continuous snowshoe hare research -- with a special focus on climate-driven seasonal camouflage mismatch for the past 10 years -- we have learned much about the intersection of evolutionary history, ecological context, and environmental change. We have found seasonal coat color mismatch in snowshoe hares to be a powerful model to consider the scope for biodiversity to locally adapt to climate change. Because seasonal coat color is a genetically-driven trait directly shaped by climate, and because fitness costs of mismatch are sufficient to cause population decline in the absence of adaptive shifts, this research prompts consideration how adaptive rescue might be nurtured by reserve selection and conservation management. I hope to foster discussion on how other research groups studying the other 5 seasonally color changing *Lepus* species might tackle key questions to broaden and deepen this framework to implement adaptive rescue for biodiversity conservation. At the same time, other traits in other lagomorph species -- genetically based, shaped by climate, and spatially mappable -- could be identified to generalize the principles. Ultimately, the goal is a research-based template that would apply beyond hares, beyond coat color, beyond lagomorphs: to identify multi-species hot spots with the greatest scope for rapid rescue of biodiversity via evolution (and/or plasticity). These hotspots for multi-species adaptive rescue would complement traditional metrics (eg species richness, diversity, focal species) to form a comprehensive platform for conservation-decision making. In this way, hare and other lagomorph research could be the *Drosophila* of applied climate change research, generating science-based general principles to foster local persistence of vulnerable wild species in a changing climate.

O4 *Open session*

Current status of the Irish hare (*L.t. hibernicus*): genomics, population size and disease

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The Irish hare (*Lepus timidus hibernicus*) is a subspecies of mountain hare (*L. timidus*) endemic to Ireland. It is distinct from other mountain hares in being large bodied (up to 4.5kg), it does not turn white in winter but retains a brown pelage throughout the year, inhabits a wide range of habitats from the seashore to mountain summits, principally grasslands, where its diet is dominated, not by browse, but grasses. Consequently, it has an ecological niche distinct from other *timidus* with a high degree of niche overlap with the European brown hare (*L. europaeus*). Recent genomic analysis suggests Irish, Alpine and Fennoscandian mountain hares split around the Last Glacial Maximum *ca.* 20Kya with the Irish hare maintaining a small effective population size (<20,000 individuals) with greater differentiation from other *timidus* than they have from one another, including a distinct mtDNA clade and evidence of ancient introgression from *L. europaeus*. Intra-population selective sweeps identified the gene *ASIP* as a candidate underlying the unique brown winter coat of the Irish hare. The species is widespread with recent camera trap Distance Sampling suggesting that current population densities are low at *ca.* 3 hares/km² with a total census size of 223,000 in the Republic of Ireland estimated during 2017-19 and 41,000 in Northern Ireland last estimated by spotlight survey during 2010 (total population *ca.* 264,000 hares which appears largely stable over the last two decades). Rabbit haemorrhagic disease 2 (RHD2) virus was first detected in domestic, and subsequently wild rabbits (*Oryctolagus cuniculus*) in Ireland during 2016 and has since been confirmed as present in 13/32 counties throughout Ireland. During 2019, two lethal cases were recorded in the Irish hare suggesting the disease could be an emerging threat. Present ongoing research focuses on GPS-tracking and accelerometry examining survival, movements, home ranges and behaviour.

O5 *Open session***No need to cull predators for enhancing brown hare (*Lepus europaeus*) populations in farmland**

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Pre-weaning mortality in brown hares (*Lepus europaeus*) is generally high and its variability might be the most important driver of brown hare population density. Leverets mostly die because of wet and cold weather, predators, and agricultural machinery. Attempts to increase hare populations have a long tradition, because hares are a valuable game species. As hunters have no influence on weather and almost none on general agricultural practices, management for hares consists mainly in culling predators. Done with appropriate tools and high intensity, this type of «gamekeeping» leads to clear reductions of potential leveret predators and consequently to high hare densities, sometimes up to ten- and twentyfold compared to normal densities in the natural steppe habitat. Besides ethical considerations (killing two and more predators in order to increase the game bag by one hare), gamekeeping is time-consuming, expensive and in Switzerland legally very constrained (some predator species protected and killing traps forbidden). In a field experiment in Northwestern Switzerland, we therefore tested another approach to increase leveret survival: offering places in the landscape where potential leveret predators do not or only rarely go and which are seldom treated with agricultural machines. These places were wildflower patches and wider-sown cereals (to allow hares to enter the fields from May to July). Predator densities were high and not influenced by management. The management lasted seven years in two experimental areas and three years in the other two. In three out of the four experimental areas, we found a more positive development of hare densities in the managed area compared to the control area. Furthermore, the distribution of the hares within the experimental areas could be best described by a model including the percentage of wildflower patches, the percentage of arable land, and the percentage of cereals in wider-sown rows.

O6 *Open session*

Influence of multiple predators decreases body condition and fecundity of European hares

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We assessed the hypothesis that there is a negative correlation between the influence of multiple predators and body condition and fecundity of the European hare, from 13 areas in the Netherlands. Year-round abundance of predators was estimated by hunters. We quantified predator influence as the sum of their field metabolic rates, as this sum reflects the daily food requirements of multiple individuals. We determined the ratio between body mass and hindfoot length of hares as an index of body condition, and the weight of their adrenal gland as a measure of chronic exposure to stress, and we counted the number of placental scars to estimate fecundity of hares. As hypothesised, we found that the sum of field metabolic rate of predators was negatively correlated with body condition and the number of placental scars, whereas it was positively related to the weight of the adrenal glands. In contrast to the sum of the field metabolic rate, the total number of predators only weakly affected hare fecundity. The sum of the field metabolic rate can be a useful proxy for the influence of multiple predators, and takes into account predator abundance, type, body weight and food requirements of multiple predators. With our findings, our paper contributes to a better understanding of the risk effects of multiple predators on prey fitness. Additionally, we identify a potential contributor to the decline of European hare populations.

O7 *Open session***Rabbit and hare population status and management considerations in the eastern United States**

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In the eastern United States, 5 species of cottontail rabbits (*Sylvilagus* spp.) and the snowshoe hare (*Lepus americanus*) are managed as a public resource by state wildlife agencies. The Eastern cottontail (*S. floridanus*), swamp rabbit (*S. aquaticus*), marsh rabbit (*S. palustris*) and snowshoe hare are hunted throughout most of their range. The New England cottontail (*S. transitionalis*) and Appalachian cottontail (*S. obscurus*), although hunted in some areas, primarily are managed for preservation purposes because of their fragmented distribution and concerns about their population status. Because rabbit and hare populations affect ecosystem health and have a high value to humans, it is important that state wildlife agencies effectively monitor their population status and manage their habitats and numbers. This is especially relevant when considering the recent threat of the invasive non-native Burmese python (*Python molurus bivittatus*) and rabbit hemorrhagic disease virus (RHDV2). The purpose of our research was to assimilate rabbit and hare status, population trend, and management-related information for 31 eastern states to include scientific literature, agency reports, and wildlife survey and hunter-based information collected by state wildlife agencies. We discovered some states had little, or no, data on rabbit population status and no long-term plan for sustaining existing populations. Other states had historical hunter-harvest data, population survey data, and detailed rabbit and/or hare management plans. Impetus for our research was the need for all state wildlife agencies to be equally cognizant of rabbit and hare population status and proactive to direct threats to those populations that could be minimized through habitat and population management. We encourage state wildlife agencies to work together to standardize population-survey methodology and to develop best management practices for each species, including contingent effects of invasive predators, sympatric species, and endemic disease.

O8 *Open session***Contrasted effects of alpine landscape on gene flow in two sympatric hare species**

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Landscape connectivity is important for animal population dynamics. Even in fragmented habitats, the possibility for individuals to disperse may improve population viability, demographics and gene flows contributing to maintain both sufficient population size and genetic diversity to avoid extinction. But, if landscape resistance prevents individual dispersal, populations will remain fragmented and viability will decrease. We used landscape genetics to understand which landscape elements influence dispersal in brown hare (*Lepus europaeus*) and mountain hare (*L. timidus*) in the French Alps. In particular, we investigated how each species was constrained by the landscape, given that in the Alps the brown hare lives at low altitude and the mountain hare at high altitude, these two species being sympatric at intermediate altitudes. We used microsatellite genotypes of 120 mountain hares and 135 brown hares. First, the genetic structure of each species within the landscape was assessed using three different methods. Second, we inferred which landscape elements influence gene flow with a recent selection and resistance optimization method applied on three landscape variables: slope, elevation and land cover. We found different genetic structures depending on the method used for both species, showing that the genetic structure of both species within this alpine landscape was weak. However, the resistance optimization approach showed that altitude (and not slopes or land cover) constrained dispersal in both species, but in opposite ways. In mountain hare, landscape resistance significantly increased below 1000 m of altitude. Conversely, in brown hare, landscape resistance significantly increased above 3000 m of altitude. Our results show that, in the Alps, mountain hares disperse through high altitudes, whereas brown hares mainly disperse along low valleys. This study also suggests that the two species are sympatric (for dispersal) from 1000 to 3000 m of altitude, and that alpine mountain hare populations might be threatened by global warming.

O9 *Open session*

Inference of positive selection in the evolution of major Lagomorph lineages

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Recent advances in high throughput sequencing have revolutionized our ability to collect and analyze massive amounts of genetic information from traditionally non-model species. RNA-sequencing is one of the high throughput techniques, which allows collecting information about the transcriptome of species, the part of the genome that is transcribed into mRNA and later translated to proteins. This gives us the opportunity to understand the major patterns of molecular evolution of genes at several evolutionary depths, from species to families or orders. In this work we produced and analyzed transcriptomic sequencing data of three species of hares (*Lepus granatensis*, *L. timidus* and *L. americanus*), together with available data on protein-coding genes from other Lagomorphs. We developed a pipeline to identify and align orthologs and use codon-based methods to infer instances where positive selection impacted the evolution of genes at particular sites in some of the major branches of the phylogeny. The inspection of the affected genes and their functions provides valuable insights on the occurrence and nature of evolution driven by natural selection that lies at the very foundation of several of the Lagomorph groups, such as Leporids and hares.

O10 *Open session***Dublin Hareport: increased aircraft related mortality of a resident population of Irish hare (*Lepus timidus hibernicus*) at Ireland's largest civil airport**

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Mammal-strikes with aircraft are a global phenomenon constituting 3-10% of strike incidents. Despite mammal strikes being 5x more likely to inflict damage to an aircraft, there has been relatively little research into the management of mammals on airfields or on mammal strike mitigation. Here we report on the unique opportunity to study mammal strikes in Ireland, by focusing on the ecology of the endemic Irish hare (*Lepus timidus hibernicus*) inhabiting the airfield at Dublin Airport. Over a 30-year period, a total of 320 strike events with the Irish hare have been recorded at the airfield, with a sharp increase in strikes reported in 2011. Hare strikes will be discussed in the context of the rate of civil aircraft movements, possible direct and indirect damage to aircraft, and airfield wildlife hazard management. Here, we demonstrate that not only are strike events increasing by 14% on an annual basis, but that the kinetic energy of such an event has the potential to cause significant damage to an aircraft. In an effort to reduce these strike events, ecological survey methods have been used to collect population level data. These data have been used to model the population size and circadian activity overlap of the hares with aircraft to identify high risk periods. Given the sensitive nature of the airport environment, paired with the protected status of the Irish hare, this work gives us a valuable insight into how to conduct ecological research in heavily restricted and anthropogenically influenced habitats.

O11 *Open session*

Two species, one pheromone? Evidence that the European rabbit *Oryctolagus cuniculus* and the Mexican cottontail *Sylvilagus cunicularius* share the same nipple-search pheromone

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The European rabbit *Oryctolagus cuniculus*, in common with other lagomorph species, has an unusual pattern of maternal care in which the mother visits her secluded young for just a few minutes once a day to nurse. To locate the mother's nipples and obtain sufficient milk and survive to the next brief nursing, the altricial young depend on chemical cues, a so-called nipple-search pheromone, on the mother's ventrum. Emission of this pheromone is under hormonal control; ovariectomized (OVX) females do not emit it, estrous females emit it to some degree, and lactating females emit it the most, eliciting immediately a highly stereotyped nipple-search behavior and nipple attachment in the young. These effects can be simulated by the administration of hormones of reproduction to OVX females. Given the similarity in the pattern of brief maternal care in the (Old World) European rabbit *Oryctolagus cuniculus* and the (New World) endemic Mexican cottontail rabbit *Sylvilagus cunicularius*, we asked whether there might be commonalities in this chemical signal between the two species. In a crossover design in which we tested the response of newborn young of each species to the ventrum of anesthetized OVX, pregnant and lactating females of each species at the field station Estación Científica La Malinche, we obtained evidence that commonalities exist; that is, pups of each species did not show nipple-search behavior or locate nipples on OVX females of either species, they searched somewhat on pregnant females of both species, and searched vigorously and located and attached to nipples of lactating females of both species. These findings call into question the narrow definition of “pheromone” as species-specific, and suggest that chemical signals of such vital importance in an unusual and highly conserved pattern of rabbit maternal care may have been retained over millennia.

O12 *Open session***Declining breeding success of the European hare in French farmland**

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The loss of biodiversity in farmland has been reported in several studies and concerns species among all taxa. In particular, the European hare *Lepus europaeus* has been declining between the 1960s and early 2000s as shown by the decrease in hunting bags throughout Europe, likely due to habitat change. We first assessed the abundance trend of several hare populations in France over the last 30 years. Despite spatial variation, we observed an overall negative trend in the population annual growth rate suggesting that hare population dynamics are slowing down. Second, to test the hypothesis that the decrease of the population growth rate was associated with a lower recruitment rate, we investigated the evolution of the age structure in the hunting bags in France over 30 years. We found that overall the age ratio in hunting bags, which was around 2 young per adult in the 1980s, decreased to 1 young per adult during the mid-1990 before stabilizing. The decline seemed to start earlier in grassland-dominated habitat than in cereal-dominated habitat. Third, we studied the distribution of birth dates of hunted young hares. We didn't observe any change in this distribution over time or habitat. This suggests that the cause of the decline of the recruitment rate occurs during the whole breeding season. For instance, a high predator density may have a negative impact on leveret survival during the entire breeding season whereas agricultural machinery which occurs over a more limited period. We thus looked at red fox (*Vulpes vulpes*) data, the most known hare predator. From different sources, we found a 2 to 6-fold increase of abundance index since the 1990s, consistent with our hypothesis. As a consequence of this declining breeding success, the fate of hare populations may become more and more sensitive to variation in maintenance than in recruitment.

O13 *Open session***Gimme, gimme shelter: Determining key habitat features used by desert cottontails (*Sylvilagus audubonii*) for improved habitat restoration and conservation**

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Throughout the world, Lagomorpha populations are declining. This decline destabilizes the key functions they play within an ecosystem. *Sylvilagus* species play multiple ecosystem roles including, being a key prey species, an ecosystem engineer and a seed disperser. Specifically, the desert cottontail (*Sylvilagus audubonii*) is the primary prey species for many predators in the western America grassland and desert ecosystems. Despite this important role, there is minimal research and monitoring on the desert cottontail. In Colorado this research is critical because of the acute threats this species faces. Most notably, the presence of Rabbit Hemorrhagic Disease Virus 2 (RHDV2) and major habitat loss due to anthropogenic and environmental factors. Our research is focused on identifying key habitat features that will allow researchers and agencies to increase rabbit populations through habitat restoration. To do this, we investigated the effects of vegetation patterns on space use and selection from desert cottontails. To determine fine-scale vegetation characteristics we used satellite imagery and object-based imagery analysis (OBIA) to produce vegetation maps. Then we overlaid telemetry data on the vegetation maps to create resource selection functions (RSF), which highlights areas of importance. Additionally, we conducted comprehensive winter vegetation surveys to identify key refugia features that cannot be identified through remote sensing technology. Our results indicate desert cottontails are selecting for high and low shrub cover. These results illuminate the relationship between diversity of key habitat features and long-term stable desert cottontail populations within the semi-arid grassland ecosystem and will allow land managers to identify and promote desert cottontail habitat.

O14 *Open session*Using genomic patterns of introgression to reconstruct the history of divergence between the sister broom and Corsican hares (*Lepus* spp.)

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Hybridization leading to genetic introgression between species is a ubiquitous evolutionary process that may strongly influence the gene pool of extant species. Characterizing patterns of introgression in species that have recurrently hybridized with neighbour close relatives can provide important insights on the history of contacts between species and the selective and demographic processes underlying the genetic exchanges. Here, we study these processes focusing on two sister hare species that are the result of a yet poorly characterized recent split from a common ancestor: the broom hare (*Lepus castroviejoi*) and the Corsican hare (*L. corsicanus*), allopatrically distributed in the Iberian and Italian Peninsulas, respectively. These sister species are known to have anciently hybridized with the mountain hare (*L. timidus*) before their split, and to have more recently differentially hybridized after their separation with the neighbouring Iberian hare (*L. granatensis*), and possibly with the European brown hare (*L. europaeus*) and again with the mountain hare. We use whole genome sequencing data to characterize and model the process of divergence between the sister broom and Corsican hares, and infer ancient and recent introgression affecting the species from the different sources. Our results will provide novel insights about the genomic and biogeographic processes underlying the separation of broom and Corsican hares, and refine our understanding of Pleistocene and post-glacial dynamics leading to recurrent contacts among southern European hare species. Furthermore, our results will show how introgression has influenced the evolutionary trajectories of broom and Corsican hares.

O15 *Open session*

Gastrointestinal parasite infestation in the Alpine mountain hare (*Lepus timidus varronis*): are abiotic environmental factors such as elevation, temperature and precipitation affecting prevalence of parasite species?

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Information concerning factors regulating Alpine mountain hare (*Lepus timidus varronis*) populations such as host-parasite interactions is missing as only a few parasitological surveys exist of this subspecies. Parasites are not only dependent on their host but also on suitable environmental conditions for infestation. Abiotic environmental factors have an important regulating role on parasites in mammals. It is estimated that the elevation range of parasites is likely to shift in response to alternate host movement and changes in climate. Here we assess the parasitic infestation in the Alpine mountain hare by analysing the parasites in faeces and comparing the parasite infestation at different elevation ranges and at varied weather conditions for two years in the Austrian Alps. Almost half of the faecal samples were free of parasites (46.2%, n=52). Most frequent was the infection by Coccidia (46.2%), whereas stomach intestine strongylids, *Trichuris* spp, and Cestoda were only found in 9.6% of all faeces. Hence, only Coccidia may be prevalent enough to regulate Alpine mountain hare populations in the Austrian Alps. Elevation had a significant positive effect on the infection of animals by *Trichuris* spp, whereas temperature had a significant negative effect on the infection by any parasite traceable in faeces and, when looking at the parasite groups individually, on Coccidia.

O16 *Open session*Sex biases the flea (*Siphonaptera*) infection on wild Mexican cottontails (*Sylvilagus cunicularius*): report from a longitudinal study

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Fleas play a critical role in population dynamics on wild rabbits. These parasites are vectors of relevant diseases among lagomorphs like myxomatosis and rabbit haemorrhagic disease (Mexico government reported an outbreak of the latter in 2021). In this way it is essential to know the ecology and population dynamics of wild rabbit fleas in order to understand what factors control flea presence and abundance. It is known that sex, reproductive status or body mass of the host influence flea abundance. Our aim was to look for biases in flea infection related to sex and reproductive state of endemic Mexican cottontails (*S. cunicularius*). For this, we captured cottontails on the Malinche volcano in central Mexico over a period of 14 years (since 2000 to 2013). We used wire (Tomahawk®) and net traps. Captured individuals were handled for obtaining body measurements and ectoparasites. We introduced every rabbit in a cloth bag and then in a plastic bag with chloroform in order to obtain adult fleas. Once we obtained samples and data from individuals, we release them in the site of capture. Generalized linear mixed models were applied to data for analyzing prevalence and total number of fleas. We obtained 526 captures of individuals, 239 from females and 287 from males. We found three flea species belonging to Pulicidae family: *Cediopsylla inaequalis interrupta* (8660 specimens), *Euhoplopsyllus glacialis affinis* (1073) and *Pulex irritans* (20). Relative to infection level we present parasite infection parameters. Overall parameters were as follows: flea prevalence 67.8%, mean abundance: 19 fleas per individual and mean intensity: 27 fleas per infected individual. Model analyses showed significant higher prevalence and number of fleas on females and higher number of fleas on non-reproductive animals. This female bias in flea infection contrasts with a general pattern in flea infection skewed to males in mammals.

O17 *Open session***Hare today gone tomorrow: the role of interspecific competition in shaping riverine rabbit occupancy and density**

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Effective species conservation requires understanding population dynamics, allowing managers to quantify the impacts of environmental changes. In the case of one of Africa's most endangered mammals, however, little is known about the ecology of the species, which inhibits conservation efforts. The riverine rabbit (*Bunolagus monticularis*) is endemic to the drylands of South Africa and is strongly associated with vulnerable riverine habitats. Critically, the influence of two sympatric competitors, namely *Lepus saxatilis* and *Lepus capensis*, on riverine rabbit occurrence has never been examined. In this study, we used non-invasive remote cameras to evaluate how interference competition affects the occupancy, temporal activity and density of the riverine rabbit. Camera trapping data were collected from 3 sites with historical records of rabbit presence in the Klein Karoo, South Africa, covering 223.24 km². Alarmingly, riverine rabbits were only detected at one of the sites. We fitted a multi-species occupancy model to assess the spatial response of riverine rabbits to varying environmental conditions and competitor presence. We also examined the temporal overlap in activity patterns between all species, and estimated their respective densities using the random encounter model. In contrast to prior studies, we found that riverine rabbits were not restricted to riverine habitat. Results showed that riverine rabbit occupancy was conditional on their competitors' absence and less rugged terrain. In contrast, hare occupancy was independent of riverine rabbit presence and terrain ruggedness. Temporal overlap was high between the species ($\Delta = 0.828$), and hares occurred in substantially higher densities. Our results suggest that conservation management underestimated the importance of competition with other lagomorphs in understanding riverine rabbit occurrence. This study furthers our understanding of the fine-scale predictors of presence for one of the world's rarest mammal species.

O18 *Open session***Saving the striped rabbits: A conservation action plan for the Annamite and Sumatran striped rabbits**

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The *Nesolagus* genus is represented by two extant species, the Annamite striped rabbit (*Nesolagus timminsi*) and the Sumatran striped rabbit (*Nesolagus netscheri*). Historically, there have been few targeted studies of either species, and their ecology has remained largely unknown. Owing to the lack of information on the species, there have been few conservation initiatives implemented for the species, and little coordination of research and conservation efforts. However, recently documented poaching and capture of both striped rabbit species has highlighted the urgency of strong conservation initiatives for the species. Recently, the IUCN SSC supported the formation and first meeting of the IUCN Lagomorph Specialist Group Striped Rabbit Working Group in Bogor, Indonesia. This was a collaborative effort to assess what is currently known of the two species and the threats that they face. The working group then prioritized research needs and the implementation of conservation actions for the two species, which we report here.

O19 Open session**Drawing the baselines for the good management of a Mediterranean key species, the wild rabbit**

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The European wild rabbit (EWR) (*Oryctolagus cuniculus*) is an endemic species in the Iberian Peninsula that has undergone a progressive decrease in abundance due to two viral diseases (myxomatosis and rabbit haemorrhagic disease (RHD)), along with habitat changes. Additionally, the emergence of a new variant of RHDV in the last decade accelerated the decline in the EWR throughout its native range, causing severe conservation problems jeopardizing the conservation of its top predators (*e.g. Lynx pardinus, Aquila adalberti*) by seriously affecting their reproductive success. Rabbit population decline is also causing socio-economic problems in rural areas where rabbit hunting is an important economic driver. In parallel, there have been local demographic explosions in farmland areas, causing notable crop damage and important economic losses. In this context, EWR population management at the Iberian Peninsula level is fundamental given its economic and ecological value. In the Iberian Peninsula, the EWR distribution and abundance are quite heterogeneous in space and time. Currently, there is an absolute lack of governance with species management occurring at local level, and measures with differing objectives being applied by different stakeholders. Furthermore, experiences are not frequently shared among parties involved in rabbit management, and knowledge and standard protocols and monitoring methodologies are usually not available, making data comparison difficult. For example, it is not even possible to define EWR population status in most peninsular areas where it is crucial to establish wide-range conservation goals. The main goal of Iberconejo LIFE project is to create a global Iberian governance structure responsible for a coordinated EWR management in the Iberian Peninsula by implementing consensual management and monitoring protocols involving all partners and stakeholders. Additionally, Iberconejo will gather information on population status and will design and implement management measures that will consider all aspects related with species conservation and its socio-economic impacts.

O20 *Open session***Serosurveillance of the myxoma virus in Iberian hares (*Lepus granatensis*) after the first outbreak**

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Myxomatosis is an infectious disease that affects wild and domestic lagomorph species, caused by a *Leporipoxvirus*, the myxoma virus (MYXV). After its first introduction in Europe in the 1950's, European wild rabbit (*Oryctolagus cuniculus*) populations declined due to initial high mortality rates. Throughout the decades, mortality decreased as virus and host undergone a co-evolution that resulted in attenuated viral strains and higher host resistance. Consequently, the MYXV is now considered endemic in the Iberian Peninsula with detected seroprevalence values around 50%, but it still produces epizootic outbreaks with significant mortality rates in susceptible rabbit populations. Despite active circulation in Iberia, no outbreaks had been reported in Iberian hares (*Lepus granatensis*), as this species was considered to have a low susceptibility to MYXV infection. However, in 2018 an event of massive mortality was notified in the Cordoba province (Southern Spain), after which reports of ill or dead individuals quickly spread throughout the Peninsula. A new recombinant strain of the MYXV was identified (ha-MYXV) that was able to successively infect Iberian hares and cause severe disease and death. A large-scale study was carried out to determine the prevalence of antibodies against MYXV in this hare species after the first outbreak. For that end, around 700 serum samples were collected between 2018 and 2022, through active surveillance conducted across most of the Iberian hare range. A commercially available indirect ELISA was employed to detect anti-MYXV antibodies. Preliminary results show seroprevalence values of around 20%, indicating that clinically health hare populations had moderate exposure to this virus and developed some degree of immunity with antibody production. Nonetheless, our study highlights the importance of long-term surveillance for a better understanding of the epidemiology of ha-MYXV in Iberian hare populations in the Iberian Peninsula.

O21 *Open session***Absence of hepatitis E virus circulation in hares collected in Italy from 2019 to 2021**

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Hepatitis E virus (HEV) is the agent of the hepatitis E disease that in Europe is mainly transmitted foodborne. Human cases in EU have increased in the last years and are linked to the consumption of raw or undercooked pork product or wild boar meat infected by the zoonotic HEV-3 genotype. Rabbit HEV (HEV-3ra) is a recent genotype of HEV detected in feral, wild and farmed rabbit species (France 23%, Netherlands 60% and Germany 37.3%), and, only recently, in humans in both France and Switzerland. The genotype is now considered zoonotic, most likely affecting immunocompromises but so far, no foodborne transmission has been described. Genetically, the virus strictly resembles the zoonotic genotype HEV-3, except for an insertion in the ORF1 and more rarely in the overlapping ORF1-ORF2 region (recombinant subtype). The infection in rabbits is similar to other animal hosts and the virus is localized in several organs besides the liver. In Italy, two studies confirmed the circulation of the virus in pet and wild rabbit populations, by detection of anti-HEV IgG. The viral RNA has been detected rarely in only a few wild animals in Tuscany region and matched with both HEV-3 and HEV-3ra. In the present study, we investigated the occurrence of HEV-RNA in liver of 328 brown hares (*Lepus europaeus*) sampled in 13 Italian regions between 2019 and 2021, in the framework of the regional surveillance plans for wildlife diseases. HEV-RNA (0/328 liver samples) and anti-HEV antibodies (0/34 meat juice) were not detected in any tested hare. In conclusion, even if the hare seems not to be involved in the epidemiology of HEV further investigation is needed to constantly monitor the HEV presence in wild hosts, and to prevent possible foodborne zoonotic spill-over of both HEV-3 and HEV-3ra genotypes.

O22 *Open session***Multidisciplinary approaches to recovering an imperiled cottontail in the presence of competing threats in a heavily impacted system**

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The New England cottontail (NEC) is a shrubland obligate lagomorph that has experienced an >86% range contraction. A large multi-state and multi-agency recovery effort is in place including active habitat management, two captive breeding facilities, two offshore breeding colonies, and multiple fenced breeding pens; however, despite this considerable effort the species continues to decline. Limited dispersal capability, a hostile matrix, and limited habitat availability limit individual fitness and population sizes of NEC, placing extant populations at high risk of extinction. However, managing for these impacts is challenging as competitive interactions with the non-native eastern cottontail alter habitat use by NEC. We use a multidisciplinary approach, incorporating information from movement and resource use, survival, population genetics, parasitology, and experimental habitat management to understand these complex interactions and inform adaptive management of NEC in this heavily impacted system. Our results indicate that as a result of limited available habitat and a hostile matrix, NEC populations are small and severely fragmented with highly restricted movement. Within suitable patches, competitive exclusion by eastern cottontail results in use of otherwise avoided cover types. However, survival is higher within these areas, potentially a result of differences in density dependent interactions and predation between attractive and unattractive cover types. We find that proper placement of managed habitat can result in rapid colonization under appropriate conditions and management prescriptions. Further, experimental habitat manipulations targeting NEC use and survival over that for eastern cottontail indicate competitive interactions can be mitigated through targeted habitat management. Herein, we highlight the importance of understanding system complexity when managing species and propose a paradigm shift to ensure recovery of NEC. Variation in such biological phenomena indicates that the functional signal conveyed for a given environmental stimulus will differ due to the variable responses of disparate skeletal structures as well as temporal variation in external loading patterns.

O23 *Open session***Abundance and habitat use of the insular endemic black jackrabbit (*Lepus insularis*) in Espiritu Santo Island, Gulf of California, Mexico**

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The black-jackrabbit (*Lepus insularis*) is an endemic lagomorph only present in the Espiritu Santo Island, Gulf of California, protected by the Mexican law, and categorized as vulnerable by the IUCN. Ecological knowledge about this species is scarce and even its population status is poorly known. Additionally, in 2021 the Rabbit Hemorrhagic Disease Virus type II was detected in some dead individuals. In response to this potential vulnerability scenario, we generated a baseline study of its current habitat use and spatio-temporal abundance. We delimited a grid composed by cells of 2.5 km x 2.5 km along the archipelago and then we selected 20 cells by random sampling, where we established a total of twenty 500-m-long transects divided in ten 50-m-long sampling points. We considered the number of fresh fecal pellets as an indicator of black-jackrabbit abundance. To reach our first objective, we measured twice a year eleven topographic and ecological variables in each point (bare ground, coverage by vegetation height, slope, soil type percentage, competitors' presence, food availability and number of fresh fecal pellets) totalizing 200 sampled points. Using a General Lineal Model, we analyzed the relationship between species abundance and habitat variables and constructed a niche model using Maxent. For our second objective, spatio-temporal abundance, we monthly counted fresh fecal pellets in eight 500-m-long transects for a year. Each transect was divided in 10 sections, totalizing 80 sampled points. Based on previously defined habitat characteristics, we assigned a habitat type to every sampling point. We estimated relative abundance monthly, annually, per season and per habitat. Our results suggest that in 2021 the black-jackrabbit was more abundant during the months of April, May and August and its abundance is related to the vegetation height.

O24 *Open session***Tularemia, common vole outbreaks and Iberian hare population trends: correlative evidence for “disease pit” situation**

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Iberian hare (*Lepus granatensis*) populations have suffered severe declines in recent decades in Spain, probably due to a combination of various factors (e.g. agricultural intensification, predation, emerging diseases, etc.). During the 1970-90s, an abrupt increase in irrigation and alfalfa cultivation occurred in the Tierra de Campos area (NW Spain) and was associated with an invasion by the common vole (*Microtus arvalis*) that colonized lowland agricultural areas from surrounding mountainous habitats. The large fluctuations in abundance of voles (population outbreaks) contribute to the amplification of *Francisella tularensis*, the etiological agent that causes tularemia that was first detected in the region in 1996. Tularemia, is a lethal disease for the Iberian hare and to assess the possible effect of vole fluctuations, and concomitant tularemia outbreaks, on Iberian hare populations, we analysed hunting bag data in the Tierra de Campos area most affected by vole outbreaks during 1996-2019. We also compiled data on tularemia prevalence in Iberian hares reported by the regional government during 2007-2016. The results showed a generally negative trend of hares' abundance based on the hunting bags for the study period. An index of Iberian hare population growth rate showed a reduced growth during common vole outbreak years as compared with non-vole outbreak years. In addition, the prevalence of tularemia in hares was significantly higher during common vole outbreak years and the year after. This suggest that tularemia may persist in hares at least one year after a vole outbreak. In general, our results indicate that vole population outbreaks may limit the recovery of hare populations by amplifying and spreading tularemia in the environment and it may be placing the lagomorph in a situation known as a "disease pit", keeping hares in a low-density equilibrium below a threshold that does not allow the population to reach a high-density equilibrium.

E1 Short talks: Ecology, Behaviour & Conservation**Reproductive isolation between European rabbit subspecies informed by genome wide hybrid incompatibilities**

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Reproductive isolation is a fundamental step towards speciation. In this context, hybrid populations represent ideal systems to explore the emergence of genetic incompatibilities and their link to differences in fitness. The European rabbit (*Oryctolagus cuniculus*) system represents a classic example of range contraction and population divergence in allopatry with subsequent range expansion and secondary contact of two subspecies (*O.c.cuniculus* and *O.c.algirus*). The hybrids from these two subspecies form a stable hybrid zone from northwest to southeast Iberia and have lower fitness than the parental populations, specifically regarding male sterility, suggesting ongoing speciation. To test this hypothesis, we sought to identify areas of the genome involved in postzygotic hybrid incompatibilities. We generated exon capture data for 190 hybrid rabbits from a single population and 20 parental male rabbits from two and three populations of *O.c.cuniculus* and *O.c.algirus*, respectively. We obtained over 4 million SNPs with which we characterized the hybrid population in terms of genetic diversity and hybrid index, performed ancestry disequilibrium mapping and searched for epistatic associations between loci, both within and between autosomal, sex-linked and mitochondrial loci. We determined that the European rabbit hybrids included in this study represent a population with around 60% of *O.c.cuniculus* proportion at the autosomal, X chromosome and mitochondrial levels, and around 80% considering the Y chromosome. We also identified multiple regions of the genome where the hybrid population has decreased nucleotide diversity compared to both parental populations that also overlap with extreme shifts in allele frequencies in the hybrid population, representing potential areas of genomic incompatibility. Gene ontology analysis of some diagnostic SNPs present in these regions show associations to processes relating to gonad development and fertility across multiple chromosomes. Taken together, these results highlight the great potential of studying hybrid populations for the identification of genomic incompatibilities in populations undergoing early reproductive isolation.

E2 Short talks: Ecology, Behaviour & Conservation**Decrease of European hare (*Lepus europaeus*) densities in a context of grassland-dominated areas: feasibility study of reinforcement operations involving captive-bred animals – first analyses**

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While European hare (*Lepus europaeus*) densities are slightly decreasing within Europe, populations have reached a critical threshold in some medium mountain areas, suggesting local losses of genetic diversity. To reverse this dynamic, we launched a 2 year-program of reinforcement operations involving captive-bred animals (2021-2022), in a selected 4,000ha grassland-dominated area. We released 74 hares in 2021, all fitted with GPS tags and accelerometers. At individual-level, we respectively (i) assessed their survival, (ii) identified the causes of death and (iii) monitored their behavioural responses to both land-cover and land-use. At population-level, we assessed the effectiveness of these operations (i) by estimating the local hare density using complementary methods to the common KAI (*i.e.* spotlight count & distance sampling) and (ii) by assessing the evolution of the genetic structure of the population onsite (faeces collection).

Survival & death causes – 13 hares were still alive in February 2022. Predation explained most of deaths (75%), followed by parasitism (13%), road collision (6%) and unknown circumstances (6%).

Behaviour – In 2021, monthly home-range median size (Kernel 95%) increased from 24 ha [95% CI: 15 - 59] to 70 ha [95% CI: 57 - 78] between July and December.

Density estimation – In Spring 2019, respectively 30, 29, 22 wild hares were detected during a 3-night spotlight count survey. Detectability ranged from 0.41 to 0.88 and density surface models predicted an average density of 7-8 hares/100ha. *Analyses are still in progress to confirm these results and make further predictions for the next years.*

Genetic structure – In 2020, within the study area, 46 different wild individuals were identified, based on 107 faeces analyses. *Parenthood analyses are in progress.*

The results of this study will improve both management and monitoring programs of reinforcement operations and will contribute to the knowledge for the conservation of the species.

E3 Short talks: Ecology, Behaviour & Conservation

Using faecal pellets to monitor the changes in mountain hare *Lepus timidus* and the European hare *Lepus europaeus* wintering distribution in the French Alps

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The mountain hare *Lepus timidus* is an artico-alpine species living in isolated relic populations in the Alps. Its distribution is expected to contract with rising temperatures, leading to population isolations. Low- to mid-altitude populations could thus disappear in the coming decades. Conversely, the European hare *Lepus europaeus* could be favored by the temperature rising and extend its distribution area higher up, causing competition or hybridization with the mountain hare. Here we developed a pilot-study to implement a rigorous protocol for tracking these changes in the long-term. The nocturnal, discreet behavior and mimetic coat of the mountain hare make individuals very difficult to detect. The development of genetic techniques based on faecal pellets collected in the field offers new opportunities to study its distribution. The pilot-study began in 2018 in several French alpine massifs. We fitted a first niche-model based on hare presence-only data combined with topography, land-cover and climate covariates. We then applied a 2km squares grid on high occurrence probability areas of the two species revealed by the niche models, excluding squares too steep or with low snow-cover. 21 squares randomly selected in the Mercantour National park were prospected by skiing or snowshoeing by 2 to 4 observers who collected faecal pellets in the snow. These data (360 presence-absence obtained by genetic analyses) were used to fit a new niche-model that significantly improved the precision of the predicted distribution of the two species. The yearly snow-cover duration was the best predictor of the two species occurrence probabilities, revealing highly segregated distributions. The application of this protocol on most of the Alpine French protected areas should provide a precise overview of the current distribution of the two hare species and help predicting and measuring the effects of long-term climate changes.

E4 Short talks: Ecology, Behaviour & Conservation

Stable individual differences in the frequency of chin-marking behavior across development in the domestic rabbit (*Oryctolagus cuniculus*): What does it mean?

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Individual differences in behavior (“personality”) are of considerable interest to behavioral biologists. Important questions include how early in life such differences emerge, what factors influence their emergence, and whether they remain stable across development and into adult life. Given the demanding nature of longitudinal studies there is a lack of information regarding these questions in mammals. Our aim in the present study was to investigate the development of individual differences in chin-marking behavior (chinning) in the domestic rabbit, a notable part of this species' system of chemical communication, and to relate this to individual differences in growth and behavior among littermates during the early post-natal period. We tested repeatedly the frequency of chinning movements from weaning to sexual maturity in 63 chinchilla-strain rabbits (35 females, 28 males) from 14 litters. Within litters, we found significant consistencies over time in this behavior, i.e. in both sexes litter-sibling differences in the frequency of chinning movements remained stable across the post-weaning period until sexual maturity. Unexpectedly, however, we found no significant association with the morphological, physiological or behavioral variables known to form a well-correlated early developmental complex in this species. We tentatively conclude that in the rabbit individual differences in the frequency of chinning have little relation to other previously studied aspects of individual developmental trajectories. The origin and functional significance of individual differences in chinning frequency, whether in reproductive or other social contexts is largely unknown and requires further investigation (Grant from PAPIIT-UNAM IN213120, ECOS-NORD-ANUIES Nos. 2999016 and M19A01, CONACyT 227352).

E5 *Short talks: Ecology, Behaviour & Conservation*

Warming climate favours the spatial overlap between mountain and European hares at the top of the Alps

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The mountain hare (*Lepus timidus*) is a boreo-alpine species with an unfavourable/inadequate conservation state in parts of its range. Its populations seem to be declining in the Western Alps: the species is threatened by climate change because of its sensitivity to temperature increase and the limited possibility to shift toward higher altitudes. Climate change might also favour the European hare (*Lepus europaeus*), a lowland species that invades the mountain hare range with a risk of introgressive hybridisation. So far, no study investigated the distribution of hare species in the Alps over time. Our research fills this gap by assessing the distribution of species in a valley in the Western Italian Alps using non-invasive genetic techniques based on mtDNA. In 2009 and 2021, we collected faecal samples of hares along 47 transects, analysing data with standard and Bayesian approaches. Results suggest a significant increase in time in the proportion of the European hare mtDNA. We also detected a range contraction at lower latitudes for mountain hare and an expansion toward higher altitudes of the European hare. Habitat use of the species changed accordingly, with an increased presence of European hares in alpine pastures. In 2021 individuals of mountain hares coexist with European hares of different sex, confirming the potential for hybridisation. This study allows to quantify the impact of a decade of climate change on these species. In the Alps, the European hare is expanding toward higher altitudes, invading the habitats of the mountain hare. The latter is retracting from the lowest altitudes. This spatial dynamic suggests that the brown-mountain hare alpine system could evolve in the medium-term towards a complete admixture of the two species. In the long term, the mountain hare risks becoming extinct due to the habitat no longer being suitable and the hybridisation with the European hare.

E6 *Short talks: Ecology, Behaviour & Conservation***The Faroes mountain hare (*Lepus timidus*) and hunting of hare in the Faroe Islands during the years 2012-2021**

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The Faroe Islands are an archipelago consisting of 18 islands, located in the North Atlantic, between Norway, Iceland and Scotland. Mountain hare (*Lepus timidus*) is a relative new species on the islands. It was first introduced for hunting in 1855, when four leverets were introduced from South Norway. They did well and multiplied rapidly. Ten years later, thousands of hares were reported roaming around in the wild. Today they populate 15 of the 18 islands in the archipelago. Since then, annual hare-hunting has taken place in the Faroe Islands, mainly during November and December. Although hare has been hunted for more than 150 years in the Faroes Islands, no official hunting statistics have been available and no assessment has been made. To improve this, I started to collect hunting data in 2012. A Facebook page for hare hunters was created. On this page hunters voluntarily reported their catch and experience. The idea of the Facebook group turned out to be a huge success, as information came directly from the hunters, who may otherwise not have come forward. For each hunting trip, information on location, date, number of hares shot and number of participants are registered. By this, citizen science was introduced as a management tool for hare hunting in the Faroes Islands. During these 10 years, the average annual number of hunted hares has been 6,265 hares. However, there is a huge fluctuation among years, from being only 2,950 hares in 2016 to 9,562 hares in 2020. In my presentation, the hunting statistics of the Faroese hare during the last 10 years, from 2012 to 2021, will be presented: How many individuals are hunted each year on each island, in each field, and village on specific days.

E7 Short talks: Ecology, Behaviour & Conservation**Experimental study on the reproductive seasonality of *Oryctolagus cuniculus* subspecies**

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The importance of the European wild rabbit (*Oryctolagus cuniculus*) in its native area, the Iberian Peninsula, stresses the need to understand its population dynamics and thereby to optimize the management of the species. Although the reproductive patterns of this species have been assessed globally, there are no studies that explore this aspect from the perspective of its subspecies: *Oryctolagus cuniculus cuniculus* (Occ) and *Oryctolagus cuniculus algirus* (Oca), which evolved independently approximately two Ma and have different geographical ranges. Variations in reproductive seasonality between rabbit subspecies could be expected as previous studies have revealed many other differences between them in terms of genetic or biometry and a genetic basis for reproductive seasonality in the European rabbit has been described. In this work we examine throughout monthly captures the proportion of sexually active rabbits of each subspecies maintained in semi-captive enclosures in Central Spain, where both subspecies naturally coexist. According to our results, Occ males present a more marked seasonality than Oca males and in accordance with this Oca specimens begin their maximum reproductive activity before Occ individuals, while both groups finish their reproductive season more or less at the same time. Nevertheless, the decline of Oca is apparently more progressive. In addition, the maximum peak of activity is observed slightly earlier in the case of Oca. These observations together could suggest the adaptation of each subspecies to the typical climatic conditions of their distribution areas, a point that would be worth investigating in greater depth as it would be important when guiding the appropriate management strategies for each subspecies, even more so in the current context of climate crisis.

E8 *Short talks: Ecology, Behaviour & Conservation*On the ecology of the Italian hare (*Lepus corsicanus*)

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The Italian hare (*Lepus corsicanus*) is endemic of Central-Southern Italy and Sicily. It is classified as Vulnerable according to the International Union for Conservation of Nature, mainly due to habitat alteration, the isolation in distant and low-density subpopulations, and ecological competition with the introduced European hare (*Lepus europaeus*). To date, information about the ecological preferences of the Italian hare is still fragmented and provided for a few local areas. Here, we show the first large scale results on habitat preferences of the Italian hare for the whole peninsular distribution range of the species, defined using a habitat suitability model based on presence data genetically validated by High Resolution Melting analysis on DNA from faecal pellets. Agricultural meadows, crops, and deciduous woods emerged as the preferred habitats for the Italian hare. Information on the ecological distribution were integrated with seasonal diet data, inferred with DNA metabarcoding and High Throughput Sequencing, to define the ecological niche of the Italian hare, considering spatial and temporal variability of all resources. The diet of the Italian hare all year round included 192 genera in 62 families. *Fagaceae*, *Fabaceae*, *Poaceae*, *Rosaceae*, and *Solanaceae* emerged as the most frequently occurred families, accounting for 90.22% of the total diet. Deepening the knowledge about the ecological requirements of the Italian hare is one of the key goals to aim for to define suitable management and conservation strategies for this threatened species.

E9 Short talks: Ecology, Behaviour & Conservation**Reproductive cost in female European and mountain hare**Marco Rughetti¹, [Maria Ferloni](#)²

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In female mammals, reproduction requires high-energy expenditure because of gestation and lactation; therefore, a fitness cost of current reproduction may lead to a decrease in future survival or reproduction. The reproductive cost differs between short-lived species with fast life history strategy, compared to long-lived species with slow life history strategy. In short-lived species, females are more likely to adopt a risky prone reproductive strategy, allocating more energy to current reproduction rather than to survival, and a negative correlation between current and future reproduction is unlikely to be observed. In long-lived species, females often adopt a conservative reproductive strategy, allocating more energy to survival rather than to reproduction, and a negative correlation between current and future reproduction is expected. We used harvest data on reproduction and body mass of two small size mammals: mountain and European hare (*Lepus timidus*, *Lepus europaeus*), to explore the reproductive cost of reproduction, and to determine how reproductive success affects body mass. Within a reproductive season, current reproduction in adult female hares was negatively affected by previous reproductive success; the effect was larger in European compared to mountain hare. Female hares with high seasonal reproductive success were larger in body mass at the end of the breeding season and experienced the highest number of litters. Our results support the hypothesis that hares, at least to some extent, adopt a prudent reproductive strategy. A reproductive strategy based on energy investment in maintenance of body mass and on a reproductive cost of current reproduction, may result in an increase number of reproductive opportunities during the breeding season. Increasing the level of iteroparity makes it worthwhile to adopt a conservative strategy of reproduction. Allocating additional energy to body mass maintenance, even at the expense of current reproduction, may increase the number of litters per year and hence the overall seasonal fitness.

E10 *Short talks: Ecology, Behaviour & Conservation*

Long-term patterns of brown hare (*Lepus europaeus*) population dynamics in Vojvodina (Serbia) in relation to agriculture, climate and predation

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European hare (*Lepus europaeus*) is a well-known farmland species that is negatively affected by agricultural intensification. While it was thoroughly researched in most European countries in Serbia most questions considering the decline hasn't been researched. We analyzed the area of Vojvodina (Autonomous Province in northern Serbia) as a typical farmland habitat with very low percentage forest areas and around 85% of agricultural land. Data was collected for the period between 1970 and 2020 and preliminary analysis is presented. We included information on hare population and annual cull, climatic factors, crop categories, and the presence of red fox as the main predator. Preliminary results show a considerable negative effect of change in crops categories (rise of industrial crops, and decline of cereals), as well as the decline of meadows. Climate changes also negatively affected the population with a rise in average annual temperatures and a decline in precipitation (mostly during reproduction season). Predation didn't seem to have a considerable effect on the population.

T1 *Workshop: Taxonomy & Conservation***Updating the global conservation status and threat assessments for world Lagomorphs**

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The IUCN Red List of Threatened Species is a comprehensive inventory of the conservation status of species worldwide. We reviewed the recent 2016/2019 Red List re-assessments of all lagomorph species to examine the current status and global trends in Lagomorph conservation in order to understand the magnitude of threats facing rabbits, hares, and pikas. While most Lagomorph species are considered to be of Least Concern (LC), more than 42% are experiencing population declines. Out of 95 species worldwide, 24% are at elevated risk for extinction: 2 Critically Endangered (CE), 13 Endangered (EN), 8 Vulnerable (VU), and 2 Near Threatened (NT). Nearly 41% of leporids, but only 17% of ochotonids, are at elevated risk of extinction or Data Deficient (DD). These differences may reflect differences in accessibility, as many species of *Ochotona* are quite isolated and unstudied, and far more has been documented on leporid population trends. The threat status or Red List criteria were changed for 29% of all lagomorph species during the recent re-assessment, although 36% of those changes were due to taxonomic revisions (10 species since 2008). With 7 species considered DD and 41% of all lagomorphs whose population trends are unknown, these results further underscore the critical need for systematic monitoring, further taxonomic work, and the development of regional conservation expertise. With accelerating environmental change, the conservation activities of the IUCN Lagomorph Specialist Group and members of the World Lagomorph Society play a pivotal role in our ability to assess conservation threats, develop conservation plans, and promote actions to reduce biodiversity loss.

T2 Workshop: Taxonomy & Conservation

Genetic diversity and population structure of the broom hare, *Lepus castroviejo*

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The broom hare (*Lepus castroviejo*) is a threatened Iberian endemic, restricted to Northwest Spain. However, the overall knowledge about this species is very limited, particularly regarding its genetic diversity. Preliminary studies infer reduced genetic diversity, albeit using a very low sample size. To accurately infer the genetic diversity and population structure we performed a genetic non-invasive sampling (gNIS) approach by collecting 185 feces during 2020 and 2021. Five tissue samples collected opportunistically from roadkill specimens, and 17 samples collected previously (2003-2007) were also included. Moreover, in order to accurately compare the genetic diversity patterns and infer admixture, samples from other European hares were also analyzed: *L. europaeus* (81); *L. timidus* (77); *L. granatensis* (68); *L. corsicanus* (20). A 108bp fragment of mtDNA cytB was amplified and sequenced, followed by 240bp fragment of transferrin, to infer species ID. A panel of 15 microsatellites was genotyped, and a 556bp fragment of mtDNA cytB was sequenced for those samples that had a genetic profile. A total of 54 distinct individuals were identified in gNIS. *L. castroviejo* showed the lowest level of nuclear diversity ($N_a=2.53$, $H_o=0.160$ and $H_e=0.180$), and very low mitochondrial ($H_d=0.75$ and $\pi=0.01553$) diversity. Nevertheless, no signals of inbreeding or population bottleneck were detected recently. Two clusters were inferred from Bayesian analysis using microsatellite markers, partially segregating the populations from west and east of the Cantabrian Mountains. No recent hybridization was observed with neighboring *L. granatensis* and *L. europaeus*. Two highly divergent clades were also observed from mitochondrial cytB, one introgressed from *L. timidus*. This study emphasizes the importance on using gNIS for conservation planning and highlights the need to underline measures to preserve this endemic threatened species. This work was partially funded by Mr. Klaus Tamm, through the World Lagomorph Society.

T3 *Workshop: Taxonomy & Conservation***Comparative landscape genomics of an imperiled native and invasive cottontail in the Northeastern US**

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The New England cottontail (*Sylvilagus transitionalis*) is the only native cottontail to the Northeastern United States and a species of conservation concern due to its dramatic decline. New England cottontail is an early successional obligate and they have been negatively impacted by habitat loss and fragmentation. An additional factor in their decline has been competition with the invasive eastern cottontail (*S. floridanus*). Eastern cottontail are habitat generalists and can occur in both rural and urban areas. Thus, the gene flow of eastern cottontail should be less restricted than New England cottontail and New England cottontail gene flow should be impacted more by habitat fragmentation and the decline of early successional habitat. We used a double digest Restriction-site Associated DNA approach to generate single nucleotide polymorphism data for New England cottontail (n=210) and eastern cottontail (n=272). Neutral patterns of gene flow showed the grouping of New England cottontail into four clusters at the regional level, which is similar to previous research using more traditional markers. Eastern cottontail also showed evidence of four genetic clusters at the regional scale; however, the genetic clusters were not as distinct. An Estimating Effective Migration Surfaces analysis found the presence of barriers to gene flow for both species, but surprisingly the barriers were stronger for eastern cottontail. We also used machine learning and a random forest approach to test the influence of environmental variables on cottontail gene flow at a regional and three local scales. The environment did not consistently have a stronger influence on New England cottontail gene flow. In general, the environmental variables had the predicted effect on each species' gene flow. However, the most important environmental variable varied by subregion and species, which shows that location and species matter. The results of our research will help inform management decisions to conserve New England cottontail.

T4 Workshop: Taxonomy & Conservation**Systematics of the Eastern cottontail rabbit group species (Lagomorpha: Leporidae: *Sylvilagus floridanus*) from Southwestern North America to South America**

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The Eastern cottontail species group, *Sylvilagus floridanus* and allies, with putative subspecies continuously and discontinuously distributed from Venezuela to Canada, has one of the broadest distributions among extant mammal species, including populations relatively resilient to anthropogenic activities, and occurring at high densities. As such, the conservation status of the species is listed as “Least Concern” in the most recent version of the IUCN Red List. Our current operative taxonomic paradigm, based on recent research on forest rabbits of the *S. brasiliensis* species group, suggests that there is a tighter correspondence between ecology and taxonomy of *Sylvilagus* species than may heretofore have been appreciated. In light of the potential for speciation to have occurred over this broad range, we examined the holotypes of all the subspecies of *Sylvilagus floridanus* from Mexico to Venezuela. We examined discrete character variation as well as mitogenomes from fresh and museum specimens, including some of the holotype, paratype, and other historical and contemporary material, and compared them with the holotype, paratypes, and contemporary topotypical material of *S. floridanus*. Our findings demonstrate that, far from constituting a single species, the floridanus group in fact is constituted by a number of species-level taxa generally congruent with biogeographic regions. Here, we describe the morphological attributes and molecular data, and their joint bearing on speciation and biogeography of *Sylvilagus* in general, and taxa associated with the *S. floridanus* species group in particular.

T5 *Workshop: Taxonomy & Conservation*Introgressive hybridization promoted by climate change: a case study on hares (*Lepus* spp.)

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Climate changes and anthropogenic activities pose serious challenges to the survival of species, forcing them to move, adapt to new environments or go extinct. The shifts of the distribution of species, either retractions of vulnerable species or expansions of favoured ones, are among the most striking impacts of climate changes. This is particularly important when these demographic trends include the invasion of retracting close relatives and the species are still able to hybridize. Introgressive hybridization might introduce maladaptive variation but may also add new genetic diversity and potentially, promote rapid adaptation to the new conditions. Assessing the impact of introgressive hybridization in the interspecific dynamics of species facing climate change is therefore imperative. For this purpose, here we study the genetic interactions between *Lepus europaeus* (brown hare), an invading temperate species and *Lepus timidus* (mountain hare), a retracting arctic/boreal species well adapted to cold environments, in two contact areas, Sweden and Scotland, where an invasion-retraction dynamics between the species is known. By using genome-wide single nucleotide polymorphism data from both species, we will characterize the patterns of genetic structure and genetic diversity on the two focal areas, investigate historical and contemporaneous patterns of hybridization during the range replacement, and model the demographic dynamics of the interacting species. With these results, we will be able to discuss the impact and relevance of introgression in the gene pool of the affected species.

T6 Workshop: Taxonomy & Conservation

Phylogeography and ecological niche modeling unravel the evolutionary history of the Yarkand hare, *Lepus yarkandensis* (Mammalia: *Leporidae*), through the Quaternary

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The Taklimakan Desert in China is characterized by unique geological and historical dynamics and endemic flora and fauna, but the influence of historical climate oscillations on the evolutionary history of endemic animals is poorly understood. *Lepus yarkandensis* is an oases-dependent Near Threatened species that live in fragmented oasis habitats in the Taklimakan Desert, China. We investigated the geological and climatic impacts on its geographical differentiation, demographic history, and influence of Pleistocene glacial-interglacial cycles on the evolutionary history of *L. yarkandensis*. Further, studied the impact of the climatic oscillation-based modification on phylogeography, distribution, and diversification pattern of Yarkand hare by using Cytb (1140 bp), MGF (592 bp), and SPTBN1 (619 bp) markers. ENM revealed the evolutionary history of this species in response to climate change during the Quaternary. Paleodistribution modeling was used to identify putative refugia and estimate their historical distributions. Both historical demographic analyses and climatic niche modeling revealed strong effects of glacial climate changes, suggesting recurrent range contractions and expansions. The EBSP results indicated clear population expansion of *L. yarkandensis* since the Pleistocene. In the “early Pleistocene”, demographic expansion continued from 0.83 MYA to the last glacial period. The ENM analysis supported a wide distribution of *Lepus yarkandensis* at high altitudes during the last interglacial period. During the last glacial maximum the suitable climate was reduced and restricted to the western part of the Taklimakan Desert. Inland aridification, oasis evolution, and river flow played major roles in population differentiation and the demographic history of Yarkand hares. The large, continuous oases in the Taklimakan Desert contained a viable and unique population of *L. yarkandensis*. A fragmented desert environment might have caused low gene flow between individuals or groups, thus leading to predominant genetic differentiation. The Pleistocene climatic cycles triggered the diversification and expansion of this species during cold and warm periods.

T7 Workshop: Taxonomy & Conservation**Splitting hares: Current and future ecological niches predicted as distinctly different for two congeneric lagomorphs**

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The congeneric lagomorphs *Lepus timidus* and *L. europaeus* share allopatric distributions in many areas of Europe characterised by competitive exclusion and hybridisation. We investigated prospects for these species under climate change in northern England uplands. We created ensemble models predicting niche realisation for these species, influenced by abiotic and biotic factors, estimating niche overlap in geo-environmental space. The two species occupy distinctly different niches, influenced more by vegetation preferences than climatic differences. The current climate niche for *L. timidus* featured higher elevations with cooler temperatures and 168 km² range extent. Its current habitat niche scale was larger at 269 km², comprised entirely of upland dwarf shrubs: heather, cotton grass, moorland grasses. By contrast, the current climate niche predicted *L. europaeus* occupying lowland areas with a milder climate and range extent of 252 km². Its current habitat niche was also greater, 401 km², being mostly improved grassland. Competition was presently limited. The current niche predictions showed very little geographic overlap between the species. Niche overlap measured by Schoener Index was low: current climate niche 0.16; current habitat niche 0.07. The future climate niches for 2050 (IPCC RCP2.6), predicted *L. timidus* range contracting to 19 km², on hilltops and *L. europaeus* range expanding to 765 km². Consequently *L. timidus* range would be wholly within the *L. europaeus* range. In many contact zones throughout Europe, *L. europaeus* outcompetes *L. timidus*; however, in the Peak District their distributions are largely distinct. Future replacement of *L. timidus* by *L. europaeus* may be engendered by dietary convergence, should a warmer climate cause a transition of upland dwarf shrub vegetation to grasses.

M1 *Workshop: Lagomorphs as a Model Morphological System***Computational biomechanical modelling of the rabbit and pika cranium during mastication**

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The crania of leporid lagomorphs are uniquely fenestrated, including the posterior cranial bones and the lateral portion of the maxilla. The posterior fenestrations have been linked to locomotion; however, the functional significance of the highly fenestrated rostrum has received considerably less attention and the mechanical function is still debated. It has been hypothesised that the fenestrations are associated with the transmission of incisal occlusal forces, or to reduce weight of the rostrum to assist with high-speed locomotion. In terms of cranial biomechanics, this is a particularly interesting feature because it is absent in other mammalian herbivores with a long rostrum. In addition, the rabbit processes food through incisor and molar biting within a single bite cycle, and the potential influence of these bite modes on skull biomechanics remains unknown. This study combined multi-body dynamics and finite element analysis to compute musculoskeletal forces associated with incisor and molar biting, and to predict the associated strains. In addition, we compare a rabbit with a pika that lacks cranial fenestrations. The results show that the majority of the cranium, including the fenestrated rostrum, transmits masticatory strains. The cranial shape in rabbits appears to accommodate a uniform strain distribution for a combination of infrequent incisor bites and more frequent cyclic molar bites. The posterior struts of the fenestrated rostrum were predominately strained during molar biting, while the dorsal and ventral regions of the rostrum are strained more by incisor biting. These results show that the rostrum plays a role in the transmission of masticatory forces, therefore it is hypothesised that the fenestrations may be optimised to facilitate this transmission while minimising bone mass.

M2 *Workshop: Lagomorphs as a Model Morphological System*

The relationships among cranial shape, locomotor habit, and visual field within leporids

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Leporids (rabbits and hares) exhibit a surprising range of cranial shape and locomotor behavior. Cranial disparity within this group has been shown to be driven by pronounced changes in cranial flexion (facial tilt). Within leporids, facial tilt angle is strongly correlated to locomotor mode and significantly predicts cranial shape variation on the major axis of cranial shape space. In short: the more leporids tilt their face downwards, the more likely they are to exhibit high-speed, cursorial locomotion. We previously hypothesized that leporid cranial transformations are driven to improve visual acuity. Here we measure orbital convergence angle in 184 leporid crania, representing 20 extant species, to test the relationships among cranial shape, locomotor behavior, and visual acuity. Our analysis shows significant correlation ($p < 0.001$) between orbital convergence and facial tilt: as leporids tilt their face downwards, they also increase orbital convergence and, therefore, the size of their binocular field. This relationship provides a functional link for the hypothesis that cranial shape variation within leporids is influenced by locomotor behavior: leporids may tilt their faces to improve visual acuity as they increase the speed of their locomotor habits. Though a relationship between orbital convergence and locomotor behavior has been proposed for primates, our study demonstrates strong quantitative links between these systems within a non-primate mammalian clade.

M3 *Workshop: Lagomorphs as a Model Morphological System*

Evolutionary integration of the leporid cranium

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Morphological integration is the biological concept that organisms are integrated to function as a whole, but the strength of integration among constituent parts differs within and between individuals. Theory suggests that lower levels of integration may facilitate morphological diversity at developmental and evolutionary levels. Understanding integration of the vertebrate skull is therefore important to understand the origins of skull disparity. The leporid skull exhibits a surprising range of shapes which are in part due to locomotor behavior. We have previously shown that disparity within this group has been driven by pronounced changes in cranial flexion (facial tilt). Using the geometric morphometric toolkit to characterize shape variation and assess statistical covariation of skull modules (discrete anatomical regions) we demonstrate the facial tilt of leporid skull is facilitated by relatively weak integration among bones of the braincase and facial region, and this pattern is comparatively conserved across species of leporids. The implications of this research inform on the developmental and environmental factors responsible for biodiversity.

M4 *Workshop: Lagomorphs as a Model Morphological System***Evolution of unique skull morphology and function in Lagomorphs: comparative phylogenetic, shape and complexity analyses**

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The leporid lagomorphs (rabbits and hares) are adapted to running and leaping (some more than others) and consequently have unique anatomical features that distinguish them from ochotonid lagomorphs (pikas) and from their rodent relatives. One such feature is an intracranial joint that circumscribes the back of the skull, thought to facilitate skull mobility. This joint separates the anterior portion of the cranium (including the dentition, rostrum and ocular system) from the posterior portion of the cranium (which encompasses the occipital and the auditory complex). Aside from the observation that the intracranial joint is absent in pikas (generalist locomotors) and appears more elaborate in the genera with cursorial and saltatorial locomotory habits, the evolutionary history, biomechanical function and comparative anatomy of this feature in leporids lacks a comprehensive evaluation. The present work analysed the intracranial joint in the context of leporid evolutionary history using a Bayesian inference of phylogeny (18 genera, 23 species) and ancestral state reconstruction to gather information about the likelihood of its presence in ancestral groups. In addition, this work used 3D reconstructions of the skull from CT scan data, geometric morphometrics and complexity analysis to reveal correlations between ecology and morphological form, skull modularity and phylogenetic signal in cranial traits. Our phylogenetic analysis found it highly likely that the last common ancestor between all living leporids had an intracranial joint (92.9% likelihood) and that the last common ancestor of all living lagomorphs did not (70.1% likelihood). Results of morphometric and complexity analyses suggest there is correlation with ecological factors such as locomotion. These findings provide a broader context to further studies of evolutionary history and will help inform the formulation and testing of functional hypotheses.

M5 *Workshop: Lagomorphs as a Model Morphological System*

Mechanobiology and adaptive plasticity in the Lagomorph skull and feeding apparatus

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Naturalistic experimental analyses facilitate a unique knowledge of how musculoskeletal elements respond to dynamic mechanical stimuli, information fundamental for understanding connective-tissue mechanobiology and phenotypic diversity. In growing mammals, diet-related variation in jaw-loading patterns induces a cascade of changes at the gross, tissue, cellular, protein and genetic levels that maintain the integrity of craniomandibular structures. Applying diverse techniques (longitudinal microCT, histology, mechanical tests) to novel models of long-term dietary plasticity in white rabbits (*Oryctolagus cuniculus*), we document the presence of considerable intracranial and hierarchical variation in reaction norms within and between masticatory and non-masticatory hard-tissue elements (i.e., bone quantity, bone quality). Further, we show that the postnatal onset, duration and pattern of loading stimuli associated with a given feeding behavior can result in levels of intraspecific variation in jaw form that mirror anatomical differences between closely related taxa with similarly disparate diets. Such findings are important for highlighting why bone should not be viewed as similar across skeletal regions with respect to its intrinsic growth potential or adaptive responses to external forces, an assumption inherent to most comparative, experimental and biomedical research. While there is undoubtedly a genetic component to variation in the mammalian skeleton due to natural selection and evolution, arguably there is an underappreciation of intrinsic determinants of bone formation that modulate phenotype responses in the skeleton within individuals and across populations. An integrative perspective to the adaptive plasticity of masticatory soft and hard tissues in growing rabbits also greatly informs our understanding of jaw-joint function and development as well as the interplay between joint organization, gene expression patterns and tissue mechanical properties. Variation in such biological phenomena indicates that the functional signal conveyed for a given environmental stimulus will differ due to the variable responses of disparate skeletal structures as well as temporal variation in external loading patterns.

M6 *Workshop: Lagomorphs as a Model Morphological System*

Pulling the rabbit out of the hat: Revealing the development of lagomorphs in microCT scans

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Nondestructive, reversible methods that increase the radio-opacity of soft tissues prior to CT scanning have paved a way for detailed quantitative studies of internal anatomy in unborn mammals. Here, I demonstrate the application of iodine staining and microCT scanning as a means for detailed examination of the development of the hearing apparatus (including the brain), using a case study focused on a dataset of whale embryological and fetal specimens. Using these new data, I describe the sequence of acquisition of neomorphic anatomical structures in the odontocete biosonar apparatus. I quantify how and when brain regions change in size or shape, and whether this corresponds to the presence or growth of hearing-related structures including the inner and middle ear. Lastly, I demonstrate how these techniques can equally be used to study the development of lagomorphs, shedding light on similarly unique and little understood morphology.

M7 Workshop: Lagomorphs as a Model Morphological System**Cranial anatomy of *Palaeolagus haydeni* from the Oligocene of North America: systematic and evolutionary implications**

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Palaeolagus, an Eocene–Miocene North American lagomorph has been long considered a basal leporid. We present new data on its cranial anatomy including the first description of intracranial structures of the nasal and auditory regions based on μ CT data and 3D reconstructions of a complete skull of *Palaeolagus haydeni* from the Oligocene of Nebraska (Orellan, Brule Formation). Our results show a puzzling pattern of extant ochotonid (e.g., elongated basicranium structure, lack of cranial pitting) and leporid (e.g., muzzle with anteriorly tapering nasals, general architecture of the zygomatic arch, shape of the orbit anteroventral rim) characters. Furthermore, *Palaeolagus* shows some unique features (e.g., two mental foramina, absence of zygomatico-orbital canal) shared with *Rhombomylus turpanensis* (basal Glires). This mosaic pattern of cranial morphology supports phylogenetic position of *Palaeolagus* as a stem lagomorph and allows us a re-evaluation and polarization of some characters in the extant crown-group. *Palaeolagus haydeni* and Leporidae show several intracranial features that can be regarded as plesiomorphic (e.g., the thin wall of the bulla tympani, flat conic cochlea). The turbinal count is similar to Leporidae and may represent the lagomorph grundplan. However, *Paleolagus* is apomorphic in showing a reduced frontoturbinal 2. Common derived features of *Palaeolagus* and extant Lagomorpha are the dendritic maxilloturbinal, and the deeply excavated nasoturbinal continuous with the lamina semicircularis. The bony labyrinth of *Palaeolagus* shows a secondary crus commune, which is lost in all extant lagomorphs; its absence is the only derived character of the crown group. Finally, the anterior anchoring pattern of the malleus in *Palaeolagus* is an important contribution to the polarization of two patterns in extant Ochotonidae and Leporidae. *Palaeolagus* resembles early ontogenetic stages of Ochotonidae and thus the adult patterns in the two living families need to be regarded as separately derived character states.

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M8 *Workshop: Lagomorphs as a Model Morphological System*

The cursoriality gradient revisited: How running ability affects limb bone proportions and integration patterns in lagomorphs

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Highly cursorial animals generally display a suite of specific morphological and functional adaptations, notably including extended distal limb elements, decreased mechanical advantage at the joints, and decreased bone robusticity. The Lagomorpha, whose members vary in cursorial ability based on lifestyle and habitat, have been observed to possess such adaptations to varying degrees. In general, hares are highly cursorial, rabbits can run but more frequently saltate, and pikas predominantly trot. Previous investigations of this clade have identified that trends in anatomy correlate with this 'cursoriality gradient', however, the phylogenetic sampling of such investigations has been limited to three species each. By combining published data on the American pika (*O. princeps*), brush rabbit (*S. bachmani*), and black-tailed jackrabbit (*L. californicus*) with unpublished data on the Eastern cottontail (*S. floridanus*) and novel data from Australian samples of the European rabbit (*O. cuniculus*) and European hare (*L. europaeus*), we increase the phylogenetic robustness of this research and are better able to assess the linearity of trends associated with the observed cursoriality gradient.

X-ray Computed Tomography was used to image ~40 specimens of both European lagomorph species, followed by digital landmarking to capture length ratios within the appendicular skeleton. Using multivariate statistical analyses to investigate relative limb proportion and joint mechanical advantage identified that the trends previously described exclusively in three American species are more complex than initially apparent. We assessed which traits most consistently correlate with cursorial ability in lagomorphs, as well as which traits may be affected by factors such as fossoriality. Furthermore, we evaluated morphological integration in the appendicular skeleton, finding that between-limb covariation patterns in lagomorphs are mostly similar to those of other mammals, despite differences on a finer scale. Broadly, these results suggest cursoriality is likely to be one of many selective forces driving lagomorph skeletal evolution and development.

M9 *Workshop: Lagomorphs as a Model Morphological System*

The timing of mountain hare (*Lepus timidus*) coat colour change in Norway is determined by elevation and latitude

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Coat colour has a critical impact on fitness as predation risk may increase when an organism is mismatched against the background. In this study we investigate the impact of latitude, altitude and a gradient from continental to oceanic climate on moult timing in a native winter-adapted, winter-white herbivore, the mountain hare (*Lepus timidus*). Data collected between 2014 and 2018 by 678 camera traps deployed across a habitat gradient within Norway was used to create a Bayesian multinomial logistic regression model that quantifies the impact that latitude, altitude and climate zones have on the timing of autumn and spring moults for each year. Timing of moult was modelled as the probability of hares being white, brown or moulting at a given date. Our preliminary results indicate that altitude had a significant impact on moulting in both spring and autumn. In spring, the date at which there was a 50 % probability of having moulted was between 16 and 47 days earlier (depending on year) at sea level, compared to 600 m.a.s.l. In autumn, the date at which there was a 50 % probability of having moulted was between 15 and 55 days later (depending on year) at sea level, compared to 600 m.a.s.l. Latitude also had a significant effect on spring moulting in all years except 2014. The date at which there was a 50 % probability of having moulted was between 13 and 38 days earlier at 59° N than at 65° N. Surprisingly, latitude did not have a significant effect on autumn moult timing. Climate zone did not appear to have a significant impact on moult timing. These results represent the first quantitative assessment of the habitat covariates that affect mountain hare moult phenology in Norway.

L1 Workshop: Lagoviruses

Emerging European brown hare syndrome virus in *Lepus europaeus* in Spain

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European brown hare (*Lepus europaeus* - EBH) populations are affected by lagoviruses from the *Caliciviridae* family, such as the European brown hare syndrome virus (EBHSV, genotype *Lagovirus europaeus*/GII.1), and the rabbit haemorrhagic disease virus 2 (RHDV2/b, genotype *Lagovirus europaeus*/GI.2). These agents are considered amongst the most pathogenic animal viruses. Since first reported in Sweden in 1980, European brown hare syndrome (EBHS) has been documented around Europe, affecting mainly EBH and, less frequently, other hare species. However, only two isolated cases of EBHS had been described in the Iberian Peninsula, the latest in 2016 in Catalonia (NE Spain). Conversely, since the first description of GI.2 affecting EBH in 2014, this virus is considered one of the major threats in all those areas where EBH is sympatric with the European rabbit (*Oryctolagus cuniculus*). This study reports an outbreak that occurred in Catalonia from December 2020 to July 2021. During this period, up to 40 EBH carcasses were submitted for necropsy and anatomopathological evaluation. EBHSV was detected by specific RT-PCR in twenty-seven hares, whilst in two other individuals GI.2 was confirmed. Macroscopic and microscopic lesions consistent with lagovirus disease were observed in twenty-five out of the twenty-nine molecularly-positive hares. Two of these PCR-positive hares did not show any alterations related to lagovirus disease, suggesting an early state or post-infection. The two remaining molecularly-positive hares were not suitable for anatomopathological study due to severe autolysis and extensive predation. The pathological lesions and the tissue distribution of viral antigen were studied by immunohistochemistry, showing antigen positivity mainly in the liver and spleen. This is the first report of an EBHS epizootic event in the Iberian Peninsula, complicated by the simultaneous presence of RHDV2/b/GI.2. The importance of this episode is high in view of the increased vulnerability of the population of this species in the area.

L2 Workshop: Lagoviruses

Retrospective study in French and Belgian European hare populations gives new insights into European brown hare syndrome virus and rabbit haemorrhagic disease virus 2 (*Lagovirus europaeus*/GII.1 and /GI.2) epidemiology

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A fatal viral disease causes severe necrotizing hepatitis in the European hare (*Lepus europaeus*), the most relevant *Lepus* species in Europe. Two genotypes of *Lagovirus europaeus* (*Caliciviridae*) giving similar clinical signs can be involved i) the European brown hare syndrome virus (EBHSV, GII.1) and ii) the rabbit haemorrhagic disease virus 2 (RHDV2, GI.2) first detected in the European rabbit (*Oryctolagus cuniculus*) in 2010. GI.2 has rapidly replaced most of the former lagoviruses (RHDV, GI.1) restricted to European rabbits. The first GI.2 outbreak in European hares was reported in Italy in 2012, then in France. Contrary to Italy where infections were sporadic, GI.2 was widely distributed in France and involved in 37% of lagovirus disease cases in 2015. A case of co-infection was also reported. Even if the GI.2 spread rate seems to differ between rabbits and hares, replacement of GII.1 in hares could also happen. To a better clinical and epidemiological description of lagovirus infections in this species, a real-time multiplex RT-PCR has been developed to discriminate both genotypes. We analyzed 2,075 liver samples from dead hares displaying clinical signs similar to EBHS between 2009 and mid-2021 in France (collected by SAGIR network) and Belgium: 42% were lagovirus-positive. The earliest GI.2 cases were reported in 2011 in both countries, showing that the crossing of the species barrier occurred at different locations soon after GI.2 emergence in rabbits. The percentage of GI.2 has gradually increased to reach a maximum of 76% in 2018 in France. Interestingly, GI.2/GII.1 ratio was significantly reversed in the following years: 16% in 2019, 14% in 2020 and 15% between January and August 2021. Co-infections have regularly occurred (1-4 % detected per year), maintaining the risk of new recombinant strain emergences. Several hypotheses can be put forward to explain GII.1 and GI.2 epidemiologic evolution in hares.

L3 Workshop: Lagoviruses

Diagnostic efforts during an outbreak of rabbit haemorrhagic disease virus 2 (*Lagovirus europaeus* GI.2) in California, US (2020-2021)

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An outbreak of rabbit hemorrhagic disease (RHD) caused by rabbit hemorrhagic disease virus 2 (RHDV2; *Lagovirus europaeus* GI.2) is occurring in the United States (US). The first cases were detected in March 2020 in New Mexico and soon after the virus spread broadly among wild and domestic leporids of several southwestern states. Later, cases were detected also in northern and eastern regions of the US. Mexico and Canada have been affected too. In California, RHDV2 was first detected in May 2020 in Riverside County (southern California). Diagnostic efforts are currently ongoing at the California Animal Health and Food Safety Laboratory (UC Davis) in conjunction with the California Department of Fish and Wildlife, and the California Department of Food and Agriculture. These efforts include gross and histological examination of affected carcasses, confirmatory diagnosis by RT-qPCR from liver, lagoviral antigen detection by immunohistochemistry on several tissues, and whole genome sequencing. To date, RHDV2 has been detected in 12 different counties in California. Southern California became a hotspot for this disease during the spring of 2021 and, more recently, there were cases in central and northern areas of the state. Cases have been confirmed in four different leporid species in California: domestic rabbit (*Oryctolagus cuniculus*), desert cottontail rabbit (*Sylvilagus audubonii*), black-tailed jackrabbit (*Lepus californicus*), and western brush rabbit (*Sylvilagus bachmani*). Hepatic necrosis typical of pathogenic lagovirus infection and associated with lagoviral antigen has been detected in affected animals of the four species. The analyzed California viral sequences are closely related irrespective of the affected species. Among all the available RHDV2 sequences originating from detections in North America before this outbreak started, the California sequences are more similar to a virus collected in British Columbia, Canada, in 2018.

L4 Workshop: Lagoviruses

Multiple introductions of rabbit hemorrhagic disease virus *Lagovirus europaeus*/GI.2 in Africa

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Rabbit hemorrhagic disease (RHD) causes high mortality and morbidity in European rabbits (*Oryctolagus cuniculus*). In Africa, the presence of the causative agent, the rabbit hemorrhagic disease virus (RHDV), was first confirmed in 1992 (genotype *Lagovirus europaeus*/GI.1). In 2015, the new genotype *Lagovirus europaeus*/GI.2 (RHDV2/b) was detected in Tunisia. Currently, GI.2 strains are present in several North and Sub-Saharan African countries. Considerable economic losses have been observed in industrial and traditional African rabbitries due to RHDV. Like other RNA viruses, this virus presents high recombination rates, with the emergence of GI.2 being associated with a recombinant strain. Recombination events have been detected with both pathogenic (GI.1b and GII.1) and benign (GI.3 and GI.4) strains. We obtained complete genome sequences of Tunisian GI.2 strains collected between 2018 and 2020 and carried out phylogenetic analyses. The results revealed that Tunisian strains are GI.3P-GI.2 strains that were most likely introduced from Europe. In addition, the results support the occurrence of multiple introductions of GI.2 into Africa, stressing the need for characterizing complete genome sequences of the circulating lagoviruses to uncover their origin. Continued monitoring and control of rabbit trade will grant a better containment of the disease and reduce the disease-associated economic losses.

L5 Workshop: Lagoviruses

Protecting the endangered riparian brush rabbit from emergent RHDV2 in California, USA

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Rabbit hemorrhagic disease virus serotype 2 (RHDV2), the cause of a highly contagious and fatal lagomorph disease, rapidly spread through the western United States and Mexico, resulting in significant mortality in domestic and wild rabbits. Since first detected in California in May 2020, the disease spread rapidly throughout the state, prompting the formation of an ad hoc interagency/zoo/academia/non-profit team to implement emergency conservation actions to protect the endangered riparian brush rabbit (*Sylvilagus bachmani riparius*), an endemic subspecies numbering less than two thousand individuals, from RHDV2. Riparian brush rabbits have lost over 90% of their historical habitat, and remnant habitat is fragmented and prone to flooding and wildfire. The team first implemented a vaccine safety trial by giving a single subcutaneous dose of the Filavac VHD K C+V® vaccine (Filavie, France) to 19 wild riparian brush rabbits that had been captured and temporarily held in captivity. Rabbits were monitored for side effects, including loss of appetite, lethargy, and development of swelling or pain at the injection site. Serum from captive rabbits was collected prior to, and at 7-10-, 14-20-, and 60-days post-vaccination for determination of antibody response. No adverse effects from vaccination were documented, and thus a large-scale ongoing field effort was initiated in September 2020 with the goal of keeping approximately 15% of the estimated wild population vaccinated to reduce extinction risk. Population estimation via remote camera transects coupled with predictive modeling were used to inform vaccination goals. Serologic testing to determine optimal booster frequency by examining duration of antibody response to vaccination is in progress. To date, 586 individuals have been vaccinated at least once and surveillance via RT-PCR of rectal swab samples from riparian brush rabbits and sympatric desert cottontails (*Sylvilagus adubonii*) indicates RHDV2 has not reached core brush rabbit habitat as of December 2021.

L6 *Workshop: Lagoviruses*

Comparison of the impact of both variants of rabbit haemorrhagic disease on European wild rabbit populations based on Spanish national hunting bags

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Hunting is an important recreational practice in many countries, but it also has a deep traditional component and an essential role in wildlife management. A species of great hunting value in Spain is the European wild rabbit (*Oryctolagus cuniculus*), a key species in the Mediterranean ecosystem. In the Iberian Peninsula, a combination of overhunting, habitat loss and changes in land use, but also the impact of two viral diseases (i.e. myxomatosis and rabbit haemorrhagic disease-RHD, henceforth GI.1), has caused a remarkable decline in rabbit populations during the last 50 years. In 2010, a novel RHD virus variant (i.e. GI.2) affecting rabbits was identified in France. Since then, the virus has rapidly spread throughout continental Europe. In this work, we used Spanish National hunting bags published by the National Institute of Statistics (INE) from 1973 to 2018 to assess the impact of both RHD variants on wild rabbit populations trends in Spain. Despite the unpopularity of hunting bags for population trend analysis, they have increased during the last years in different countries such as Germany, Portugal, and New Zealand. Our results show that, at the national level, the number of rabbits hunted significantly decreased after the first outbreak of GI.1, and this trend continued during at least the following 5 years. Surprisingly, the outbreak of GI.2 did not match a clear trend in rabbits' populations after its detection in Spain in 2012. Furthermore, we observed variability between provinces, and unlike for GI.1, no clear trend for GI.2 even considering the provinces with an overpopulation of rabbits. In conclusion, hunting bags can provide an overall abundance index that can be useful for detecting population trends and especially relevant for surveillance and understanding the effect of emerging diseases.

L7 Workshop: Lagoviruses**Longitudinal semi-quantitative serological study of myxoma and rabbit haemorrhagic disease viruses in southwestern Iberian rabbit populations**Joana Coelho ^{1,2,3}, Henrique Pacheco ^{1,2,3}, Paulo Célio Alves ^{2,3,4,5}, Nuno Santos ^{2,3}

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Myxoma (MYXV) and Rabbit Haemorrhagic Disease (RHDV) viruses are important drivers of the population decline of the European rabbit (*Oryctolagus cuniculus*), however their epidemiology is still imperfectly known, particularly for the emerging and currently dominant RHDV GI.2 strain. This study aimed to uncover the epidemiology of MYXV and RHDV in wild rabbits using semi-quantitative serology. A serological assessment of MYXV and RHDV was performed over 3 years in free-ranging (n=2) and enclosed (n=3) populations of the southwestern Iberian subspecies *Oryctolagus cuniculus algirus*, in a capture-mark-recapture study. Data on gender, weight, and ear length were recorded and the scaled mass index estimated as a proxy of body condition. The semi-quantitative indirect ELISA (iELISA) standardized results for antibodies against MYXV and RHDV GI.2 on 398 sera were analysed using linear mixed models. Overall apparent seroprevalence for MYXV was 51.9% (CI95 47.4-56.4%) and 26.2% (CI95 22.0-30.8%) for RHDV. The MYXV model revealed a significant positive relationship between the iELISA results and body condition. The RHDV GI.2 model included the seropositivity status for MYXV and site, with MYXV-seronegative rabbits showing lower RHDV iELISA results. Overall, the MYXV iELISA results increased by 0.006 units/month and RHDV iELISA results increased by 0.008 units/month. We found evidence of the presence antibodies against MYXV and RHDV GI.2 in some juveniles, possibly of maternal origin, declining up to 250g body weight, but seropositive animals were all over 500g body weight. Apparent survival of seropositive rabbits was higher than of seronegative rabbits in a free-ranging population, but similar in enclosed populations. Semi-quantitative serological data provides epidemiological information, otherwise lost when considering only binomial (positive/negative) results. Semi-quantitative serology suggests the presence of maternal passive immunity to RHDV GI.2 and MYXV in juvenile European rabbits and likely lifelong humoral immunity to both viruses after natural infection.

L8 Workshop: Lagoviruses**The role of recombination in the emergence and evolution of rabbit hemorrhagic disease virus (RHDV)**Ana Margarida Lopes^{1,2,3}, Joana Abrantes^{1,4,2}

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RNA viruses are characterized by their rapid evolution that allows adaptation to new or changing environments. Their large population sizes combined with high levels of genetic diversity, which are the result of high mutation and substitution rates, are responsible for the rapid evolution. While RNA virus evolution is dominated by mutation, much larger variation is achieved through recombination. Recombination can occur when two distinct strains coinfect the same host cell and exchange genetic information, originating a hybrid virus. Due to the extensive genetic changes produced, recombination is frequently associated with extreme changes in virus phenotype, which might contribute to virus escape either from the host immune response or from antiviral therapies, or changes in cell or host tropism. Moreover, recombination has been associated with an increase in viral pathogenicity. Rabbit haemorrhagic disease virus (*Lagovirus europaeus*; RHDV) is an RNA virus that infects the European rabbit (*Oryctolagus cuniculus*). This calicivirus emerged in 1984 in China (genotype GI.1) and dispersed worldwide, putting at risk rabbit populations and their predators, in particular in the Mediterranean area. In 2010, a new genotype (GI.2) emerged in France. G2 rapidly disseminated worldwide and in some countries replaced the circulating GI.1 strains. In addition, in many wild rabbit populations, GI.2 became endemic and causes regular outbreaks. Non-pathogenic strains (genotypes GI.3 and GI.4) related to RHDV also exist and circulate in rabbit populations. Intra- and inter-genotype recombination events have been extensively documented in RHDV, particularly for GI.2. Here we review the role of recombination in the emergence and evolution of RHDV.

L9 Workshop: Lagoviruses

Recombination between viral genomes as a potential mechanism for speciation: the example of rabbit haemorrhagic disease type 2 (RHDV2) - BG12

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Diseases in lagomorphs caused by caliciviruses emerged in the 1980s with the identification of RHDV in China and EBHSV in Europe. Today, the *Lagovirus* genus consists of several members, both pathogenic and non-pathogenic, including RHDV2 which emerged in Europe around 2010. Within a few years, RHDV2 almost replaced RHDV, spreading to several continents, including North and Central America. In 2012, we received a wild European hare from northern Italy with suspected EBHS but we identified RHDV2 (RHDV2_Bg12). Based on findings of multiple recombinant events among RHDV2 strains, we subsequently analyzed the full genome sequence of the RHDV2_Bg12 to investigate the occurrence of such event also for this "hare" strain. Phylogenetic and SimPlot analysis performed with the ORF1 lagovirus sequences present in GenBank, showed a recombination event between the non-structural proteins of an EBHSV-like virus, not yet identified, and the structural protein of RHDV2 virus. Consequently, we orally infected seronegative adult rabbits with RHDV2_Bg12. Surprisingly, they did not contract RHD and neither develop a specific antibody response, suggesting that RHDV2_Bg12 is not able to infect rabbits. Despite repeated cases of RHDV2 in rabbits in the same areas and in subsequent years, none of the isolates matched RHDV2_Bg12. Moreover, after RHDV2_Bg12 identification, we did not find any more cases of RHDV2 in hares for years. Therefore, the new virus 'RHDV2_Bg12' can be classified as a failed attempt of a new viral emergence occurred in a hare due to a recombination process between two related lagoviruses. While the case of RHDV2_Bg12 had no practical implications, it prompts more speculations on the scientific side i.e. the host spectrum of lagoviruses is determined not only by the sequence of the VP60 gene, but it likely also depends on certain NSP genes involved in the intracellular replication of the virus.

L10 Workshop: Lagoviruses**Detection and differentiation of RHDV genotypes GI.1 and GI.2 by a duplex lateral flow assay**

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Rabbit Haemorrhagic Disease Virus (RHDV), a member of the genus *Lagovirus* (family *Caliciviridae*), causes a fatal disease of domestic and wild European rabbits (*Oryctolagus cuniculus*) and was first reported in China in 1984. Since, it has been reported in over forty countries in the five continents, being endemic in most parts of the world where European rabbits are domesticated. The primary target organs of the virus are the liver, the spleen and the lungs. RHD is characterized by acute necrotizing hepatitis, splenomegaly and haemorrhages in several organs, generally associated with massive disseminated intravascular coagulation. In 2010, a new pathogenic lagovirus, commonly called RHDV2, was identified in France and classified within genogroup I as genotype 2 (GI.2). It presents a unique antigenic profile and it has rapidly spread since then throughout other European countries and continents, replacing most of the circulating former RHDV (GI.1). So far, several techniques can be employed for the detection of GI.1 or GI.2 as RT-PCR and commercial and non-commercial ELISA tests. Here, we describe the development of a rapid and easy-to-use test, a lateral flow assay that allows by first time the simultaneous detection and differentiation between both RHDV genotypes GI.1 and GI.2 in liver homogenate and liver exudate samples. Results indicate a specificity of 100% and a sensitivity of 93.1% and 95.5% for GI.1 and GI.2, respectively. In summary, the results show that this duplex lateral flow assay is a quick and cheap antigen diagnostic tool that does not require the use of specific laboratorial equipment. Therefore, this test could be used as a reliable and rapid test for the continuous surveillance of RHD in the rabbitries, especially in vaccination strategies, but also in the field.

L12 Workshop: Lagoviruses**Understanding U.S. rabbit owners' willingness to engage in biosecurity measures to prevent transmission of RHDV2**Elizabeth Pienaar, [Hannah Shapiro](#), Mark Ruder*University of Georgia, USA*Email contact: elizabeth.pienaar@uga.edu

In March 2020, RHDV2 was confirmed in domestic and wild rabbits in New Mexico and has since spread to 19 states. Trade in domestic rabbits and rabbit-related products has played a role in the transmission of RHDV2, as the most recent cases have been detected in states outside the range of infected wild lagomorphs. Thus, it is essential for rabbit owners to engage in biosecurity behaviors to protect the health of their rabbits and lower the risk of RHDV2 spreading to new areas. We investigated rabbit owners' willingness to engage in nine commonly recommended biosecurity practices (e.g., the use of disinfectants, housing rabbits indoors, vaccinating rabbits) and determinants of these behavioral intentions. From April – August 2021, we surveyed 1,807 U.S. rabbit owners (breeders, pet owners, rabbit rescues). Most respondents were likely to engage in all biosecurity measures, with respondents being most likely to report suspicious rabbit deaths (92.8%) and least likely to acquire a health certificate before transporting their rabbits between states (56.6%). However, rabbit breeders were less likely to engage in biosecurity measures, likely owing to concerns about the costs to their operations. Respondents' willingness to engage in biosecurity was positively correlated with the importance they placed on biosecurity, their recognition that the domestic trade is contributing to the spread of RHDV2, and their concern about the health of rabbit populations and the economic viability of domestic rabbit industries. Educational materials should be developed by trusted sources that articulate RHDV2's risk to rabbits and rabbit-related industries and how engaging in biosecurity measures can lower this risk. Participants in the domestic rabbit trade are more likely to vaccinate their rabbits and obtain health certificates if the costs of these interventions are reduced, and the movement of domestic rabbits between states is better monitored.

L13 *Workshop: Lagoviruses*

National rabbit biocontrol optimisation - assessing the potential of RHDV2 as a registered biocide

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For over 70 years viral biological control of rabbits has been successfully used in Australia. The use of self-disseminating viral biocontrol agents and resulting long-term reduction of rabbit impacts has delivered massive benefits to the agricultural industries and allowed for recovery of many vulnerable ecological communities. Despite these past successes, biological control is never a silver bullet for rabbit control, and host-pathogen co-evolution often leads to a reduction in the effectiveness of biocontrol agents over time. With the aim to preserve the long-term gains made by previous biocontrol initiatives, an innovation pipeline approach is being pursued in Australia to investigate and develop new biocontrol tools and strategies to be implemented at regular intervals, to maintain low rabbit population numbers and associated benefits. In this context, Australia is currently investigating if more targeted applications of the rabbit biocontrol viruses already in the country could be explored as an additional means to improve rabbit biocontrol. As part of this approach, RHDV2 is currently being investigated for its potential as an additional registered biocide to complement local control operations. While RHDV2 is already circulating naturally in wild Australian rabbit populations, it has unique features warranting further investigations in this context, such as its ability to infect and kill young rabbits. Work is underway to quantify the virulence and welfare impacts of RHDV2 compared to other control methods, as well as the extent to which it can overcome immunity to other strains in wild and domestic rabbits. In addition, naturally occurring virus activity and diversity are being monitored across Australia, which is essential to understand how the different RHDVs present in Australia interact and if this can be exploited for rabbit control. The project also supports the development of a vaccine that covers all virulent Australian RHDVs to protect domestic pet and farmed rabbits.

L14 *Workshop: Lagoviruses***Leporid herpesvirus-4: potential new additional biocontrol for pest *Oryctolagus cuniculus***

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In 1990 two rabbitries in northern Canada reported outbreaks of an acute, fatal herpesvirus infection. Though the herpesvirus wasn't characterised, these outbreaks resulted in high morbidity and mortality. Further outbreaks describing similar symptoms with approximately 50% morbidity and 29% mortality, were reported on a farm in Wasilla, Alaska (USA), in 2006 and 2007, from which a new alphaherpesvirus, leporid herpesvirus-4 (LHV-4), was described. LHV-4 was subsequently detected in a dead pet rabbit from northern Ontario Canada in 2010, and in 2018 from a dead pet rabbit in Wasilla, Alaska.

This virus has been identified as a potential new biocontrol for pest rabbits in Australia. Its positive attributes include reports of it affecting all age groups, and causing stillbirths and neonatal deaths in a doe infected the previous year likely due to viral reactivation from latent infection. In addition, this virus can cause death with minimal visible symptoms.

The myxoma virus is a benign disease in its native host, *Sylvilagus andinus*, but an effective biocontrol for pest *Oryctolagus cuniculus*. It has been hypothesised that LHV-4 may be a benign disease in the snowshoe hare, *Lepus americanus*, that has occasionally had a spill over via biting insects into *O. cuniculus*. This hypothesis arises from the 16 deceased rabbits in the 2006 Wasilla outbreak. These animals had been individually housed outdoors, summer mosquito and biting fly activity was high, and there were snowshoe hares in the area. LHV-4 has morphology similar to human herpes simplex virus and hence is likely to also spread by contact such as during copulation. With recent Australian research showing sub-adult rabbits using multiple warrens up to 700m away, 32.2% off-warren male siring, and evidence of multiple paternity, the effective spread of LHV-4 by contact transmission is likely to be much more effective than previously anticipated.

R1 *Workshop: Successes and Failures of European Rabbit Translocations*

Lessons from the 16th to 18th century and today for improving wild rabbit *Oryctolagus cuniculus* conservation

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Introduced in the Netherlands in the Middle Ages as free ranging wildlife, wild rabbits have found their niche and are now valued by nature managers for their keystone role in the coastal dune ecosystem. However, rabbits in the Netherlands have declined since the 1950 due to myxomatosis and Rabbit Haemorrhagic Disease. In this talk, we will present historical approaches to managing rabbits in the dunes from the 16th to 18th century, and together with a review of translocation studies of the 20th and 21st century formulate approaches for effective and active rabbit conservation in our coastal dunes.

R2 *Workshop: Successes and Failures of European Rabbit Translocations*

How a single introduction of wild rabbits triggered the biological invasion of Australia

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Biological invasions are a major cause of economic and environmental disruption. While ecological factors are key determinants of their success, the role of genetics has been more challenging to demonstrate. The colonisation of Australia by the European rabbit is one of the most iconic and devastating biological invasions in recorded history. Here, we show that despite numerous introductions over a 70-year period, this invasion was triggered by a single release of a few animals that spread thousands of kilometres across the continent. We found genetic support for historical accounts that these were English rabbits imported in 1859 by a settler named Thomas Austin, and traced the origin of the invasive population back to Austin's birthplace in England. Combining genomic and historical data we show that, contrary to the earlier introductions which consisted of domestic animals, these rabbits had wild ancestry. This was replicated in New Zealand and Tasmania, where rabbits only became a pest several decades after being introduced. We argue that the common denominator to these invasions was the arrival of a new genotype that was better adapted to the natural environment. These findings demonstrate how the genetic composition of invasive individuals can determine the success of an introduction and provide a mechanism by which multiple introductions can be required for a biological invasion.

R3 *Workshop: Successes and Failures of European Rabbit Translocations*

Not born to be wild: the European rabbit in North America

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Since its widespread introduction to North America in the 19th century, the European rabbit has been an important agricultural species, laboratory animal, and, more recently, popular house pet whose nature and needs take many unprepared owners by surprise. Abandonment of domestic rabbits leads to formation of seasonal or year-round feral colonies, most of them located in urban and suburban areas. While these colonies have historically had minimal impact on native ecosystems, the arrival of RHDV2 to North America in 2018 has raised concern for transmission of the virus between feral European rabbits and native lagomorph species.

North America presents a unique situation where the public and even government officials are too often confused about the distinction between the invasive European rabbit and native cottontails as well as other native species which many domestic rabbits visually resemble. 'Cottontail' is often and mistakenly used to describe a breed of European rabbit rather than a distinct species. The term 'wild' is often applied to European rabbits who live in a feral state. The public sees feral European rabbits grazing in city parks or on university campuses and gets the impression that the animals are living a good life, not realizing that only the survivors are on display. Added to this is the rudimentary education that North American veterinarians receive in rabbit medicine, perpetuating the second-class status of these animals as pets and hence the relative ease with which they are abandoned. Thus, for the sake of European rabbits' welfare as well as the health of native lagomorph populations, education efforts must be aimed at the public, the veterinary profession, and government officials in charge of wildlife management.

R4 *Workshop: Successes and Failures of European Rabbit Translocations*

Wild European rabbit recovery plans: are we learning from the mistakes?

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The wild European rabbit (*Oryctolagus cuniculus*) is an endemic species in the Iberian Peninsula that has undergone a progressive decrease in abundance due to two viral diseases (i.e. myxomatosis and RHD), acting together with human-induced habitat changes (e.g. agricultural intensification, habitat loss and fragmentation). On top of that, the arrival of a new variant of rabbit haemorrhagic disease virus in the last decade yielded another decline in wild populations throughout their native range, even recording local extinctions. In this regard, wild rabbit scarcity has become a major concern given its economical and its ecological value, being recently listed as an endangered species within its native range according to the IUCN Red List categories (IUCN 2019). In order to recover or boost wild rabbit populations, a wide variety of management measures have been traditionally implemented: habitat management, rabbit restocking or translocations, predator control or exclusion, vaccination campaigns or game regulation. Nevertheless, many recovery attempts have failed in spite of both massive efforts and bulky investments. In many cases, management strategies have been misdirected since they focus on the species conservation without accounting the entire ecosystem. Despite of the recommendations made by researchers, there are still many wildlife or hunters managers that implement unplanned and improvised activities, compromising the viability of wild populations. In this sense, the coordination among different researchers, managers, stakeholders and government working on wild rabbit recovery plans, is critical to guarantee the overall success of the program. Additionally, a rigorous, standardized monitoring protocol is needed to evaluate the status of the species and help to solve any problem during management operations. Here we review some examples of why management measures may have flawed and discuss actuations aimed at boosting wild rabbit populations in the context of rabbit conservation in Spain, pointing out both good practices and deficiencies, as well as suggesting potential solutions.