

Mértola Evolution Conferences– 2025 edition: Speciation: from field studies to genomics



PROGRAM

DAY 1, 5th of April

Chair: Jeremy Searle

9:30-10:00 - Welcome Coffee and Cakes

10:00-10:30 - Opening Ceremony

10:30-11:45 - **Peter Grant:** "Ecology of speciation in the adaptive radiation of Darwin's Finches"

11:45-13:00 - **Rosemary Grant:** "Speciation and Hybridization in Darwin's Finches"

13:00-14:30 - Lunch

14:30-15:30 - **Leif Andersson:** "Atlantic herring - an adaptive radiation with incomplete reproductive isolation"

15:30-15:45 - José Cerca: "Consistent transposable element accumulation in the face of hybridization and rapid speciation in Galápagos giant daisies (*Scalesia*)"

15:45-16:00 - Martim Melo: "Signatures of selection despite ephemeral population dynamics in "Darwin's Sparrow" (*Passer iagoensis*, Cabo Verde endemic)"

16:00-16:30 - Coffee Break

16:30-16:45 - Borja Milá: "Diversification and local adaptation between and within oceanic islands: the Chaffinch radiation in Macaronesia"

16:45-17:00 – Jan T. Lifjeld: "Sperm and speciation in songbirds"

17:00-17:15 – Salomé Barreto: "Ecological differentiation influences the evolution of prezygotic isolation in spider-mite species"

17:15-17:30 – Marta Berluenga: "Host-parasite interactions drive speciation in crater lake cichlid fish"

17:30-17:45 - Ester Serrão: "Climate-driven evolution at range margins of marine forests"

17:45-18:00 - Kari Saikkonen: "Extreme polar light regimes promote hybrid zones at higher latitudes and biodiversity globally?"

18:00 – Cante Alentejano

19:00 – Dinner

DAY 2, 6th of April

Chair: Leif Andersson

09:30-10:30 - **Joana Meier**: "The roles of hybridisation and chromosomal rearrangements in rapid adaptive radiations"

10:30-11:00 - Coffee Break

11:00-12:00 - **Rui Faria**: "The role of chromosomal inversions in *Littorina* adaptation and speciation"

12:00-13:00 - **Roger Butlin**: "Hybrid zones and reproductive isolation"

13:00-14:30 - Lunch

14:30-15:00 - **Jeremy Searle**: "Despeciation"

15:00-15:30 - **Rikard Holmdahl**: "Why we became humans"

15:30-15:45 - Carl Vangestel: "How ancient chromosomal inversions shaped a parallel Galápagos beetle radiation."

15:45-16:00 - Hannes Svardal: "Introgression dynamics of sex-linked chromosomal inversions shape the Malawi cichlid adaptive radiation"

16:00-16:30 Coffee Break

16:30-16.45 - Alexandre Blanckaert: "Interactions between mechanisms of reproductive isolation"

16:45-17:00 - Silu Wang: "Mitonuclear divergence predicts gradual speciation in animal hybrid zones"

17:00-17:15 - Sofia L. Mendes: "Hybridization is prevalent but outcomes are distinct across highly differentiated Iberian chub species"

17:15-17:30 – Giovanni Forcina: "Neglected human-driven species diversification: the case of the Javan Red Junglefowl (*Gallus gallus bankiva*) "

17:30-19:00 – Close of Conference and Free time to visit Mértola

ORGANIZATION

Leif Andersson, Uppsala University

Miguel Carneiro, CIBIO-BIOPOLIS

Rui Faria, CIBIO-BIOPOLIS

Paulo Célio Alves, FCUP, CIBIO-BIOPOLIS & EBM

Jeremy Searle, Cornell University, FCUP & EBM

ABSTRACTS

INVITED TALKS

5th of April, 10:30-11:45

Ecology of speciation in the adaptive radiation of Darwin's Finches

Peter R. Grant
Princeton University, USA

I will discuss what we have learned about speciation by combining insights from genomics with long-term studies of finch populations in the Galápagos. I will conclude by considering how evolution of contemporary populations can throw light on the causes of speciation and diversification in the past.

5th of April, 11:45-13:00

Speciation and Hybridization in Darwin's Finches

Rosemary Grant
Princeton University, USA

In this talk, I highlight our recent discoveries of reproductive isolation in Darwin's finch populations in the Galápagos archipelago. I describe the evolutionary consequences of episodic genetic exchange between species and conclude with our exciting discovery of the formation of a new lineage via hybridization.

5th of April, 14:30-15:30

Atlantic herring – an adaptive radiation with incomplete reproductive isolation

Leif Andersson

Department of Medical Biochemistry and Microbiology, Uppsala University, Sweden

An adaptive radiation is characterized by rapid speciation and genetic differentiation. A classical example of an adaptive radiation is Darwin's finches in the Galápagos archipelago, in which one species has diversified into 18 different species within the last 1-2 million years. In this presentation I will compare the degree of genetic differentiation among species of Darwin's finches with that among ecotypes of the Atlantic herring that is not recognized as distinct species. I will show that genetic differentiation at loci under natural selection is equally strong or stronger in herring than among some recognized species of Darwin's finches. A striking difference between the two groups is that Atlantic herring ecotypes show essentially no genetic differentiation at neutral loci in contrast to the situation in Darwin's finches. The difference can be explained by striking differences in prezygotic reproductive isolation. Birds have well elaborated mate choice based on song, plumage and morphology that can rapidly drift in small populations, whereas Atlantic herring is an abundant broadcast spawner with no mate choice. Gene flow occurs even between Atlantic and Pacific herring that split about 3 million years ago. However, reproductive isolation occurs between ecotypes in Atlantic herring, due to their homing behavior and genetic regulation of spawning time, but it is incomplete.

6th of April, 9:30-10:30

The roles of hybridisation and chromosomal rearrangements in rapid adaptive radiation

Joana Meier

Department of Zoology, University of Cambridge & Wellcome Sanger Institute, Cambridge, UK

Species richness is very unevenly distributed across the tree of life. While some lineages diversify rapidly into many species given ecological opportunity, others are much less prone to do so. For instance, one lineage of cichlid fishes repeatedly diversified into hundreds of species in each lake in the Lake Victoria region, whereas four other cichlid lineages that colonised the same lakes did not speciate. Here, I show that hybridisation facilitated the rapid diversification by providing ecologically relevant gene variants. Multiple cycles of hybridisation and diversification characterise the evolutionary history of the cichlid lineage that led to diversification into 500 species in just 16,000 years in the most recent radiation in Lake Victoria. Next, I explore if gene exchange generally facilitates rapid diversification and specifically, if it facilitated rapid adaptive radiation in certain lineages of South American ithomiine butterflies. We find that in addition to gene exchange, chromosomal rearrangements play an important role. Whereas most butterflies have 31 chromosomes, ithomiine butterflies range from 5 to over a hundred chromosomes. Complex chromosome fusions and fissions lead to reproductive isolation between closely related species in some ithomiine butterfly lineages, facilitating their rapid adaptive radiations.

6th of April, 11:00-12:00

The role of chromosomal inversions in *Littorina* adaptation and speciation

Rui Faria

(and the *Littorina* Research Community)

CIBIO - Research Center in Biodiversity and Genetic Resources, BIOPOLIS & Faculty of Sciences of the University of Porto, Portugal

Chromosomal inversions are practically known since the beginning of genetics. Because inversions can have both direct (e.g., altering genes at breakpoints) and indirect effects (as recombination modifiers) on fitness, they have the potential to play a major role in evolutionary processes such as adaptation and speciation. However, inversions are influenced by many interacting processes (for example, reduced recombination also increases the effects of genetic drift). Thus, understanding the underlying mechanisms as well as the sequence of evolutionary events by which inversions play a role in adaptation or speciation is challenging. As result, despite the increasing genomic evidence for the presence of polymorphic inversions across many systems, their evolutionary significance is not yet fully understood. In order to contribute to fill this gap, I will present the collective efforts of the *Littorina* Research Community to understand the role of inversions in adaptation and speciation in *Littorina* marine snails. By combining genomic and phenotypic data from multiple natural hybrid zones across the *Littorina saxatilis* distribution with QTL analyses, I will argue that: i) some inversions are enriched for SNPs showing strong differentiation between ecotypes; ii) traits that evolved in parallel in multiple populations facing similar divergent pressures map to inversions; and iii) inversions contribute to (rapid) ecotype divergence, but their role in completing speciation in this system is less clear. Finally, I will describe our current efforts trying to infer the evolutionary history of these inversions and put our results into a wider taxonomic context aiming to understand the evolutionary significance of inversions across the tree of life.

6th of April, 12:00-13:00

Hybrid zones and reproductive isolation using *Littorina* examples

Roger Butlin

University of Sheffield, UK & University of Gothenburg, Sweden

Hybrid zones are often described as natural laboratories for the study of evolution. In particular, they provide valuable insights into the barriers to gene flow between divergent populations. I will use examples from the marine snail genus *Littorina* to introduce some of the principles of hybrid zone analysis and then to review what they have revealed about reproductive isolation. Some *Littorina* hybrid zones show bimodal distributions of phenotypes and hybrid indices at their centres. This suggests strong reproductive isolation but it is not predicted by classical cline theory. I will describe some simulations aimed at dissecting the factors that might explain bimodality.

6th of April, 14:30-15:00

DESPECIATION

Jeremy B. Searle

Department of Ecology and Evolutionary Biology, Cornell University, USA

Hybrid zones between major genetic forms within species can act as what Godfrey Hewitt called “natural laboratories for evolutionary studies” and those studies are all the more fascinating because hybrid zones may be hotbeds for important evolutionary processes. There has long been an interest in hybrid zones as sites of speciation by reinforcement, a process championed by Theodosius Dobzhansky. Reinforcement is a potential outcome when there is sufficient selection against hybrids between the major genetic forms. However, substantial selection against hybrids doesn't necessarily have to lead to speciation, there is the possibility that it can go the opposite direction – reducing reproductive isolation of the genetic forms – and that's what I mean by 'despeciation'. I will describe this process as postulated for a small mammal (the common shrew), based on studies using hybrid zones between chromosomal forms as natural laboratories.

Why we became human

Rikard Holmdahl
Karolinska Institutet, Sweden

The human genome project has produced massive sequence information of individuals all around the world revealing numerous polymorphisms. However, it has been difficult to conclusively associate these polymorphisms to explain complex traits, like common diseases. We have taken a shortcut through inbred mice and rats and were able to identify a single nucleotide polymorphism (SNP) in the NCF1 gene, to be causative for many autoimmune diseases in rats (1). To translate this information to humans we realized that the NCF1 gene was not sequenced at the time due to copy number variation (CNV). We made an assay for the CNV and also sequence all exons and could identify both CNV and an amino acid replacement SNP (R90H) to be causative for several major autoimmune diseases (2) (3) (4). Expression of the human SNP (R90H) in the mouse could reproduce the human disease and could also be demonstrated to influence numerous complex traits in which reactive oxygen species plays a role (5) (6) (7, 8). The question remained however, why NCF1 is polymorphic in rats and humans. We assumed that the strongest natural selection factor for rats would be behaviour leading us to send our rat strains, with one nucleotide difference, for blind testing in an experimental behavioural test centre. The only significant test were tests for risk behaviour (9). This could explain the well-known scouting behaviour in rats (*Rattus norvegicus*), which could likely be a strong natural selection factor. The house mouse (*Mus musculus musculus* or *Mus musculus domesticus*) do not have any NCF1 polymorphism and no scouting behaviour. But humans clearly have this. The CNV appeared in humans and can be detected in both neanderthals and us. In our subspecies we do have the R90H occurring, but it has not been so far seen in neanderthals, although very few sequences have so far been revealed. We therefore speculate that the few individuals with the 90H mutation, leading to a low reactive oxygen species response in the brain allowing them to take more risks than others, were instrumental for migration and building hierarchies and larger societal networks.

1. Olofsson P, Holmberg J, Tordsson J, Lu S, Akerstrom B, Holmdahl R. Positional identification of Ncf1 as a gene that regulates arthritis severity in rats. *Nat Genet.* 2003;33(1):25-32.
2. Olsson LM, Nerstedt A, Lindqvist AK, Johansson AC, Medstrand P, Olofsson P, et al. Copy number variation of the gene NCF1 is associated with Rheumatoid Arthritis. *Antioxid Redox Signal.* 2012;16(1):71-8.
3. Olsson LM, Johansson AC, Gullstrand B, Jonsen A, Saevarsdottir S, Ronnblom L, et al. A single nucleotide polymorphism in the NCF1 gene leading to reduced oxidative burst is associated with systemic lupus erythematosus. *Ann Rheum Dis.* 2017;76(9):1607-13.
4. Zhao J, Ma J, Deng Y, Kelly JA, Kim K, Bang SY, et al. A missense variant in NCF1 is associated with susceptibility to multiple autoimmune diseases. *Nat Genet.* 2017;49(3):433-7.
5. Luo H, Urbonaviciute V, Saei AA, Lyu H, Gaetani M, Vegvari A, et al. NCF1-dependent production of ROS protects against lupus by regulating plasmacytoid dendritic cell development and functions. *JCI Insight.* 2023;8(7).
6. Li Y, Li Z, Nandakumar KS, Holmdahl R. Human NCF1(90H) Variant Promotes IL-23/IL-17-Dependent Mannan-Induced Psoriasis and Psoriatic Arthritis. *Antioxidants (Basel).* 2023;12(7).
7. Zhang J, Wang Y, Fan M, Guan Y, Zhang W, Huang F, et al. Reactive oxygen species regulation by NCF1 governs ferroptosis susceptibility of Kupffer cells to MASH. *Cell Metab.* 2024.
8. Li Y, Coelho A, Li Z, Alsveld M, Li Q, Xu R, et al. The systemic lupus erythematosus-associated NCF1(90H) allele synergizes with viral infection to cause mouse lupus but also limits virus spread. *Nat Commun.* 2025;16(1):1593.
9. Colaïanna M, Schiavone S, Zotti M, Tucci P, Morgese MG, Backdahl L, et al. Neuroendocrine profile in a rat model of psychosocial stress: relation to oxidative stress. *Antioxid Redox Signal.* 2013;18(12):1385-99.

CONTRIBUTED TALKS

5th of April, 15:30-15:45

Consistent transposable element accumulation in the face of hybridization and rapid speciation in Galápagos giant daisies (*Scalesia*)

José Cerca

NRM - Swedish Museum of Natural History, Stockholm, Sweden & CEES - Centre for Ecological and Evolutionary Synthesis

Transposable elements (TEs) have been hypothesized to play a pivotal role in driving diversification by facilitating the emergence of novel phenotypes and the accumulation of divergence between species. Hybridization and adaptation to novel niches are hypothesized to influence TE accumulation in genomes by disrupting genomic regulation, including the suppression of TE replication. The rapid speciation and ecological diversification characteristic of adaptive radiations offer a unique opportunity to examine the link between TE accumulation and speciation, diversification, hybridization and adaptation. Here, focusing on all 15 species of the genus *Scalesia* (Asteraceae), a radiation endemic to the Galápagos Islands, we test whether hybridization or shifts in ecological niche are associated with changes in TE accumulation in genomes. Our analyses reveal little to no variation in TE accumulation among *Scalesia* species nor its hybrid populations. Shifts in ecological niches, linked to climatic variation, did not result in discernible changes in TE accumulation, a surprising finding given the anticipated selective pressure imposed by aridity, a factor often linked to genome size reduction. We found no distinct patterns in the temporal accumulation of TEs, and no effects at the class or superfamily level. Our findings challenge the assertion that TEs have directly driven diversification, speciation and local adaptation. Instead, we suggest that TEs may simply be 'along for the ride,' rather than actively contributing to plant diversification.

5th of April, 15:45-16:00

Signatures of selection despite ephemeral population dynamics in "Darwin's Sparrow" (*Passer iagoensis*, Cabo Verde endemic)

José Cerca, Ângela M. Ribeiro, Michael Matschiner, Rosa Alicia Jiménez, Hugo Pereira, Zheng Oong, Gabriel David, Per Unneberg, Yan Wong, Gabriele Maria Sgarlata, Pim Edelaar, Tomáš Albrecht, Glenn-Peter Saetre, Pedro Cardia, Augusto Faustino, Evandro P. Lopes, Rauri C. K. Bowie, Mark Ravinet, **Martim Melo**

Understanding how genetic variation evolves and persists despite population reductions and selective pressures is a central question in evolutionary biology. We explored how genetic diversity is maintained in the ephemeral nature of island populations under natural selection, using the Iago Sparrow (*Passer iagoensis*), an endemic species of the Cabo Verde archipelago, as a model. Using whole-genome sequencing and phenotypic data, we examined the species' evolutionary history, population structure, and signatures of selection. Our results show that the Iago Sparrow diverged from its closest relative approximately 4.26 million years ago, with intraspecific diversification occurring within the last million years. Population structure analyses revealed three distinct lineages, corresponding to geographic divisions within the archipelago, with the Rombos islets population exhibiting significant phenotypic divergence, particularly in bill morphology. Genomic scans identified signatures of selection in genes associated with bill size (*HMG20B*) and, to a lesser extent, bill shape (*ALX1*), suggesting adaptive evolution in response to local environmental conditions. Coalescent analyses indicate that much of the adaptive variation arose after colonisation, contrasting with patterns seen in other island radiations, where ancestral variation plays a key role. Our findings highlight the interplay of genetic drift, gene flow, and selection in shaping island species' evolutionary trajectories and demonstrate that *de novo* mutations can facilitate adaptation to novel environments. The Iago Sparrow, a generalist thriving across diverse habitats, provides key insights into the mechanisms driving persistence and diversification in island lineages despite the challenges of small population sizes and environmental instability.

5th of April, 16:30-16:45

Diversification and local adaptation between and within oceanic islands: the Chaffinch radiation in Macaronesia

Milá, B (1); Fernández, M (1); Rancilhac, L (1); Recuerda, M (1,2)

(1) Department of Biodiversity and Evolutionary Biology, National Museum of Natural Sciences (MNCN-CSIC), Madrid, Spain; (2) Cornell Laboratory of Ornithology, Cornell University, Ithaca, USA

Oceanic archipelagos provide ideal systems for understanding the relative roles of selection and geographic isolation in the process of speciation. We used phylogenomics and patterns of genetic diversity to infer the diversification of chaffinches following the colonization of Macaronesian archipelagos. A molecular phylogeny and ancestral range biogeographic analyses revealed that the common chaffinch (*Fringilla coelebs*) underwent a rapid radiation across Macaronesia that was driven by the sequential colonization of the different archipelagos, from the mainland to the Azores, followed by Madeira, and finally the Canary Islands. Furthermore, on the island of La Palma (Canary Islands), where chaffinches expanded their range from the humid laurel forest to the extensive dry pine forests, we explored whether this habitat shift has resulted in evolutionary divergence between locally adapted populations. Birds in the two habitats show significant differences in diet, morphology and plumage coloration. A genome-wide survey using SNP loci revealed strong neutral genetic structure consistent with geography, revealing markedly restricted natal dispersal despite high dispersal capacity. Genome scans and Genotype-Environment Association (GEA) methods revealed numerous loci involved in local adaptation distributed across the genome, and a redundancy analysis (RDA) indicates that populations in the two habitats diverge at loci associated with vegetation greenness (NDVI). Our results suggest a strong role for polygenic selection in driving local adaptation in chaffinch populations on La Palma, a promising insular model for studying the evolutionary mechanisms of adaptive divergence.

5th of April, 16:45-17:00

Sperm and speciation in songbirds

Jan T. Lifjeld

NHMO - Natural History Museum, University of Oslo, Oslo, Norway

Speciation phenotypes are traits whose divergence contributes to reduced gene flow during speciation. In this talk I explore the hypothesis that rapid sperm length divergence promotes speciation in songbirds. Songbirds are characterized by a wide range of species-specific sperm lengths. There are also multiple examples of geographic variation in sperm length within species, which suggests that this trait evolves rapidly. Furthermore, songbirds vary in the extent of female promiscuity, which exerts selection for reduced sperm length variance in a population. In a comparative study of 20 populations pairs at different stages of the speciation continuum, I found that sperm length diverged faster, in terms of reduced overlap between populations, in more promiscuous species. Reduced overlap was caused by smaller variance in sperm length in promiscuous species, and not by different evolutionary rates of the mean sperm length. Since female promiscuity promotes non-overlapping sperm length distributions in allopatry and exerts selection on the trait, conspecific sperm precedence based on sperm length can be expected when populations make secondary contact. Thus, female promiscuity can drive prezygotic isolation through sperm length as a speciation phenotype. This “gametic speciation” hypothesis predicts that promiscuous lineages have elevated speciation rates. I will present some indirect support for this prediction in songbirds.

Ecological differentiation influences the evolution of prezygotic isolation in spider-mite species

Barreto, S (1); Grandela, A (1); Henriques, S (1); Cruz, MA (1); Sousa, VC (1); Magalhães, S (1,2); Zélé, F (3); Fragata, I (1); Blanckaert, A (1);

(1) cE3c - Centre for Ecology, Evolution and Environmental Changes & CHANGE - Global Change and Sustainability Institute, FCUL University of Lisbon, Lisbon, Portugal; (2) Wissenschaftskolleg zu Berlin, Berlin, Germany; (3) ISEM - Institut des Sciences de l'Évolution de Montpellier, University of Montpellier, CNRS, IRD, EPHE, Montpellier, France;

Understanding how speciation occurs requires the study of reproductive isolation and its evolution. The characterization of the role of the different reproductive barriers (e.g., local adaptation, mate choice, hybrid load), and how they arise and are strengthened has been largely studied. Yet, the evolution of their interactions remains somewhat elusive. Using experimental evolution, we investigated how prezygotic barriers may evolve in the presence of ecological differentiation and pre-existing postzygotic isolation, using two sister species of spider mites: *Tetranychus urticae* (Tu) and *T. cinnabarinus* (Tc). This system displays incomplete reproductive isolation (infertile F1 hybrid), strong first male sperm precedence, and both Tc and Tu males mate preferentially with Tc females. We created three isolated regimes: Tu on bean, Tu on tomato, and Tc on bean; and two connected regimes formed by pairs of populations exchanging individuals. The connected regimes differed only in hosts: Tu and Tc on bean versus Tc on bean and Tu on tomato. After 8 generations, we quantified changes in assortative mating and in the ability of females to remate successfully. Tu males showed stronger preference for mating with conspecific females when coming from the connected regimes with different hosts, than males coming from the isolated populations. Additionally, Tu females from this same regime produced more non-hybrid daughters when mating first with heterospecific males and then with a conspecific. This suggests a shift in the first male sperm precedence, allowing for a rescue of the production of fertile daughters. Altogether, our results show both a shift towards conspecific assortative mating, and a weakening of the impact of heterospecific matings by changes in male sperm precedence. Overall, contact between populations in the presence of ecological differentiation enabled the evolution of stronger prezygotic barriers, a step towards the completion of the speciation process.

5th of April, 17:15-17:30

Host-parasite interactions drive speciation in crater lake cichlid fish

Leal-Cardín M; González-García P; Bracamonte SE, **Barluenga, M**

Department of Biodiversity and Evolutionary Biology, National Museum of Natural Sciences CSIC

Divergent adaptation to distinct ecological niches can, over remarkably short periods of time, generate animal diversification. Some biotic features such as parasite communities are capable of driving diversification exerting strong selective pressures on their hosts. This is probably due to the ability of the host immune system to rapidly evolve in response to local parasites. There is evidence that immunity genes evolve more rapidly and are under more positive selection than the rest of the genome, and that respond to natural selection modulating defenses to parasites. These genes also play an integral role on reproductive isolation contributing to the discrimination of mating partners, and therefore to diversification. Here we explore the role of host-parasite interactions in promoting diversification and ultimately speciation in prime models for adaptive radiation, cichlid fishes in crater lakes. We studied the recent adaptive radiations of the Neotropical Midas cichlid in the Nicaraguan crater lakes and their associated parasite communities, to investigate how changes in parasite communities induce changes in the fish immune system. We discuss how these changes might start, maintain or enhance species differentiation

Climate-driven evolution at range margins of marine forests

Serrão, EA (1,2); Almeida, S (1); Madeira, P (1); Neiva, J (1); Assis, J (1); Pearson, GA (1)
(1) CCMAR, University of Algarve, Faro; (2) CIBIO-INBIO, University of Algarve, Faro

Climate-driven range shifts that shape the geographical distribution of genetic diversity can drive different modes of speciation including divergence in allopatry or recombination at contact zones and allopolyploidy. Empirical evidence for these predictions in marine forests was discovered by analysing the geographical distribution of genetic variability and modelling species range shifts. This revealed novel recombined genomic diversity at recent expansion fronts that form contact zones, in addition to the more expected high and unique genetic diversity in ancient populations at estimated long-term persistence zones, some of them presently located in shrinking climatic refugia. Hotspots of diversity and evolution have also resulted from diversity and reticulation within lineages with clearly discernable ancestry and geographical distribution at sympatric contact zones. Phylogroup distributions compared with habitat suitability over time further demonstrate a role of cycles of isolation in disjunct persistence areas intercalated with ephemeral expansions and admixture at high-latitude contact zones. Multi-glacial cycles thus acted as a speciation pump for marine organisms otherwise exhibiting cosmopolite amphiboreal distributions.

5th of April, 17:45-18:00

Extreme polar light regimes promote hybrid zones at higher latitudes and biodiversity globally?

Kari Saikkonen

Biodiversity Unit, University of Turku, Finland

Climate change-driven biodiversity loss represents one of the greatest global challenges. In our Perspective (Saikkonen et al. 2024), we propose a theoretical and working framework to understand biodiversity recovery by bringing together key evolutionary processes which are individually thoroughly studied but separated by the different branches of biological sciences. We emphasize the importance of microbes to plant adaptations, and hypothesize that the Polar light environment with seasonal continuous light (“polar day”) and dark (“polar night”) creates circumpolar hybrid zones by increasing the synchrony of reproductive phenology among species. On a geologic time scale, species’ range shifts across latitudes with different light environments during the Earth’s cooler and warmer periods together with circumpolar hybrid zones and consequent introgressive hybridization may play significant roles in maintaining genetic admixture and species diversity. Thus, biodiversity can, in the long term, recover after disturbances and mass extinctions, but ecosystems will restructure as novel species assemblages. This calls for increased attention to the importance of ensuring sufficient genetic, species and species interaction potential to support future diversification and ecosystem functions and services.

Saikkonen, K., T. Birge, B. Fuchs, M. Helander, J.A. Ihalainen, R. Nissinen and P. Puigbò (2024) Toward an integrated understanding of how extreme polar light regimes, hybridization, and light-sensitive microbes shape global biodiversity. *One Earth*, 7, 1529-1541. <https://doi.org/10.1016/j.oneear.2024.08.002>

How ancient chromosomal inversions shaped a parallel Galápagos beetle radiation.

Vangestel C.; Hendrickx F.

RBINS - Royal Belgian Institute of Natural Sciences, OD Taxonomy and Phylogeny, Brussels,
Belgium

A most intriguing feature of adaptive radiation within islands is the repetitive occurrence of similar phenotypes along repeated environmental gradients. Recent studies have highlighted the significance of chromosomal rearrangements in such evolutionary phenomena, however, its ubiquitous importance remains yet to be determined. Within this framework, we study a progressive parallel adaptive radiation of caterpillar-hunter beetles (*Calosoma*) at the Galápagos along. Beetles show wing reduction at high altitude on all major islands of the archipelago, and the magnitude of within-island phenotypic and genetic divergence between high- and lowland ecotypes follow the island chronosequence. We inferred the genomic basis of this gradual divergence and revealed that the genomic regions underlying the repeated divergence entail massive chromosomal inversions, whose origin could be traced back to the initial high-lowland divergence on the oldest island. Highland alleles subsequently spread to younger islands through dispersal of highland individuals as well as dispersal of lowland individuals carrying introgressed highland alleles and thereby facilitating in-situ evolution. In conclusion, a complex interplay between colonization and introgression of chromosomal inversions gave rise to this parallel beetle radiation at the Galápagos. These results enhance our understanding on the molecular underpinnings and rapid evolution of island biodiversity.

Vangestel C. et al. (2024). Chromosomal inversions from an initial ecotypic divergence drive a gradual repeated radiation of Galápagos beetles. *Science Advances*, 10, eadk7906. DOI:10.1126/sciadv.adk7906

Introgression dynamics of sex-linked chromosomal inversions shape the Malawi cichlid adaptive radiation

Svardal, H (1,19); Blumer, LM (2); Burskaia, V (1); Artiushin, I (1); Saha, J (1); Camacho Garcia, J (1); Campuzano Jiménez, F (1); Hooft van der Huysdynen, A (1); Elkin, J (3); Fischer, B (2); Van Houtte, N (1); Zhou, C (2,4); Gresham, S (1); Malinsky, M (5); Linderoth, T (6); Sawasawa, W (1); Vernaz, G (2,10); Bista, I (7,8); Hickey, A (3); Kucka, M (9); Louzada, S (10); Zatha, R (11); Yang, F (12); Rusuwa, B (11); Santos, ME (3); Chan1, YF (13,9); Joyce, DA (14), Böhne, A (15); Miska, EA (16,2); Ngochera, M (17); Turner, GF (18); Durbin, R (2,4);

(1) Evolutionary Ecology Group, Department of Biology, University of Antwerp, Belgium; (2) Department of Genetics, University of Cambridge, UK; (3) Department of Zoology, University of Cambridge, UK; (4) Wellcome Sanger Institute, Tree of Life, Wellcome Genome Campus, UK; (5) Institute of Ecology and Evolution, Department of Biology, University of Bern, Switzerland; (6) W.K. Kellogg Biological Station, Michigan State University, USA; (7) Senckenberg Research Institute and Natural History Museum, Germany; (8) LOEWE Centre for Translational Biodiversity Genomics, Germany; (9) Friedrich Miescher Laboratory of the Max Planck Society, Germany; (10) Wellcome Sanger Institute, Wellcome Genome Campus, UK; (11) School of Natural and Applied Sciences, University of Malawi, Malawi; (12) School of Life Sciences and Medicine, Shandong University of Technology, China; (13) Groningen Institute for Evolutionary Life Sciences (GELIFES), University of Groningen, The Netherlands; (14) Evolutionary and Ecological Genomics Group, School of Natural Sciences, University of Hull, UK; (15) Leibniz Institute for the Analysis of Biodiversity Change, Museum Koenig Bonn, Germany; (16) Department of Biochemistry, University of Cambridge, UK; (17) Department of Fisheries Headquarters, Malawi; (18) School of Environmental and Natural Sciences, Bangor University, UK; (19) Naturalis Biodiversity Center, Leiden, The Netherlands

Chromosomal inversions can contribute to adaptive speciation by linking co-adapted alleles. Querying 1,375 genomes of the species-rich Malawi cichlid fish radiation, we discovered five large inversions segregating in the benthic subradiation that each suppress recombination over more than half a chromosome. Two inversions were transferred from deepwater pelagic *Diplotaxodon* via admixture, while the others established early in the deep benthic clade. Introgression of haplotypes from lineages inside and outside the Malawi radiation coincided with bursts of species diversification. Inversions show evidence for transient sex linkage and a striking excess of protein changing substitutions points towards selection on neuro-sensory, physiological and reproductive genes. We conclude that repeated interplay between depth adaptation and sex-specific selection on large inversions has been central to the evolution of this iconic system.

Interactions between mechanisms of reproductive isolation

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Speciation is responsible for the diversity of species observed today and corresponds to the build-up of reproductive isolation between populations. Reproductive isolation can be generated by different mechanisms that have been extensively characterized, yet how their interactions affect speciation remains largely unknown. Here, we explicitly model the interaction of three key mechanisms (local adaptation, mate choice and genetic hybrid incompatibilities) quantifying their relative contribution to the evolution of reproductive isolation. We modeled two populations exchanging migrants using Fisher Geometric Model for local adaptation, phenotype matching for mate choice, and multiple pairs of Bateson-Dobzhansky-Muller Incompatibilities (DMI). All three mechanisms were determined by the same set of loci, creating conditions for interactions between barriers both at the genetic and population levels. We found no cases where the three barriers evolved. Instead, two barriers could evolve depending on the migration rate: either local adaptation and genetic incompatibilities for limited migration, or local adaptation and mate choice for higher migration. Our results showed that local adaptation due to ecological differentiation was the first to evolve and by far the most effective reproductive barrier. Finally, we demonstrated that in a polygenic model, populations could become locally adapted and evolve strict mate choice, yet they would not accumulate incompatibilities provided that there was sufficient gene flow.

6th of April, 16:45-17:00

Mitonuclear divergence predicts gradual speciation in animal hybrid zones

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Speciation is underpinned by genetic incompatibilities underlying the evolution of reproductive isolation. Hybrid zones provide unique opportunities to unravel the evolutionary rate of reproductive isolation in the origin of species. The selection against hybrids accrues with increased genetic incompatibilities, promoting the evolution of reproductive isolation in the face of gene flow. There have been decades of debates over the relationship between the selection against hybrids and the genetic divergence between parental lineages. The debates occur primarily among three models: (1) the Additive Effect Model predicts a linear growth of selection against hybrids with the divergence of parental lineages; (2) the Snowball Effect Model predicts exponential growth of selection; whereas (3) the Slowdown Effect Model predicts a logarithmic growth of selection. Here, we tested the three models with 116 animal hybrid zones worldwide. The Slowdown Effect Model is best supported with the full dataset. We refined the three models to consider independent and interactive effects of mitochondrial (mtDNA) and nuclear genetic (nDNA) divergence on the selection against hybrids. There is greater mtDNA distance and greater selection on mtDNA than the nDNA. Together, the refined Linear Model was most supported by the data, revealing a significant mitochondrial effect as well as a marginal and heterogeneous nuclear effect. Collectively, this data synthesis in the early stage of animal speciation reveals a gradual development of reproductive isolation with mitonuclear genetic divergence.

Hybridization is prevalent but outcomes are distinct across highly differentiated Iberian chub species

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The exchange of alleles between lineages through hybridization is increasingly recognized as a common phenomenon in nature. However, our efforts to characterize the prevalence and consequences of hybridization in natural systems often overlook highly divergent allopatric species, presumably because they are viewed as less likely to hybridize. Yet, such species provide an opportunity to investigate the later stages of the speciation process. Here, we study such a system: the Iberian chubs (*Squalius* spp.), a group of primary fish species with allopatric distributions across distinct environments and river basins in the Iberian Peninsula. Despite their current distributions, throughout their evolutionary history the rivers these species inhabit suffered profound changes, potentially allowing for several periods of isolation and secondary contact. We generated whole genome re-sequencing data from ~170 individuals from eight Iberian chub species. Our analysis uncovered three, potentially four, contrasting cases of hybridization, spanning different geographical and time scales. First, we found evidence of ancient hybridization between two species at the origin of a third one that now inhabits a broad area in the Iberian Peninsula. Second, we uncovered a case of recent, possibly ongoing, hybridization restricted to a localized stream, with introgression of nuclear and mitochondrial DNA. Third, we detected, at a regional scale, a case of nuclear introgression but with no detectable mitochondrial introgression. Finally, we found a case where two very distinct mitochondrial lineages persist at balanced frequencies in a putative hybrid population, despite no detectable nuclear introgression. Notably, the ancient hybrid was involved in all other hybridization cases, raising interesting possibilities regarding the role of lineages of admixed origin in promoting further gene flow with other species.

6th of April, 17:15-17:30

Neglected human-driven species diversification: the case of the Javan Red Junglefowl (*Gallus gallus bankiva*)

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Human actions have a significant influence on biodiversity, which is rapidly declining due to factors like changes in land use and overexploitation. However, there are some instances where human influence has not only prevented the loss of genetic diversity in wild vertebrates but has also led to its increase. This phenomenon, which occurred over relatively short evolutionary periods, may go unnoticed without historical records or phenotypic evidence. However, the growing use of genome-wide technologies is providing new opportunities to uncover these overlooked cases of human-driven genetic differentiation. For instance, by analyzing the entire genomes of modern and historical samples collected around 110-150 years ago, we demonstrate that the most distinct subspecies of Red Junglefowl (*Gallus gallus*), the wild ancestor of domestic chickens, likely resulted from a recent genetic mixing with the Green Junglefowl (*G. varius*) on the island of Java. Gene flow analysis suggests that this event occurred either as the result of the Red Junglefowl colonization of new favorable habitats in Java or from the introduction of feral *G. gallus* to this island several centuries ago. This study highlights how human activities—whether through habitat alteration or the introduction of domesticated species into the wild—can shape the evolutionary path of wild species, often leading to misinterpretations that attribute such changes to long-standing natural differentiation.