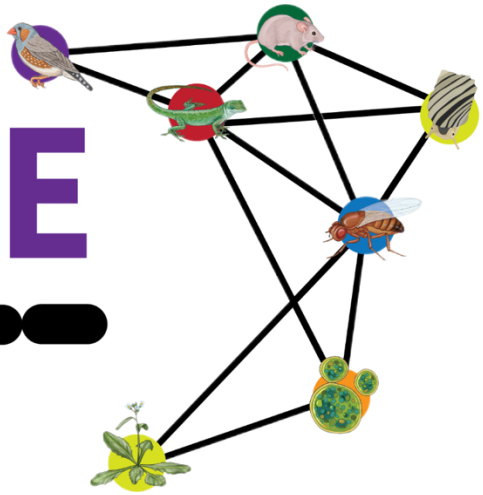
TiBE STRiVE

Trends in Biodiversity and Evolution

The evolutionary role of structural genomic variation



TiBE-STRIVE Conference 2026

8th-10 July

Vila do Conde

Portugal

Abstract book

TiBE-STRiVE Conference

Conference on the evolutionary role of structural variation

8th-10th July 2026

Vairão, Vila do Conde

Portugal

STRiVE is a Special Topic Network funded since 2026 by the European Society for Evolutionary Biology

The Trends in Biodiversity and Evolution (**TiBE**) conference is an annual meeting organized by BIOPOLIS-CIBIO

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Venue

The venue comprises two buildings: the CIBIO-BIOPOLIS Headquarters (Building 1 – top image), which will host the morning sessions, and the newly renovated buildings of Quinta do Crasto, a former farm and agricultural museum that has recently been transformed into a biodiversity research laboratory for CIBIO – Associação BIOPOLIS, University of Porto, Portugal (Building 3 – bottom image), which will host the afternoon sessions.

Building 1 - BIOPOLIS Headquarters, Campus de Vairão; Vairão, Vila do Conde, Porto, Portugal.

Building 3 - BIOPOLIS Quinta do Crasto, Campus de Vairão; Vairão, Vila do Conde, Porto, Portugal.

Detailed program

DAY 0, 7th of July

Centro de Memória Building, Vila de Conde

18:00-19:30 – Registration & Welcome Reception

DAY 1, 8th of July

8:00 Shuttle from Vila do Conde to the Venue (Building 1)

8:30 – 9:00 Registration

9:00 – 9:30 Open Ceremony: Nuno Ferrand - CIBIO/BIOPOLIS director, Susana Ribeiro - CM Vila do Conde, Claire Mérot - STRiVE Network, Rui Faria - Main TiBE-STRiVE organizer

Chair: Claire Mérot

9:30 – 10:15 Plenary Talk – Mark Kirkpatrick - Chromosome inversions as pre- and postzygotic isolating mechanisms

10:15 – 10:30 Carolina Segami – The role of inversions in the reproductive isolation of recently diverged cryptic mouse lemur species.

10:30 – 11:00 *Coffee Break*

Chair: Marcial Escudero

11:00 – 11:30 Mini plenary: Ashwini V Mohan – Genomic rearrangements underlie barriers to recombination in holocentric sedges

11:30 – 11:45 Alistair Hockey – Massive genomic flux and rapid differentiation in a young autogamous diploid

11:45 – 12:00 Léa Nicolas – Evolutionary consequences of recombination suppression: the case of a chromosomal inversion in the seaweed fly

12:00 – 12:15 Carina Mugal – Population-level PacBio HiFi data enable the investigation of structural variants in the speciation process of two songbirds

12:15 – 12:30 Desanka Lazić – A graph-based pangenome of European beech (Fagus sylvatica) reveals the landscape of structural variation across the distribution range

12:30 – 14:00 *Lunch (Building 3)*

Chair: Marina Rafajlovic

14:00 – 14:15 Pierre Barry – Origin and fates of chromosomal inversions in *Littorina* marine snails

14:15 – 14:30 Katie Lotterhos – Comparison of population-genetic vs. read-based calls of inversions in Atlantic cod

14:30 – 14:45 Claire Lemaitre – Representation and detection of inversions in pangenome graphs

14:45 – 15:00 Mélody Temperville – SVJedi-Tag: a novel method for genotyping large inversions with linked-read data

15:00 – 15:15 Jana Wold – The good, the bad, and the complex: Characterizing structural variants using genome graphs

15:15 – 16:00 Parallel Discussions – session I

16:00 – 16:15 *Coffee Break*

16:15 – 17:00 Parallel Discussions – session II

17:00 – 17:30 Discussion reporting and conclusions

17:30 – 19:00 Poster Session

19:00 *Shuttle to Vila do Conde*

DAY 2, 9th of July

8:30 – 9:00 Shuttle from Vila do Conde to the Venue (Building 1)

Chair: Kay Lucek

9:00 – 9:45 Plenary Talk – Joana Meier - Structural variation facilitating speciation in butterflies and spiders

09:45 – 10:00 Amin Ghane – Genomic drivers of persimmon adaptive radiation in New Caledonia, a biodiversity hotspot

10:00 – 10:15 Guillaume Martin – Unravelling genomic drivers of speciation in *Musa* through comparison of wild banana ancestors genomes.

10:15 – 10:30 Simone D'Alessandro –Multiple chromosomal inversions shape the genomic landscape of a marine broadcast spawner

10:30 – 11:00 *Coffee Break*

Chair: Aurora Ruiz-Herrera

11:00 – 11:30 Mini plenary: Océane Mion – Uncovering the role of structural variations in the evolution and adaptation of a devastating fungal pathogen

11:30 – 11:45 Heidi Yang – Role of chromosomal inversions in local adaptation in California endemic oak

11:45 – 12:00 Laure Segurel – Adaptation of the bedbug *Cimex lectularius* to a new (human) host

12:00 – 12:15 Hugo Corval – A 38-Mb region underlies an ancient climate-linked inversion in barn owls

12:15 – 12:30 Malin Hasselgren – Structural variation in Iberian lynx (*Lynx pardinus*)

12:30 – 14:00 Lunch (Building 3)

Chair: Benjamin Dauphin

14:00 – 14:15 Jessica Purcell – The role of gene flux in the evolutionary trajectory of supergenes

14:15 – 14:30 Vitor Sudbrack – The effect of supergene evolution on the structure and stability of the G-matrix

14:30 – 14:45 Trevor Krabbenhoft – Structural variants and the genetic diversity – population viability paradox

14:45 – 15:00 Eleftherios Darzentas – The role of gene Copy Number Variations (gCNVs) in the local adaptation of major european tree species

15:00 – 15:15 Pascal Milesi – Show Case of the 'rCNV', a comprehensive framework to call gene copy number variations from SNPs data.

15:15 – 16:00 Parallel Discussions – session III

16:00 – 16:15 *Coffee Break*

16:15 – 17:00 Parallel Discussions – session IV

17:00 – 17:30 Discussion reporting and conclusions

17:30 *Shuttle to Vila do Conde*

18:00 Walking city Tour

DAY 3, 10th of July

8:30 – 9:00 Shuttle from Vila do Conde to the Venue (Building 1)

Chair: Thomas Aubier

9:00 – 9:45 Plenary Talk – Jeffrey Groh - Ancient rhythms of sex alternation in flowering plants

09:45 – 10:00 Dominique Hicks – Macro-evolutionary perspectives on a large chromosomal rearrangement underlying alternative life-histories in seaweed flies

10:00 – 10:15 Eva Koch – The role of a sex chromosome–autosome fusion in the evolution of live-bearing and speciation in the common lizard

10:15 – 10:30 Nikolas Vellnow – Sex-linked structural variation and paralogy shape genomic diversity in a songbird

Chair: Petr Neguyen

10:30 – 11:00 *Coffee Break*

11:00 – 11:30 Mini plenary: Katarina Stuart – Structural variants and transposable elements under weakened selection in invasive populations

11:30 – 11:45 Paul Battlay – Local PCA reveals widespread structural variation across the tree of life

11:45 – 12:00 Caitlin Price – Uncovering the complex genomic history of *Araneoidea* and the role of TEs on Intrachromosomal Rearrangements

12:00 – 12:15 Anna-Sophie Fiston-Lavier – Exploring Transposable Elements dynamic in human population in the Human Pangenome Reference Consortium Release 2 Data

12:15 – 12:30 Janina Rinke – Transposable element islands at the interface of 3D genome architecture and karyotype evolution in ants

12:30 Closing

12:45 – 14:30 *Lunch (Building 3)*

14:30 Visit to Hall of Biodiversity - Porto

19:00 Bus from Porto to the conference dinner

20:00 Conference Dinner

11th of July, After-Conference Excursion

Oral communications

Plenary talks

Plenary talk 1 | **Mark Kirkpatrick - Chromosome inversions as pre- and postzygotic isolating mechanisms**

The University of Texas at Austin, USA

Abstract

Inversions often reduce fertility, and when that happens they contribute to postzygotic isolation between populations or species. In this talk I discuss models showing they can also (at the same time) contribute to prezygotic isolation. Clines in the frequencies of locally adapted haplotypes can generate troughs in the density of continuous populations. Under some conditions, these troughs can divide one population into two populations, potentially leading to parapatric speciation.

Plenary talk 2 | **Joana Meier - Structural variation facilitating speciation in butterflies and spiders**

The Wellcome Sanger Institute and University of Cambridge, UK

Abstract

Structural variation, from large-scale chromosomal fissions and fusions to small-scale inversions, has long been hypothesised to facilitate speciation by decreasing hybrid fitness and/or reducing recombination rates, thereby linking together co-adapted genes. By assembling reference genomes at the chromosome level, we can now test this hypothesis in great detail and deepen our understanding of the roles of these structural variants in speciation. With genome assemblies of over 100 Ithomiini butterflies, we are studying how chromosomal fissions and fusions contribute to speciation in these rapidly speciating butterflies with high karyotype variation. With 1200 additional moths and butterfly genomes generated via Project Psyche - a large-scale project to sequence European Lepidoptera, and genomes from other orders (Coleoptera and Diptera) generated via the Darwin Tree of Life, we can elucidate the generality of our findings. Lastly, I would like to introduce peacock spiders as an exciting study system to elucidate the role of inversions in very rapid species radiations.

Plenary talk 3 | **Jeffrey Groh - Ancient rhythms of sex alternation in flowering plants**

University of California Berkeley, USA

Abstract

Discrete mating type systems offer compelling evidence for the selective maintenance of genetic variation through long-term balancing selection. Such systems inform our understanding of the forces shaping sexual reproduction strategies, the evolution of genome architecture, and the molecular and developmental regulation of sex. One example is heterodichogamy - dimorphism for the direction of temporal separation of sexes within hermaphrodite plants. Male-first and female-first flowering types mate disassortatively and are thus maintained near equilibrium through negative frequency-dependent selection. Similar to separate sexes, heterodichogamy has convergently evolved across angiosperms and has a simple inherited basis. Our recent work has uncovered the genomic basis of this trait in the walnut and laurel families, revealing an important role of ancient structural variants, novel regulatory models, and genomic convergence. Yet, even within a single family, several distinct genetic mechanisms are found among closely related genera, suggesting dynamic evolution during the establishment of genetic inheritance for heterodichogamy. In this talk, I will discuss our recent findings from the walnut family to illustrate dynamics of heterodichogamy polymorphisms and propose developmental models for the joint regulation of male and female flowering time. Structural variants appear to play an important role, both directly in effecting context-specific gene regulation, as well as indirectly as a consequence of recombination suppression.

Mini Plenary talk 1 | **Genomic rearrangements underlie barriers to recombination in holocentric sedges**

Mohan, A.V. (1); Sánchez-Villegas, R. (2,3); Sargheini, N. (4); Marín-Gual, L. (5); Gomez-Ramos, I. (3), Escuer, P. (1); Martin-Bravo, S. (2); Ruiz-Herrera, A. (5); Marques, A. (4); Escudero, M.(3); Lucek, K. (1)

(1) UniNe - Department of Biology, University of Neuchâtel, Neuchâtel, Switzerland; (2) UniPab - Universidad Pablo de Olavide, Seville, Spain; (3) UniSev - Department of Plant Biology and Ecology, University of Seville, Spain; (4) MPI-PBR – Max Planck Institute for Plant Breeding Research, Cologne, Germany; (5) UAB - Universitat Autònoma de Barcelona, Barcelona, Spain

Abstract

The plant family *Cyperaceae* (sedges) shows outstanding species diversity associated with high rates of chromosomal fusions and fissions. This is likely because sedges have holocentric chromosomes, *i.e.* chromosomes with centromere-like regions across their entire length. However, we do not yet understand the genomic underpinnings of such rearrangements, and their role in the formation of new species. Heterokaryotypic crosses provide the opportunity to study the impact of rearrangements on rates of recombination and therefore the buildup of reproductive barriers. Here we utilize such a cross of *Carex laevigata,* which shows a gradient of karyotypes across populations in the Iberian Peninsula and combine karyotyping, chromosome-resolved genome assemblies, whole genome resequencing, and Hi-C across four generations. We show that heterokaryotypic crosses result in highly unstable chromosome pairings in the F1s and F2s, producing mono- to tetravalent chromosomes. The F3s seem to stabilize towards the parental karyotype with larger chromosome numbers, and consequently smaller chromosome sizes. We hypothesize that this could reflect high segregation distortion experienced by missegregation of smaller chromosomes in the irregular pairings during meiosis. Further, synteny breakpoint regions in the F1s and F2s are enriched for LTR gypsy repeats, whereas the F0 parents and the F3s show no such enrichment in the corresponding regions, suggesting that these repeats may facilitate chromosomal rearrangements. TAD-like regions are either retained or re-established in F3s, consistent with high conservation of 3D genomic features. In this system, holokinetic drive seems to favor smaller chromosomes, chromosomal fissions, and shows loss of repeat elements. Together, our study provides insights into the mechanisms of how rapid genomic rearrangements occur and stabilize in just four generations, and how these properties can contribute to species diversification in holocentric organisms.

Mini Plenary talk 2 | **Uncovering the role of structural variations in the evolution and adaptation of a devastating fungal pathogen**

Mion1, O (1*); Lorazo, M (1*); Lambert, M (1); Berard, S (1); Nabholz, B (1); Fiston-Lavier, A-S (1,2); Puechmaille, S (1,2)

(1) ISEM, University of Montpellier, CNRS, IRD, Montpellier, France (2) IUF, Institut Universitaire de France, Paris, France *co-first authors

Abstract

Structural variants (SVs) are increasingly recognised as major drivers of genome evolution and adaptation. In fungal pathogens, SVs often constitute a substantial proportion of genomic variation, yet their role in adaptation remains poorly characterised. Here, we investigate SVs, focusing on inversions and transposable elements, in *Pseudogymnoascus destructans* (Pd), a psychrophilic, haploid filamentous ascomycete causing White-nose disease, the most severe disease-driven mortality recorded in non-human mammals. Pd comprises two closely related but independently evolving species, Pd-1 and Pd-2, associated with different but partially overlapping bat hosts and distributed across a broad thermal gradient in Europe (ca. 2–16 °C), providing an opportunity to examine genome organisation and adaptation. We generated over 200 de novo assembled genomes from 28 European countries using Oxford Nanopore long-read sequencing. Combined SV detection pipelines (Syri with Minimap2 or Nucmer, and Cactus) enabled high-resolution identification of SVs, including large transposable elements such as Starship, while simultaneously quantifying genome-wide methylation. Preliminary analyses show that the Pd genome comprises 14 core and three accessory chromosomes. TEs represent more than 35% of the genome, with evidence of recent activity. TEs occur at 70% of inversion boundaries, and more than 6,000 inversions were detected, including large events (>100 kb). Methylation levels were higher within TEs than in surrounding regions and varied among TE families, suggesting differential epigenetic regulation. Ongoing analyses integrate SNPs and SVs to identify genomic regions under selection associated with host specificity and temperature, highlighting the major contribution of SV to genome architecture and adaptation in this emerging fungal pathogen.

Mini Plenary talk 3 | **Structural variants and transposable elements under weakened selection in invasive populations**

Stuart, KC (1,2,3); Whibley, A (3); Atsawawaranunt, K (3); Johnson, R (4); Major R (5); Ewart KM (5); Rollins, LA (2); Santure AW (3)

(1) Macquarie University, Sydney Australia; (2) University of New South Wales, Sydney, Australia; (3) University of Auckland, Auckland, Aotearoa/New Zealand; (4) Smithsonian Institution, National Museum of Natural History, Washington, DC, USA; (5) Australian Museum, Sydney, Australia

Abstract

Structural variants (SVs) are a major contributor to genomic variation, yet their evolutionary dynamics remain poorly understood relative to single nucleotide polymorphisms (SNPs). The frequency and persistence of any genetic variant within a population is strongly influenced by demographic history. For example, when populations experience bottlenecks and reduced effective population sizes, weakened purifying selection may allow mildly deleterious variants to accumulate. However, the extent to which this process affects SVs relative to SNPs remains unclear. This is particularly important when considering that SVs encompass a diverse range of variant types and sizes, and it is unknown whether different classes of SVs respond similarly to weakened selection or whether their evolutionary dynamics differ across demographic contexts. Here, we investigate how demographic disruption shapes genome-wide structural variation in the globally invasive avian species *Acridotheres tristis*. Using genome resequencing data from 82 individuals sampled across one native and four invasive countries, we profile and compare genome-wide SNPs, SVs, and transposable elements. This invasion system provides a natural experiment for examining how successive introduction bottlenecks and population expansions influence the prevalence and distribution of complex variants. We focus specifically on distinguishing between standing and novel variants, as well as SVs arising from TE activity from those of non-TE origin, allowing us to test whether these classes of variants respond differently to demographic change. Thus, we can assess separately how weakened selection regimes shape their frequency, genomic distribution, and potential functional impacts across populations that have experienced repeated founder events. Ultimately, this study aims to examine how genome-wide variation interacts with demography to shape genome evolution in small and recently expanded populations.

Regular talks

Talk 1 | **The role of inversions in the reproductive isolation of recently diverged cryptic mouse lemur species**

Segami, JC (1); Kania, H (1); Goel, M (1); Hyde Roberts, S (1); Yoder, AD (1)

(1) Biology department, Duke University, Durham NC, USA

Abstract

Inversions are strong candidates to serve as barriers to gene flow in diverging lineages due to their ability to prevent recombination and build suitable ground for the buildup of genetic differences. These linked differences are shielded from geneflow and allow selection to act on them. Documented examples of inversions aiding speciation through the buildup of reproductive isolation include *Drosophila*, *Anopheles*, *Littorina*, *Mimulus*, and more. These examples are associated with inversions bigger than 1Mb, often acting as "supergenes", where traits have accumulated or proper chromosome pairing is disrupted. However, there are theoretical arguments and some examples in *Helianthus* and *Littorina* that suggest that several small inversions could also have a synergic effect aiding divergence. *M. murinus* and *M. griseorufus* are two cryptic sister species that diverged less than a million years ago. Demographic modelling shows evidence for divergence with constant but small gene flow that stopped altogether very recently (thousands of years ago). While *M. murinus* is a known generalist and has a wide distribution, *M. griseorufus* is considered a specialist restricted to the dry spiny forests found in southern Madagascar. They both share a sympatric area in the Andohahela region (SE Madagascar) where –while using many of the same resources and territories– they show complete reproductive isolation. Using two high quality de-novo assemblies and low coverage population data, we identified several fixed but small inversions. Here we investigate how these inversions between the two species could have contributed to the recent completion of reproductive isolation.

Talk 2 | **Massive genomic flux and rapid differentiation in a young autogamous diploid**

Hockey A, (1); Syme, R (1, 2); Cizkova, J (3); Croser, J (1, 4); Ryan, M (1); Hribova, E (3); Lichtenzveig, J (1)

(1) The UWA School of Agriculture and Environment, University of Western Australia, Crawley, Western Australia, 6009, Australia; (2) Seqera Labs, Barcelona, 08005, Spain; (3) The Institute of Experimental Botany, Czech Academy of Sciences, Olomouc, 77900, Czech Republic; (4) South Australian Research and Development Institute, Urrbrae, South Australia, 5064, Australia

Abstract

Species cohesion depends on gene flow to maintain a unified evolutionary pathway. Recombination suppression within structural variants, such as inversion polymorphisms, disrupts this flow and drives genetic differentiation between haplotypes. While the role of inversions in the divergence and speciation of diploid species is increasingly recognised, most studies document ancient polymorphisms (>1 MYA) in outcrossing (allogamous) species. Here, we present evidence of extensive, rapid genome differentiation driven by structural variation in a young, self-fertilising (autogamous) diploid species. *Cicer echinospermum* P.H. Davis (2n = 16) is a young legume species that shared a common ancestor with cultivated chickpea (C. arietinum L.) just 95 to 127 KYA. Despite its recent origins and autogamous reproductive strategy, we discovered massive structural variations within and between geographically distinct populations. Two large inversion polymorphisms were fully validated through a combination of assembly comparisons, breakpoint mapping, and karyotyping using fluorescent in situ hybridisation. Furthermore, local patterns in sequence variation revealed dozens of similar haplotype blocks across the genome. These blocks are comparable to well-studied, older inversion polymorphisms in allogamous species but possess distinct SNP signatures that demonstrate their highly recent occurrence. This provides the first evidence of rapid, large-scale genomic differentiation in an autogamous species, suggesting we are documenting a rare and active case of contemporary evolutionary flux.

Talk 3 | **Evolutionary consequences of recombination suppression: the case of a chromosomal inversion in the seaweed fly**

Nicolas, LA (1); Mérot C (1)

(1) ECOBIO - Ecosystemes, Biodiversity, Evolution - University of Rennes, Rennes, France

Abstract

Chromosomal inversions, which strongly reduce recombination and form blocks of linked genes, are increasingly recognized for their role in intra-specific diversity and local adaptation, protecting adaptive combinations of alleles. Inversion polymorphisms are frequently maintained over large spatio-temporal scales through balancing selection, often forming parallel patterns across distant locations. However, the lack of recombination also limits the purging of deleterious mutations, particularly in inversions found at low frequency. This paradox raises multiple questions about the functional, demographic, and selective mechanisms associated with large polymorphic inversions. In this study, we investigated the evolutionary dynamics of a large inversion - Cf-Inv(4.1) - harbored by the worldwide-distributed seaweed fly Coelopa frigida, which displays parallel latitudinal clines of frequencies in Europe and North America, suggesting a role in adaptation to an environmental gradient. With experiments, we found a significant impact of Cf-Inv(4.1) on egg-to-adult survival and fecundity, partially interacting with temperature. We speculate that inversion fitness may be shaped by subtle life-history differences whose relative advantage depends on climate. Next, we uncovered the evolutionary history of the inversion and the evolution of its sequence. Combining long- and short-reads from America, Europe, and Japan, we reconstructed the demographic history of Cf-Inv(4.1), inferred an ancestral recombination graph, and investigated the conservation of its structure across continents. Lastly, we performed simulations to elucidate how the clinal distribution of the inversion affects the purging of deleterious mutations and compared the results with empirical data. Overall, this study provides an empirical example that illustrates the contrasting evolutionary impacts of recombination suppression, highlighting both its possible adaptive and deleterious effects.

Talk 4 | **Population-level PacBio HiFi data enable the investigation of structural variants in the speciation process of two songbirds**

Chase MA(1,2); Leal L(3); Kraft FL(3); Lerat E(4); Segami JC(1); Ålund M(1); Qvarnström A(1); Wheatcroft D(3); Mugal CF(1,4)

(1) Department of Ecology and Genetics, Uppsala University, Uppsala, Sweden; (2) Swiss Ornithological Institute, Sempach, Switzerland; (3) Department of Zoology, Stockholm University, Stockholm, Sweden (4); CNRS UMR 5558, Laboratory of Biometry and Evolutionary Biology, University of Lyon 1, Villeurbanne, France

Abstract

The recent rise of long-read sequencing technologies has significantly improved our ability to identify structural variants (SVs), typically defined as mutations affecting more than 50bp. As a result, increasing empirical evidence demonstrates that SVs encompass a significant portion of the genome and can have large phenotypic effects. In addition, SVs may play a substantial role in speciation, which could previously have been overlooked because of difficulties in identifying them with short-read data. However, due to the cost of long-read sequencing data, SV detection between species is still frequently based on the alignment and comparison of reference genome assemblies rather than population-level data, which does not permit distinguishing between polymorphic SVs and those that are differentially fixed between species. To address this limitation, we generate population-level long-read sequencing data of 10 collared flycatcher (*Ficedula albicollis*) and 10 pied flycatcher (*Ficedula hypoleuca*) individuals, an ecological model system of speciation research with approximately 6% mixed breeding pairs and fully sterile F1 hybrids. This experimental setting enables us to show that only a small fraction (<1%) of SVs identified by alignment of the two reference genome assemblies are differentially fixed between the two species. The vast majority of those differentially fixed SVs is represented by INDELs, with less than a handful fixed inversions and translocations. We then use this dataset to study the association of SVs with species differentiation, separately for SVs segregating in one or both species and differentially fixed ones. This analysis reveals that, inversion and translocation polymorphism is associated with a local reduction of nucleotide diversity within species and elevated levels of differentiation between species, consistent with local suppression of recombination and a mechanistic role of SVs in speciation.

Talk 5 | **A graph-based pangenome of European beech (*Fagus sylvatica*) reveals the landscape of structural variation across the distribution range**

Lazić, D (1); Müller, N (1)

(1) Thünen Institute of Forest Genetics, Großhansdorf, Germany

Abstract

Structural variants (SV) are increasingly recognised as major contributors to genomic diversity and environmental adaptation, yet their characterisation in forest trees remains limited due to the lack of high-quality long-read sequencing data and pangenomic analyses. Here we present a pangenome graph of European beech, one of the dominant tree species in Europe, constructed from 132 haplotype-resolved genome assemblies, representative of the species range. Using long-read PacBio HiFi sequencing and haplotype-resolved de novo assemblies, we built two complementary pangenome graphs with PGGB and Minigraph-Cactus, enabling a direct comparison of reference-free and reference-anchored approaches for structural variant discovery. Reference-free graph construction substantially expands the detected structural variants relative to the reference-anchored approach. Pangenome growth analysis reveals an open pangenome with substantial private and shell sequence. These results highlight the extent of sequence that is lacking from a single reference genome. Using the pangenome as the foundation, we are investigating the spatial distribution of structural variants across the species range to identify if rare and common SVs are shared broadly or concentrated in specific geographic regions. Genome annotation and gene space characterisation will further differentiate core from non-core genes, and identify possible connections between dispensable genes and structural variants. Together, these analyses position the beech pangenome graph as the basis for understanding how structural genomic variation contributes to the evolutionary resilience and adaptive potential of a forest tree species facing rapid environmental change.

Talk 6 | **Origin and fates of chromosomal inversions in Littorina marine snails**

Barry, P (1,2); Choo, L (3); Le Moan, A (4); Reeve, J (5), Stankowski, S (6); Westram, A (7); Johannesson, K (5); Butlin, Roger (3); Faria, Rui (1,2)

(1)CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal; (2)BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal; (3)Ecology and Evolutionary Biology, School of Biosciences, University of Sheffield; (4)Adaptation et Diversité en Milieu Marin, UMR7144, Station Biologique de Roscoff, Sorbonne Université; (5)Department of Marine Sciences, Tjärnö Marine Laboratory, University of Gothenburg; (6)Department of Ecology and Evolution, University of Sussex; (7)Faculty of Biosciences and Aquaculture, Nord University

Abstract

How reproductive isolation barriers accumulate between nascent species remains a long-standing question in speciation research. Recently, chromosomal inversions have been proposed as strong candidates to generate barriers to gene flow due to their reduced recombination rate, which helps to maintain high linkage disequilibrium between arrangements and loci under divergent selection. However, little is still known about the complete evolutionary history of inversions, i.e., the determinants of their appearance within genomes and how selection, gene flux, mutation load, and recombination shape genetic divergence between arrangements. Here, we investigate the evolutionary history of inversions and their impact on speciation in 166 whole-genome sequences of 8 different species of Littorina marine snails, whose 2 (L. saxatilis and L. fabalis) are split into different ecotypes that have different shell phenotypes, behavior, and habitat preferences. We first confirmed the presence of more than 30 polymorphic inversions longer than 1 megabase pair; most inversions separating ecotypes were found to be private to either L. fabalis or L. saxatilis. By combining Hi-C contact maps and synteny approaches, we found that chromosomal inversions are preferentially found in repeat-rich, gene-poor regions and nearby telomeres. Most inversions were found to be old, but we found no evidence that associative overdominance generating by the differential accumulation of deleterious mutation in both arrangements can explain their maintenance as polymorphism. We did not find elevated differentiation around inversion's breakpoints (i.e., suspension bridge patterns) for most inversions, suggesting that gene flux is occurring mostly via gene conversion rather than double cross over. We argue that this is a powerful system to improve our understanding of the evolutionary history of chromosomal

inversions and their role in the evolution of barriers to gene flow in multiple closely related species.

Talk 7 | **Comparison of population-genetic vs. read-based calls of inversions in Atlantic cod**

Lotterhos, KE (1); Curtis, L (1); Schaal, S (2)

(1) Northeastern University Marine Science Center, Nahant, MA USA (2) National Oceanic and Atmospheric Administration, USA

Abstract

Inversions are of great interest to evolutionary biologists due to their role in concentrating the genetic basis of adaptation in the face of gene flow. While inversions are typically detected by the characteristic 3-cluster patterns from population genomic data in principal components space, this approach driven by patterns of linkage disequilibrium (LD) does not accurately identify breakpoints and probably misses many different inversions segregating in the genome. Recent theory that we've developed have shown that multiple overlapping inversions can evolve in adaptation, but are not apparent in population genomic data. Read-based approaches for detecting inversions offer a way to detect multiple, potentially overlapping, inversions. In this study we apply read-based structural variant callers to test for overlapping inversions in Atlantic cod using whole-genome short read data at 15X coverage. While we find evidence for overlapping inversions, we also find low correspondence between read-based and population-genomic based inversion calls, which complicates inference. Nevertheless, our results suggest that multiple overlapping inversions may arise in adaptation and be "hidden" by long-range signals of LD.

Talk 8 | **Representation and detection of inversions in pangenome graphs**

Romain, S (1,4); Dubois S. (1,2); Legeai F. (1,3); Lemaitre C. (1)

(1) Univ Rennes, Inria, CNRS, IRISA - UMR 6074, Rennes, France; (2) GenPhySE, Université de Toulouse, INRAE, ENVT, Castanet Tolosan, France; (3) IGEPP, INRAE, Institut Agro, University of Rennes, Le Rheu, France; (4) Current affiliation: Bart's Cancer Institute, Queen Mary University London, London, UK

Abstract

Inversions are a major class of balanced structural variants that play key roles in recombination suppression, local adaptation, and genome evolution. At the same time, pangenome graphs are increasingly used to represent genomic diversity across individuals and species, progressively replacing the single linear reference genome. Numerous pangenomic studies have focused on SNPs and insertions and deletions. In contrast, inversions remain largely unexplored despite their evolutionary importance. Here we provide, to our knowledge, the first investigation of how inversion variants are represented in pangenome graphs. We describe the expected graph topologies produced by inversions and show that current state-of-the-art graph construction pipelines represent them in two distinct ways, only one of which preserves the biological structure of the variant. We introduce INVPG_annot, an open-source tool that enables the detection and topological annotation of inversion-associated bubbles in pangenome graphs. Using simulated and real human datasets, we show that inversion representation depends on sequence divergence, variant size, haplotype complexity, and algorithmic choices. Our results reveal substantial differences between pipelines in simulated graphs, with some inversions either misrepresented or lost. In addition, recovery rates are strikingly low in real human datasets, highlighting major challenges in analyzing inversions through pangenomic approaches.

Talk 9 | **SVJedi-Tag : a novel method for genotyping large inversions with linked-read data**

Temperville M (1), Benoit F (2), Mérot C (2), Legeai F (1,3), Lemaitre C (1)

(1) Inria/IRISA - Université de Rennes, CNRS URM 6074, Rennes, France; (2) ECOBIO - Université de Rennes, CNRS UMR6553, Rennes, France; (3) IGEPP - Université de Rennes, INRAE Institut Agro, Le Rheu, France

Abstract

Structural Variants (SVs) are an important but overlooked aspect of genetic variation. In particular, inversions are known for their role in the evolution of biological diversity and particularly studied in non-model species using population data. One of the major steps in the study of SVs is genotyping. Linked-read data provide a cost-efficient alternative to long-reads to genotype many individuals, by combining the low sequencing cost of short reads with long-distance information thanks to the use of barcodes tagging long molecules. Whereas several methods have been proposed to discover SVs with linked-reads, there are currently no tool for genotyping with this type of sequencing data. In this paper, we present SVJedi-Tag, the first inversion genotyping method dedicated to linked-read data. We tested SVJedi-Tag on simulated and real linked-read data in the seaweed fly *Coelopa frigida*, and showed that SVJedi-Tag is able to genotype with high accuracy large inversions above 25 kb, with a read depth as low as 3X.

Talk 10 | **The good, the bad, and the complex: Characterizing structural variants using genome graphs**

Wold, J (1); Mérot C (1)

(1) Université de Rennes, Rennes, Bretagne, France

Abstract

Single nucleotide polymorphisms (SNPs) have been the de facto genomic marker for population and functional genomics. To date, structural variants (SVs) have been largely overlooked due to challenges associated with accurately characterizing and genotyping them at scale, yet recent advancements in sequencing technologies and bioinformatic methods have enabled sequencing consortia to generate high-quality genome assemblies rapidly at-pace. As a result, a growing body of evidence is demonstrating that SVs impact a higher proportion of the genome and are generally more deleterious than SNPs. Nevertheless, insights into the full breadth of SV complexity remain somewhat limited as SVs are challenging to reliably characterize and genotype using a single reference genome. Reads from individuals carrying rearrangements that differ from the reference are less likely to map reliably. As a result, large, often complex SVs remain challenging to investigate. Genome graphs aim to address reference bias by representing alternative alleles as different paths for reads to map to. This has been shown to increase read mapping and SV genotyping rates. However, there is little consensus around how best to apply genome graphs to species with high intra-specific variation with indications that performance declines with high levels of diversity. We evaluate the utility and limitations of genome graphs for the seaweed fly (*Coelopa frigida*), a globally populous species with well described SV diversity and explore the implications for assessments of mutation load within and outside complex SVs. Ultimately, this work aims to identify a practical approach to incorporating genome graphs into the study of non-model organisms, providing a more holistic perspective of SV diversity in natural populations.

Talk 11 | **Genomic drivers of persimmon adaptive radiation in New Caledonia, a biodiversity hotspot**

Ghane, A (1); Khastgir TS (1); Emelianova K (1); Bruy D (2); Robert V (2); Munzinger J (3); Paun O (1)

(1) Univie - Department of Botany and Biodiversity Research, University of Vienna, Vienna, Austria; (2) IRD - Research and Development Institute, New Caledonia, France; (3) IRD - Research and Development Institute, Montpellier, France

Abstract

Adaptive radiation, the rapid evolution of many species from a common ancestor, is a major source of biological diversity. While ecological opportunity is traditionally emphasized as its main driver, growing evidence suggests that genome dynamics may also play an important role by increasing evolutionary potential. However, how such genomic processes contribute to plant diversification remains poorly understood. The *Diospyros* (persimmons) genus provides a powerful system to address this question. New Caledonia, a global biodiversity hotspot, hosts more than 30 endemic *Diospyros* species that arose from a single, rapid radiation, while three other independently colonizing lineages remain species-poor and ecologically restricted. The radiated lineage occupies a wide range of environments, including extreme ultramafic soils that are nutrient-poor and rich in toxic metals. Strikingly, species in this clade have genomes roughly twice as large as those of non-radiating relatives, despite no change in chromosome number, suggesting major shifts in genome dynamics. To investigate the role of genome dynamics in this radiation, we combined high-quality genome assemblies, population resequencing, gene family evolution analysis, structural variation detection, and ecological measurements across species adapted to contrasting soils. We find that the radiated lineage shows increased activity of transposable elements along with a higher rate of gene duplication. These changes appear to be associated with genes involved in stress tolerance, metal detoxification, and root development, and are associated with environment-specific gene expression patterns. Our results suggest that genome expansion and copy number variation may have enhanced the capacity of this lineage to adapt to diverse and challenging environments. More broadly, this study highlights how changes in genome architecture can promote diversification and help drive adaptive radiation in plants.

Talk 12 | **Unravelling genomic drivers of speciation in *Musa* through comparison of wild banana ancestors genomes.**

Martin, G (1,2); Istace, B (3); Baurens, FC (1,2); Belser, C (3); Hervouet, C (1,2); Labadie, K (4); Cruaud, C(4); Noel, B (3); Salmon, F (2,5); Mahadeo, J (2,6); Wincker, P (3); Yahiaoui, N(1,2); Aury, JM (3); D'Hont, A (1,2)

(1) CIRAD, UMR AGAP Institut, F-34398 Montpellier, France; (2) UMR AGAP Institut, Univ Montpellier, CIRAD, INRAE, Institut Agro, Montpellier, France; (3) Génomique Métabolique, Genoscope, Institut François Jacob, CEA, CNRS, Univ Evry, Université Paris-Saclay, 91057 Evry, France; (4) Genoscope, Institut François Jacob, CEA, CNRS, Univ Evry, Université Paris-Saclay, 91057 Evry, France; (5) CIRAD, UMR AGAP Institut, F-97130 Capesterre-Belle-Eau, Guadeloupe, France ; (6) CIRAD, UMR AGAP Institut, CRB-PT, F-97170 Roujol Petit-Bourg, Guadeloupe, France

Abstract

Cultivated bananas are the result of hybridisation between wild species and subspecies of Musa that diverged in the region of Southeast Asia and New Guinea. These hybridisations produced diploid and triploid hybrids, some of which yielded parthenocarpic seedless fruit, which were selected and propagated by humans. As a result, banana genomes are complex mosaics of large blocks of sequences involving nine genetic groups including one unknown contributor. We generated continuous genome assemblies of these contributors including a hybrid that provided access to part of the unknown ancestor's genome. Comparative genomic and phylogenetic analyses between those genomes revealed chromosomal rearrangements and centromere diversification. The centromeric regions have incorporated different types of repeated sequences, notably tandem rDNA repeats that may reduce fertility in hybrids. Chromosome rearrangements are mainly reciprocal translocations, sometimes with complex structures, that reduce recombination in structural hybrids and were generally found preferentially transmitted to progenies. These factors could contribute to an ongoing speciation process within *Musa* by reinforcing reproductive isolation, which probably originated from past fluctuations in climatic conditions and land connections in the Southeast Asia/New Guinea region.

Talk 13 | **Multiple chromosomal inversions shape the genomic landscape of a marine broadcast spawner**

D'Alessandro S (1,2), Humble, E (3), Hoogakker, B(1), Porter, JS (4), Kaiser, MJ (1), Ogden, R (3)

(1) HWU - The Lyell Centre for Earth and Marine Science, Heriot-Watt University, Edinburgh, UK; (2) UoE - School of Geosciences, University of Edinburgh, Edinburgh, UK; (3) UoE - Royal (Dick) School of Veterinary Studies and the Roslin Institute, University of Edinburgh, Edinburgh, UK; (4) HWU - International Centre for Island Technology, Heriot-Watt University, Stromness, UK

Abstract

Chromosomal inversions maintain genome-wide divergence by accumulating private mutations in each orientation and suppressing recombination between heterozygous individuals, allowing sets of locally adapted alleles to persist despite gene flow. These rearrangements are increasingly associated with adaptive traits, with important implications for management and conservation. In the commercially important king scallop (*Pecten maximus*), a previous RAD-seq study identified three large putative inversions associated with temperature-related allele frequency differences and genes involved in oocyte maturation, suggesting a role in regulating spawning time at small spatial scales. Here, we characterise the genomic landscape of chromosomal inversions in P. maximus using medium-coverage whole genome sequencing of 160 specimens sampled across UK waters. We identify 15 chromosomal inversions ranging from 0.8 to 15.5 Mbp, all exhibiting high linkage disequilibrium and elevated homozygosity within, but not between, arrangements - consistent with suppressed recombination and genetic isolation at these loci despite broader connectivity. Ancestral genome reconstruction across seven inversions reveals independent segregation patterns, suggesting distinct inversion origins and the potential for multiple routes through which natural selection may act. When inversions were excluded, a shallow geographical cline emerged. Gene Ontology enrichment analysis further shows that four inversions are enriched for genes associated with reproductive processes, including oocyte maturation, cyclic AMP signalling, and steroid hormone pathways. Collectively, these findings show that chromosomal inversions generate strong genetic differentiation within specific genomic regions without causing complete reproductive isolation, and their association with reproductive processes suggests they may influence key reproductive traits at spatial scales relevant for management.

Talk 14 | **Role of chromosomal inversions in local adaptation in California endemic oak**

Yang, Heidi (1); Sork, Victoria (1)

(1) UCLA - Ecology & Evolutionary Biology Dept., Univeristy of California, Los Angeles, Los Angeles, United States of America

Abstract

Chromosomal inversions are a form of genomic structural variation that can significantly influence the evolution of local adaptation by suppressing recombination in heterozygotes, thereby producing large, non-recombining sequences that contain sets of adaptive loci. In this talk, we document patterns of inversions among individuals sampled throughout the species range of valley oak (*Quercus lobata*), a California endemic oak. Valley oak exhibits both genetic and phenotypic signals of local adaptation despite widespread gene flow. Previous studies have identified significant associations between genetic and environmental variation using candidate genes, SNPs, and levels of DNA methylated positions. Here, we test the contribution of inversions to local adaptation. We hypothesize that inversion frequencies will exhibit significant genotype-environment associations, be evolutionarily old, and impact genes involved in environmental response. To identify putative inversions, we use structural variant calling programs and indirect discovery using signatures of high genetic divergence and linkage disequilibrium. We identified 330 putative inversions across all 12 chromosomes, ranging from 890 bp to 13.8 Mb. We then correlated inversion frequencies and frequencies of SNPs inside putative inversions with climate gradients to identify significant genotype-environment associations, constructed time-scaled phylogenies to estimate inversion age, and documented nearby genes to identify functional impacts. Our findings identify inversions that are associated with climate gradients and may contribute the adaptation of populations to their local environments. This work advances our understanding of the role of inversions to the adaptive evolutionary process.

Talk 15 | **Adaptation of the bedbug *Cimex lectularius* to a new (human) host**

Ségurel, L (1); Roscigni, N (1); Castex, C (2); Christe, P (2); Varaldi, J (1)

(1) LBBE, UMR CNRS 5558 – University Lyon 1, France; (2) University of Lausanne, Switzerland

Abstract

Cimicidae are obligate blood-sucking insects ancestrally associated with bats. Within this clade, a few host switches occurred towards birds and humans. Within *Cimex lectularius* (the common bed-bug), two lineages coexist: one associated with bats and one associated with humans (causing well-known damages). These two lineages present some neutral genetic structuration (Balvin et al. 2012, Booth et al. 2015, Castex et al. 2025) and have been shown to be strongly differentiated at VGSC, a gene associated with insecticide resistance (Balvin et al. 2018). However, they are still inter-fertile, at least in lab conditions (DeVries et al., 2020). While most studies to date have been based on a small number of nuclear or mitochondrial markers, we perform here a genome-wide study to identify the regions associated with adaptation to the human host. To perform such a population genomic study, we generated short-read sequencing data for 71 individuals sampled in Switzerland and France coming from both lineages: 40 bat-associated and 31 human-associated individuals. Using Fst as a measure of genetic differentiation between human- and bat-associated lineages, we observed a 30Mb region on chromosome 3 with extreme differentiation (Fst=0.72), as compared with the rest of the genome (Fst=0.17). The borders of this region are very sharp, as can be expected under the hypothesis of an inversion underlying this differentiated locus. We are currently investigating this hypothesis and assessing whether this locus could be associated with reduced gene flow between lineages. In parallel, moderate peaks of Fst were observed on other chromosomes, including an elevated differentiation on chr14 associated with insecticide resistance. Diversity levels around this locus were reduced in the human-associated lineage, likely due to the selective pressures at play that we will now better characterize.

Talk 16 | **A 38-Mb region underlies an ancient climate-linked inversion in barn owls**

Corval, H (1); Cumer, T (1); Pulido, A (1); Bachmann Salvy, M (1); Topaloudis, T (1); Ducrest, AL (1); Simon, C (1); Iseli, C (2, 3); Guex, N (2, 3); Burns, A (3); Roulin, A (1); Goudet, J (1)

(1) UNIL – Department of Ecology and Evolution, University of Lausanne, Lausanne, Switzerland. (2) BICC – Bioinformatics competence centre, University of Lausanne, Lausanne, Switzerland. (3) BICC – Bioinformatics competence centre, Ecole Polytechnique Fédérale de Lausanne, Lausanne, Switzerland.

Abstract

Large structural variants can reshape genomic architecture, alter gene content and regulation and create potential novel evolutionary trajectories. In the Western-Palearctic barn owl (*Tyto alba*), a genome scan for local adaptation at the European scale highlighted a low-recombination haploblock linked with environment. Using a new chromosome-level, haplotype-resolved genome, we described the structure of this ~38 Mb rearrangement, which consists of a primary inversion containing several secondary nested inversions. To place this complex architecture in an evolutionary context, we analysed historical museum samples across the *Tyto* genus. Local PCA on whole genome sequences from three closely related species confirmed the presence of the rearrangement throughout the range of *T. alba*, revealed its presence in *T. furcata* (Americas), but absence in *T. javanica* (South East Asia). Considering that introgression is unlikely between the populations from Europe and the Americas and according to a mitochondrial phylogeny, we hypothesised that this inversion has been segregating in the two sister species for at least ~5 million years. Here, we explore evolutionary forces (i.e., neutrality, climatic-driven selection, ...), that could explain the persistence of this ancient and structurally complex inversion.

Talk 17 | **Structural variation in Iberian lynx (*Lynx pardinus*)**

Hasselgren, M (1,2); Godoy, JA (2)

(1) Department of Zoology, Stockholm University, Stockholm, Sweden (2) Estación Biológica de Doñana, CSIC, Sevilla, Spain

Abstract

Large structural variants (SVs) have long been hypothesised to play a central role in adaptation by bundling together co-adapted alleles, yet empirical understanding remains fragmented across a small number of well-studied systems. Recent advances in analysing variation in local population structure along the genome, particularly using local PCA, provide a robust framework for identifying large SVs across diverse systems using widely available short-read sequencing data. Within the RepAdapt consortium, which brings together population genomic datasets from hundreds of species and tens of thousands of individuals, we are now positioned to move beyond case studies toward a comparative understanding of structural variation across the tree of life. Here, I present a scalable pipeline developed for the RepAdapt structural variation subgroup to systematically identify candidate SVs using local PCA. The workflow combines genome-wide windowing, dimensionality reduction, and targeted visualisation to detect regions exhibiting distinct local population structure consistent with large SVs, and is designed for distributed implementation across research groups, enabling coordinated and reproducible analyses at scale. Early results reveal that genomic regions consistent with large structural variants are widespread across species, and moreover that these regions are frequently enriched for signatures of local adaptation. By standardising SV detection across datasets, this framework enables the construction of a cross-species atlas of structural variation and provides a foundation for testing long-standing evolutionary predictions about how genome architecture shapes adaptation, gene flow, and range expansion.

Talk 18 | **The role of gene flux in the evolutionary trajectory of supergenes**

Purcell, J (1); Brelsford, A (2)

(1) University of California Riverside, Department of Entomology, Riverside, United States; (2) University of California Riverside, Department of Ecology, Evolution, and Organismal Biology, Riverside, United States

Abstract

Genomic structural rearrangements often result in locally reduced or suppressed recombination. Some structural variants are beneficial for the organism and thus either sweep to fixation or persist in a polymorphic state, because low recombination regions can maintain sets of co-adapted alleles that shape complex traits or local adaptations. However, regions of suppressed recombination can also accumulate deleterious alleles, and they may lock organisms into a restricted set of alternative strategies. Gene flux allows for the exchange of alleles between heterokaryotypes. This exchange of alleles may 'rescue' degrading haplotypes or generate novel combinations of alleles that could take on new or modified functions. Here, we examine the frequency of gene flux in an ancient supergene in ants. Specifically, we ask whether the rate of gene flux events differs among species, if gene flux rates vary across the supergene region, and what the consequences of gene flux are in this system. We find a surprisingly high rate of gene flux in the Formica ant supergene system, with novel haplotypes sometimes taking on new functions. However, the frequency of gene flux varies strikingly across the supergene region and across congeneric species. This study, combined with similar studies in other systems, suggests that gene flux can contribute to the persistence of supergene variants, as well as to the appearance of novel haplotypes.

Talk 19 | **The effect of supergene evolution on the structure and stability of the G-matrix**

Sudbrack, V (1); Mullon, C(1)

(1) Department of Ecology and Evolution, University of Lausanne, Lausanne, Switzerland

Abstract

The additive genetic variances and covariances of traits provide the raw material for phenotypic evolution, influencing both the rate and direction of multivariate responses to selection. These (co)variances, summarised by the G-matrix, are shaped by pleiotropy and genetic linkage, two features often associated with supergenes, particularly those formed by chromosomal inversions. However, how the evolution of supergenes affects the structure and long-term stability of the G-matrix remains poorly understood. Here, we combine quantitative genetics, population genetics, and adaptive dynamics to investigate the evolution and genetic consequences of inversions that capture multiple pleiotropic loci underlying traits subject to correlational selection. We show that, when such inversions arise, they can be maintained by balancing selection, preserve co-adapted allelic combinations, and promote the emergence of discrete phenotypic morphs. By reducing recombination between co-adapted loci, inversions increase additive genetic variance and hence heritability, while also stabilising the G-matrix at mutation–selection–drift equilibrium by reducing drift-driven fluctuations across generations. When dominance modifiers are allowed to evolve, selection can further concentrate genetic variation into a single major-effect supergene with coordinated dominance across inverted alleles. Despite this reorganisation of the genetic architecture, genetic variance at the population level remains predominantly additive.

Talk 20 | **Structural variants and the genetic diversity - population viability paradox**

Krabbenhoft, TJ (1)

(1) University at Buffalo, New York, USA

Abstract

Invasion genetics presents a classic paradox: how do species successfully spread despite severe population bottlenecks? The brown treesnake (*Boiga irregularis*) in Guam represents a striking example of this phenomenon, having been introduced with only a handful of individuals. We show that the population endured an extreme bottleneck, with roughly half of the genome exhibiting runs of homozygosity, comparable to species of conservation concern. Despite this, we uncovered extensive diversity in the form of nearly 19,000 genomic structural variants, which affect almost eight times more of the genome than single-nucleotide variants and provide material for 'rescuing' the population from inbreeding-driven declines. Structural variant density was highest in gene promoters, where recombination and DNA repair often occur, providing a mechanism for rapid evolution of gene-linked diversity. This diversity is enriched in genes vital for adaptive immunity and olfaction, suggesting genomic diversity in key chromosomal regions can rescue populations from inbreeding. This work has critical implications for invasion biology and conservation genetics practitioners.

Talk 21 | **The Role of Gene Copy Number Variations (gCNVs) in the Local Adaptation of Major European Tree Species**

Darzentas, E(1); Milesi, P(1)

(1) UU - Department of Ecology and Genetics, Uppsala University, Uppsala, Sweden and (2) SciLifeLab Uppsala, Uppsala, Sweden.

Abstract

Gene copy number variations (gCNVs) are unbalanced structural variants in which the number of copies of a given gene varies among individuals of the same species. gCNVs are common in eukaryotic genomes and have a multiallelic nature. Because gene dosage affects gene expression levels, gCNVs also have a quantitative nature. Therefore, when studying their role in evolutionary processes, it is important to consider the number of copies. A recent study of Norway spruce (Picea abies) showed that approximately 12% of protein-coding genes display copy number variations. Of these, around 10% participate in adaptation along environmental gradients, with a direct relationship observed between the number of copies, the environment, and the phenotype. In this study, we used the GenTree dataset (Milesi et al., 2024), consisting of an extensive exome capture experiment for over 3,500 trees sampled across a large environmental gradient. These trees included four deciduous species: silver birch, European beech, sessile oak, and European black poplar, as well as three conifer species: Norway spruce, maritime pine, and Scots pine. We used recent chromosome-level assemblies for each species to call gCNVs using the same framework across species. We then conducted population and quantitative genomics analyses (e.g., PCA, isolation by distance, genome scans, genotype environment association), using gene copy numbers as genotypes, to assess and compare patterns of variation across populations and study their role in local adaptation.

Talk 22 | **Show Case of the 'rCNV', a comprehensive framework to call gene copy number variations from SNPs data**

Zhou Q. (1); Lindstedt F. (1), Karunarathne P. (1), and Milesi P.(1)

(1) IEG- Department of Ecology and Genetics and SciLifeLab, Uppsala University, Uppsala, Sweden

Abstract

Over the last decade, significant advances in high-throughput sequencing have made it possible to conduct genomic studies at the population level at an affordable cost. These studies have notably revealed the extent of gene copy number polymorphism in eukaryotic species. However, the evolutionary importance of these polymorphisms has been overlooked, partly due to our limited ability to detect them in genomes, particularly in non-model organisms.

In this presentation, I will introduce the 'rCNV' framework that we have developed and implemented as an R package (https://piyalkarum.github.io/rCNV/). This framework identifies SNPs in putative multi-copy regions and can be used to produce a clean set of SNPs for population genetics studies or as markers of CNVs in population and quantitative genomics studies. The method was initially optimised for reduced-representation and reference-free sequencing data (e.g. RAD-seq and exome capture). Recently, however, we developed a novel algorithm optimised for SNP data obtained from whole genome sequencing (Zhou et al., in preparation). I will briefly introduce the core methods behind the 'rCNV' approach and demonstrate how it can be used to study gene copy number variations, for example for their role in adaptation along environmental gradients.

Talk 23 | **Macro-evolutionary perspectives on a large chromosomal rearrangement underlying alternative life-histories in seaweed flies**

Hicks, D (1); Ashton, D (2); Wellenreuther, M (2,3); Mérot, C (1)

(1) ECOBIO - CNRS UMR 6553, University Rennes 1, Rennes, France; (2) BSI - Bioeconomy Science Institute, Nelson, New Zealand; (3) University of Auckland, Auckland, New Zealand

Abstract

Discrete alternative phenotypes, such as morphotypes and ecotypes, are often underpinned by supergenes, or complex genomic architectures, which commonly involve large-scale structural rearrangements such as successive inversions or translocations. At the evolutionary level, supergenes have been associated with parallel evolution, introgression, and trans-species balancing selection. Hence, one way to improve our understanding of supergene evolution over long evolutionary timescales is to study the genomic and phenotypic dynamics of a supergene in a multi-species system with a large geographical distribution. In the seaweed fly *Coelopa frigida*, a 25-Mb supergene formed by nested chromosomal inversions is associated with polymorphism in several life-history traits. Indeed, males harbouring one arrangement have a larger size, longer development time, and higher reproductive success than males with the other arrangement. Interestingly, similar male size polymorphisms were qualitatively reported in other *Coelopidae* species across the globe, suggesting that this chromosomal rearrangement may be shared across species boundaries. To address this hypothesis, we quantified development time in 5 Coelopa species and size in 13 Coelopidae species, using machine learning-assisted high-throughput phenotyping. This supported the presence of phenotypic polymorphism comparable to *C. frigida* in some coelopid species – but not all. We mapped this phenotype on a new coelopid phylogeny constructed with a combination of short- and long-read data from 17 species, and we used a species vs. gene tree approach to characterize the supergene's phylogenetic origin and evolution. We also assembled 4 new genomes to study inter-species synteny and thereby retrace the structural dynamics in this genomic region. Altogether, our results provide valuable information on multi-species evolution of phenotypic polymorphism, as well as genomic structural rearrangements associated with an adaptive supergene.

Talk 24 | **The role of a sex chromosome–autosome fusion in the evolution of live-bearing and speciation in the common lizard**

Koch, EL; Elmer, KR (1)

(1) SBOHVM - School of Biodiversity, One Health & Veterinary Medicine; University of Glasgow; Glasgow; United Kingdom

Abstract

'Neo-sex' chromosomes, formed by fusions of autosomes and sex chromosomes, are ideal for studying early sex chromosome evolution and the role of large structural variants in this process. However, their evolutionary drivers and adaptive impacts remain poorly understood. We use the common lizard to investigate a sex chromosome – autosome fusion, including detailed molecular changes and the resulting evolutionary consequences. This species is exceptional in being polymorphic for reproductive mode: egg-laying and live-bearing lineages coexist and hybridise, producing intermediates with thin eggshells and faster hatching. It has a ZW system and live-bearing lineages carry a W–autosome fusion. Leveraging phenotype and whole-genome sequencing of >600 individuals, we show that the fused W ('neo-W') acts as a major reproductive barrier: F1 females with the neo-W are viable but sterile, reducing gene flow between lineages. Using short-read whole-genome and PacBio-HiFi sequencing, we found that the neo-W exhibits characteristic signatures of sex chromosome evolution. We detected suppressed recombination adjacent to the W-fusion site across half of the ancestral autosome due to large inversions and found repeat accumulation, gene degeneration, and gene silencing by increased promoter methylation in this region. Using a hybrid zone, including admixed individuals of intermediate phenotypes, we could map variation in reproductive traits to the neo-sex chromosomes, suggesting an adaptive role of the W–autosome fusion. By linking formerly autosomal alleles to the female-determining locus, the fusion may have facilitated female-specific adaptations for live-bearing in ancestral populations. Ongoing degeneration of the neo-W and resulting genetic incompatibilities further reduce maladaptive gene flow from egg-laying lineages. Overall, this system highlights how large-scale structural changes involving sex chromosomes can drive evolutionary innovation and contribute to speciation.

Talk 25 | **Sex-linked structural variation and paralogy shape genomic diversity in a songbird**

Vellnow, N (1); Gossmann, TI (1)

(1) Computational Systems Biology, TU Dortmund University, Dortmund, Germany

Abstract

Structural genomic variation and gene duplication are widespread in avian genomes, yet their impact on population genetic inference remains underexplored. Sex-linked genomic regions, in particular, may generate artefactual signals when sex-specific structural variation or paralogy is not properly accounted for. Using chromosome 6 as a representative test case in a songbird system, we investigate both the origins and consequences of such regions. Under relaxed, literature-based filtering parameters, we identify loci with elevated F_ST, sex-biased heterozygosity, coverage differences, and distortions in the site frequency spectrum. These patterns are consistent with off-mapping from sex chromosomes, the germline-restricted chromosome and autosomal paralogs. Applying more stringent repeat masking as well as coverage and mapping-quality thresholds substantially reduces these signals, demonstrating that structural variation can bias estimates of diversity and differentiation, particularly under uneven sex ratios. Comparative analyses of high-confidence orthologs will assess whether these regions show signatures of relaxed purifying selection and elevated π_n/π_s, potentially reflecting pseudogenization or functional divergence. This work aims to disentangle pervasive methodological bias from genuine evolutionary signal and to evaluate the broader impact of structural variation on population genomic inference.

Talk 26 | **Local PCA reveals widespread structural variation across the tree of life**

Battlay, P (1); Yeaman, S (2); Hodgins, KA (1)

(1) School of Biological Sciences, Monash University, Clayton, Victoria, Australia; (2) Department of Biological Sciences, University of Calgary, Calgary, Alberta, Canada

Abstract

Large structural variants (SVs) have long been hypothesised to play a central role in adaptation by bundling together co-adapted alleles, yet empirical understanding remains fragmented across a small number of well-studied systems. Recent advances in analysing variation in local population structure along the genome, particularly using local PCA, provide a robust framework for identifying large SVs across diverse systems using widely available short-read sequencing data. Within the RepAdapt consortium, which brings together population genomic datasets from hundreds of species and tens of thousands of individuals, we are now positioned to move beyond case studies toward a comparative understanding of structural variation across the tree of life. Here, I present a scalable pipeline developed for the RepAdapt structural variation subgroup to systematically identify candidate SVs using local PCA. The workflow combines genome-wide windowing, dimensionality reduction, and targeted visualisation to detect regions exhibiting distinct local population structure consistent with large SVs, and is designed for distributed implementation across research groups, enabling coordinated and reproducible analyses at scale. Early results reveal that genomic regions consistent with large structural variants are widespread across species, and moreover that these regions are frequently enriched for signatures of local adaptation. By standardising SV detection across datasets, this framework enables the construction of a cross-species atlas of structural variation and provides a foundation for testing long-standing evolutionary predictions about how genome architecture shapes adaptation, gene flow, and range expansion.

Talk 27 | **Uncovering the complex genomic history of *Araneoidea* and the role of TEs on Intrachromosomal Rearrangements**

Price, C (1); Schöneberg Y (2); Farré M (1,3)

(1) UoK - Natural Sciences, University of Kent, Canterbury, United Kingdom; (2) Trier University, Trier, Germany (3); QMUL - Queen Mary University London, London, United Kingdom

Abstract

Spiders (*Araneae*) are a diverse and ancient order, originating ~400 Million Years ago, and comprising of more than 52,000 species. Spiders are important both ecologically and economically, through their diverse adaptions and utilisation of venom and silk. It has been shown that chromosomal changes and structural rearrangements can drive the proliferation and evolution of novel traits and aid speciation. Ancestral reconstructions provide the novel opportunity to understand and quantify the important chromosomal changes that drive these events. Despite this spider genome evolution has remained understudied, however, the influx of publicly available chromosomal level assemblies, provides the opportunity to study the dynamics of genomic rearrangements and how they are involved in the evolutionary genomic histories of spiders. We focused our analysis on *Araneoidea*, of which are a diverse and widespread superfamily originating over 100 Million Years ago; providing an ideal group to begin uncovering insights into the ancestral genome evolution of Spiders. We aimed to identify conserved ancestral gene groups and define ancestral chromosomal scaffolds across *Araneoidea*. Using, 20 publicly available chromosome-level assemblies, we identified orthologous genes throughout the clade using TOGA and then we inferred ancestral gene groups using AGORA. Using DESCHRAMBLER, we reconstructed predicted ancestral chromosomal fragments using whole-genome pairwise alignments. We then explored how transposable elements (TEs) impact the large intrachromosomal variance we observe across the clade. We find evidence for extensive intrachromosomal rearrangements throughout the clade, coupled with the high concentration and variation of TEs, we observe a complex history of genomic evolution. These findings enhance our understanding of evolution in invertebrate genome structure and provide a foundation for further research within comparative spider genomics.

Talk 28 | **Exploring Transposable Elements dynamic in human population in the Human Pangenome Reference Consortium Release 2 Data**

Mayoud, C (1) ; Shahatit, S (1) ; Groza, C (2) ; Monlong, J (3), Makova, K.D (4), Fiston-Lavier, A-S (1,5)

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Abstract

Transposable elements (TEs) comprise nearly half of the human genome and are major drivers of structural and regulatory variation. Leveraging the second release of the Human Pangenome Reference Consortium (HPRC), comprising 230 diploid assemblies (440 selected haplotypes). We explored population-scale TE diversity across five continental groups. Using the GraffiTE pipeline, we identified 28,354 high-confidence insertions. To ensure robustness, we benchmarked these calls against TE variants extracted from classic pangenomic approaches, namely Minigraph-Cactus and PGGB, highlighting the respective strengths and limitations of mapping-based vs. graph-based approaches. A longitudinal comparison with HPRC Phase 1 (94 haplotypes) shows that increasing haplotype number is essential for capturing the full range of human TE polymorphism. Among the detected insertions, 5,945 are common polymorphisms (allele frequency 5–95%). Our analysis reveals that while intra-superpopulation diversity remains low, admixed populations (e.g., Caribbean) exhibit intermediate profiles. African haplotypes harbor the highest number of TE insertions, primarily driven by LINE/L1 and SINE/Alu elements enriched in intronic and intergenic regions. We identified superpopulation-specific patterns, particularly involving distinct Alu subfamilies, and observed a relative decrease in TE frequencies in non-African groups, consistent with known demographic bottlenecks. Future work will investigate the evolutionary mechanisms of TE activity through comparative analyses with great apes and archaic hominins (Neanderthal, Denisovan), focusing on sequence divergence, genomic context, and selection pressures acting on full-length mobile element insertions.

Talk 29 | **Transposable element islands at the interface of 3D genome architecture and karyotype evolution in ants**

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Abstract

Ants of the genus *Cardiocondyla* display exceptionally dynamic genome evolution that distinguishes them from most other ants. A striking feature of their genomes is an unusual distribution of transposable elements (TEs), with slowly evolving, TE-poor regions sharply separated from highly divergent, TE-rich regions (TE Islands). How such an extreme genomic architecture emerged and how it relates to the biology and diversification of *Cardiocondyla* remain largely unexplored. Here, we use comparative genomic analyses across several closely related *Cardiocondyla* species and outgroups to reconstruct the evolutionary processes shaping their genomes. Our results reveal extraordinary levels of genome rearrangements within the genus, leading to highly divergent chromosome structures and strong karyotype diversity even among closely related species. These rearrangements are tightly associated with the occurrence of TE Islands, suggesting feedback between TE activity and large-scale genome restructuring. We propose that the distinctive TE landscape of *Cardiocondyla* both drives and is reinforced by rapid genome evolution, contributing to the remarkable genomic diversity observed within the genus. By linking TE dynamics, genome architecture, and species divergence, our study highlights *Cardiocondyla* ants as a powerful model for understanding how genome instability can shape evolutionary trajectories and biological diversity.

Poster communications

Poster 1 | **SyBR: a scalable Snakemake workflow for synteny inference, evolutionary breakpoint detection, and functional enrichment analysis**

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Abstract

Comparative analyses of genome structure are essential for understanding chromosomal evolution; however, existing workflows are fragmented across multiple tools and require extensive manual integration. SyBR (Synteny and Breakpoint Region analyzer) is introduced as a fully automated, reproducible workflow implemented in Snakemake that unifies synteny detection, evolutionary breakpoint identification, and downstream functional analysis. SyBR comprises seven modular, independently configurable stages, enabling flexible deployment across diverse datasets. The pipeline supports optional whole-genome alignment, followed by bidirectional filtering and SyntenyTracker-based identification of homologous synteny blocks. Evolutionary breakpoint regions are resolved using the Evolutionary Breakpoint Analyzer, which provides high-resolution mapping of rearrangement events. Functional interpretation is facilitated through integration with getENRICH, and ancestral genome reconstruction is supported via DESCHRAMBLER. SyBR is designed for portability and scalability, executing efficiently on both local systems and high-performance computing clusters with parallelized workflows. A centralized configuration file ensures reproducibility and simplifies parameter tuning across analyses. By consolidating multiple analytical steps into a single extensible framework, SyBR reduces technical complexity and enables systematic investigation of genome rearrangements and their functional consequences across species.

Poster 2 | **Stepwise Integration of Functional Genetic Elements in a Spider Morph Determining Supergene**

Chen, MY (1,2); Vangestel, C (2); Sonet, G (2); Van Belleghem, S (1); Hendrickx, F (2)

(1) KU Leuven,Leuven, Belgium (2) RBINS,Brussels,Belgium

Abstract

The maintenance of advantageous trait combinations is essential for the evolution of discrete morphs but can be disrupted by genetic recombination. Recombination suppression preserves these combinations by preventing exchange between homologous chromosomes and may lead to the formation of "supergenes", being large genomic regions containing multiple linked loci involved in morph development. However, the evolutionary processes underlying supergene formation remain poorly understood. The dwarf spider *Oedothorax gibbosus* exhibits a striking male dimorphism in which "hunched" males, characterized by cephalic protuberances, coexist with "flat" males whose cephalic morphology resembles that of females. This dimorphism is controlled by a unique 12 Mb genomic segment present only in the hunched-determining allele. Uncovering the genomic content and evolutionary history of this sequence offers a valuable opportunity to investigate how supergenes evolve and more specifically, whether this morph-specific region originated from a structural variation initiating morph differentiation, followed by the recruitment of additional genes under positive selection. We will employ a multi-omics approach to investigate the function and evolution of the O. gibbosus supergene. Transcriptomic, Iso-seq and single-cell RNA-seq analyses will reveal expression patterns across sexes, developmental stages and morphs, while CRISPR-Cas9 experiments will test the roles of candidate genes in morphological differentiation.

Poster 3 | **Structure and function of chromosomal inversions in a parallel Galápagos beetle radiation**

De Paepe, O (1, 2); Van Belleghem, S (1); Hendrickx, F (2); Vangestel, C (2)

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Abstract

Within the Galápagos archipelago, caterpillar-hunter beetles (*Calosoma* sp.) exhibit a striking case of parallel adaptive radiation, in which a short-winged highland ecotype has repeatedly evolved from a long-winged lowland ecotype across multiple islands. Previous research has shown that the magnitude of morphological and genomic divergence between ecotypes within each island follows the islands' chronosequence. Genomic regions of elevated highland-lowland divergence are clustered into large genomic blocks that are shared across islands. Structural variants, especially chromosomal inversions, are hypothesized to underlie these genomic blocks of differentiation. Preliminary results of genome alignments have now corroborated the presence of structural variants including inversions. Yet, it remains unclear whether these inversions encompass a single adaptive gene, a cluster of co-adaptive genes or are the result of gene accumulation. The aim of this study is to distinguish between these scenarios by analyzing gene expression patterns within inversions and comparing those across multiple genomes and ecotypes. Integrating data of different islands along the chronosequence will enable us to assess whether the gene content within the inversions supports an accumulation of functional elements over time. Ongoing work focuses on refining genome assemblies and integrating RNA-seq data to explore the functional role of the detected inversions in the development of wing length.

Poster 4 | **Supergene evolution through the recruitment of morph-specific genes in a male-dimorphic spider**

Hendrickx, F. (1); Chen, M. (1,2); Vangestel, C. (1); Sonet, C.(1), Van Belleghem, S.M. (2)

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Abstract

Supergenes, being large genomic regions of tightly linked non-recombining loci, underlie some of the most striking polymorphisms within species. A central question in their evolution is whether supergenes comprise multiple co-adapted loci that accumulate progressively, with each new gene enhancing morph differentiation. However, answering this question is challenging, as suppressed recombination obscures the individual contributions of genes within a supergene. We focus on the locus controlling male dimorphism in the dwarf spider *Oedothorax gibbosus*, where males develop either as ornamented "hunched" morphs or as "flat," female-like morphs. We identify the hunched-determining allele as a 15-Mb repeat-rich, de novo insertion containing several genes that are among the most differentially expressed between the two morphs. Their role in morph-specific development is further supported by their complete suppression in females carrying the supergene. Notably, these genes originated through duplication and translocation from multiple chromosomes, subsequently diverging functionally or expanding within the supergene. This demonstrates that supergenes can evolve through the stepwise accumulation and functional divergence of genes involved in morph differentiation. Together, our findings reveal that complex adaptive polymorphisms can evolve through the assembly of multiple, independently acquired genes into a single non-recombining genomic architecture.

Poster 5 | **Genome-wide resolution of phylogenetic uncertainty in a rapid evolutionary radiation within an oceanic island system**

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Abstract

The capacity to resolve phylogenetic relationships depends strongly on the evolutionary rate and informativeness of the genetic markers employed, as well as on the temporal scale of divergence among lineages. In this context, approaches based on a limited number of loci, such as those typically generated through Sanger sequencing, often provide insufficient resolution across multiple evolutionary depths. This challenge is particularly pronounced in cases of rapid evolutionary radiations, where diversification occurs over short timescales and phylogenetic signal is consequently limited. This is the case for the tenebrionid beetle genus Oxycara, which has undergone an evolutionary radiation in Cabo Verde. Previous phylogenetic analyses based on Sanger sequencing data (COX1 and ITS2) have successfully resolved deeper nodes but are unable to establish phylogenetic relationships among the most recently diverged lineages, resulting in a large polytomy. To address this limitation, we propose a whole-genome approach to investigate the evolutionary history of this group. By generating and analysing genome-wide data, our primary aim is to identify informative genomic regions capable of resolving shallow phylogenetic relationships and clarifying species-level diversification. In parallel, our sampling includes individuals of the same species distributed across distinct altitudinal ranges, providing an opportunity to investigate genomic variation along an environmental gradient. This framework allows us to explore whether ecological differences associated with altitude may have contributed to diversification, and to identify candidate genes potentially involved in local adaptation. In particular, we aim to identify candidate genes potentially involved in

adaptation to altitude. Here, we present the conceptual framework and objectives of this ongoing Project.

Poster 6 | **Toxins among the branches: Evolution of xenobiotic processing gene families in bats**

Lauterbur, M. E. (1); Bat1K 21-families group

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Abstract

Animals encounter an enormous diversity of xenobiotic compounds from plant secondary metabolites and insect toxins to heavy metals and anthropogenic pesticides. Their ability to metabolize these chemicals depends on large, rapidly evolving detoxification gene families. Cytochrome P450 monooxygenases (CP450s), glutathione S transferases (GSTs), sulfotransferases (SULTs), and ATP binding cassette (ABC) transporters frequently undergo lineage specific expansions and contractions, yet the tempo, mode, and ecological drivers of this gene family evolution remain poorly resolved across mammals. Bats provide a powerful comparative system for studying toxin adaptation because they occupy chemically diverse dietary niches and are represented by a rapidly growing collection of high quality genomes in public repositories. Leveraging more than 100 bat assemblies available as part of the Bat1K Project, we examine the evolutionary dynamics of major detoxification gene families across Chiroptera. To address challenges inherent to large scale reuse of heterogeneous genomic data, we compare multiple strategies for gene family identification and gene–species tree reconciliation. This framework reveals repeated and independent shifts in CP450 and GST copy number, including striking variation among closely related *Myotis* species that suggests recurrent responses to insect derived toxins. Across deeper phylogenetic scales, we identify additional cases of convergent copy number evolution in xenobiotic processing pathways, consistent with shared selective pressures imposed by chemically similar diets and environmental contaminants. By integrating diverse genomic resources and systematically mining existing datasets, this work uncovers the molecular signatures of toxin adaptation in bats and highlights the broader potential of public genomic archives for studying the evolution of complex, environmentally responsive gene families.

Poster 7 | **The impact of whole genome duplication on evolutionary trajectories via structural variation and centromere evolution**

Pehlivanoglu, E (1); Sandeen, R (1); Renner, D (1); Pan, X (1); Šrámková, G (2); Kolar, F (2,3,4); Koch, M (5,6,7); Mandáková, T (8); Yant, L (1)

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Abstract

Whole-genome duplication (WGD) is a transformative macromutation that reshapes evolutionary trajectories by increasing genetic variation at SNPs and structural variants (SVs). WGD doubles the number of chromosomes (leading to polyploidy) and therefore affects evolutionary dynamics by increasing all mutation classes, reducing the impact of purifying selection, and possibly destabilizing centromere architecture and chromatin organization. Recent long-read-based population-scale work in plants has shown that WGD increases genetic diversity, SV accumulation, and genetic load in both Cochlearia (Hämälä et al., 2024) and Arabidopsis arenosa (Vlček et al., 2025), with the latter study integrating empirical data with forward-time population genetic modelling to make first steps in disentangling opposing forces caused by WGD at the population and selective level. These studies used long reads to profile SVs at the population scale, but they did not used reference-free pangenomes, nor enabled generalization of principles by applying comparative context. This PhD project addresses these gaps through comparative pangenomic and multi-omic analyses across paired diploid and autopolyploid cytotypes, initially focusing on these Cochlearia and Arabidopsis arenosa. Leveraging existing long-read pangenomes encompassing hundreds of phased haplomes (built with HiFi, Hi-C, and Cifi data), we are establishing computational pipelines to intersect SV landscapes with transcriptomic, chromatin accessibility (ATAC-seq), and 3D genome architecture. We aim to build predictive, integrative models, linking structural genomic features to regulatory outcomes and allele frequency dynamics across ploidy levels.

Cross-system comparisons will test whether WGD drives convergent functional signatures, moving toward a mechanistic and predictive understanding of polyploid genome evolution. Therefore, we present the conceptual framework and initial pipeline architecture for this PhD.

Poster 8 | **When do hybrid zones lack hybrids?**

Rafajlović, M (1); Butlin, RK (2)

(1) University of Gothenburg, Gothenburg, Sweden; (2) University of Sheffield, Sheffield, UK

Abstract

The theory of hybrid zones has classically been focused on the balance between natural selection and migration. In hybrid zones generated by these processes, adaptive phenotypes and hybrid indices exhibit locally unimodal distributions. In nature, however, hybrid zones can also be locally multimodal, mostly bimodal or trimodal. In the central parts of hybrid zones, such distributions signal local deficit of true hybrids – forms intermediate between the two extreme parental types established at the opposite ends of the hybrid zone. Earlier empirical studies suggested that strong prezygotic reproductive barriers, including assortative mating, are critical to the establishment and maintenance of multimodal hybrid zones. An alternative verbal suggestion assigns a key role to very strong divergent natural selection. However, there has been no systematic theoretical exploration of the role of different evolutionary mechanisms (e.g., natural selection, genetic incompatibilities, assortative mating, niche choice) or intrinsic genomic characteristics (e.g., inverted arrangement of adaptive loci) in the establishment and maintenance of multimodal hybrid zones. This is the focus of the present work. We use individual-based computer simulations to examine the modality of hybrid zones established after secondary contact of ecologically diverged populations in dependence of the strength of divergent environment-dependent natural selection, assortative mating, genetic incompatibilities, niche choice, and the arrangement of adaptive loci in the genome (collinear vs. inversion polymorphism). One finding is that inversions can strongly facilitate the maintenance of multimodal hybrid zones, but multimodality occurs only when the cumulative effect of the different barriers to gene flow (including both pre- and postzygotic) is strong enough.

Poster 9 | **Modelling the co-evolution between chromosomal inversions and their mutational load during local adaptation**

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Abstract

An increasing body of literature on structural genomic variation show that chromosomal inversions are abundant across taxa and frequently play a role in local adaptation. One key feature of inversions is their ability to reduce recombination, thereby maintaining the genetic linkage between the captured alleles. In a context of local adaptation, this reduction in recombination tends to favour inversions that capture locally beneficial alleles. However, inversions also capture widespread deleterious mutations which can ultimately determine the evolutionary fate of the inversions themselves. Indeed, because inversions reduce recombination, they tend to accumulate unique sets of deleterious mutations. In addition, in heterokaryotypes (individuals carrying only one copy of the inversion), partially recessive mutations are rarely expressed, creating an overdominant effect. Ultimately, this interplay between mutation accumulation and associative overdominance should strongly influence the evolutionary trajectory and maintenance of inversions involved in local adaptation. This requires further theoretical investigation. Our study builds upon established island-continent agent-based models to investigate the evolutionary dynamics of a locally-favored inversion and the accumulation of its internal mutational load. To isolate the effects of deleterious mutations, we model the adaptive benefit of the inversion as a fixed fitness advantage, representing the successful capture of locally adapted alleles. We show how the evolution of the mutational load contributes substantially to the inversion's evolutionary trajectory, frequently leading to its extinction. By providing new insights into the feedback loop between inversion evolution and their allelic content, our study provides testable predictions about the genomic properties that enable certain inversions to be implicated in long-termsustain local adaptation.

Poster 10 | **Whole genome detects a putative large chromosomal inversion in blue sharks**

Alves, JS (1,2,3,4); Marques, JP (1, 3); Farelo, L (1, 3); Arnaud-Haond, S (4); Queiroz, N (1, 3); Melo-Ferreira, J (1,2,3)

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Abstract

Rapid ocean change and overfishing threaten the persistence of many marine predators. The blue shark (*Prionace glauca*) is the most widely distributed and heavily fished shark species globally and is particularly vulnerable to ocean warming and deoxygenation due to its ectothermic physiology and highly active predatory behaviour. These characteristics make it an ideal model for investigating how pelagic predators facing environmental and anthropogenic pressures can adapt and persist. Here, we aim to address this question by applying whole-genome sequencing to investigate the genetic diversity and structure of the blue shark across the Atlantic and Mediterranean. Genome-wide population structure analysis showed no clear genetic structure. However, analysis of genetic differentiation (Fst) across the North Atlantic, South Atlantic, and Mediterranean regions, detected a region of elevated differentiation on chromosome 23 (~20 Mb), primarily associated with South Atlantic individuals. Synteny analysis using long-read data from two individuals identified a large inversion in this genomic region. In parallel, analyses based on short-read data, including principal component analysis and individual heterozygosity, revealed three genetic clusters, with intermediate individuals showing elevated heterozygosity, a pattern consistent with inversions. Ongoing work aims to characterize the architecture of this inversion and test its potential association with local adaptation. This study presents the first evidence of a chromosomal inversion contributing to localized genetic divergence in a highly migratory pelagic shark species.

Poster 11 | **How structural variants rewire chromatin architecture and shape evolution across time scales**

Aurora Ruiz-Herrera (1,2)

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Abstract

The functioning of cells depends on far more than DNA sequence alone. Chromatin folding, orchestrated by regulatory elements and long-range genomic contacts, plays a crucial role in shaping gene expression and genome stability. Structural variants (SVs) can disrupt or reshape these 3D architectures, altering regulatory interactions and potentially driving evolutionary change. In this talk, I will explore how SVs can rewire chromatin folding and influence evolutionary trajectories across multiple time scales. I will begin by outlining the general principles that govern chromatin organization in the germ line, where heritable structural rearrangements arise. I will then examine emerging evidence showing how SV-induced changes in chromatin topology affect both local regulatory environments and broader nuclear architecture. Finally, I will discuss how lineage-specific chromatin interaction landscapes may predispose certain groups to recurrent patterns of structural variation, ultimately shaping their evolutionary paths across deep and recent evolutionary time.

Poster 12 | **Rapid evolution of genome size mediated by centromere expansion and contraction in Formica ants**

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(1) University of California Riverside

Abstract

How and why does genome size evolve? We estimate centromere size in 1,800 Formica ants of over 100 species, by measuring the frequency of a centromere-associated satellite repeat in whole-genome sequence data. Species vary in satellite content from less than 3% to over 40% of the genome, with substantial changes in centromere proportion even between closely related species. Long-read genome assemblies show that the non-centromeric component of the genome has remained stable and largely collinear across the genus, while validating short-read-based estimates of centromere size and genome size variation. We trace the evolution of centromere size along the Formica phylogeny, identifying a ten-fold expansion of satellite DNA early in the diversification of the genus resulting in a 50% increase in genome size. We also identify several recent reductions in satellite content and genome size. Variation within and between species is correlated with climate, with larger genomes observed in colder climates, suggesting that genome size may be locally adapted.

Poster 13 | **Massive transposable element expansion and RIP defence reveal evolutionary dynamics in the widespread ectomycorrhizal fungus *Cenococcum geophilum***

Benjamin Dauphin (1); Tobias Baril (2); Emmanuelle Morin (3); Ursula Oggenfuss (2,4); Stephanie Pfister (1); Maira De Freitas Pereira (3); Igor V. Grigoriev (5,6); Annegret Kohler (3); Francis Martin (3); Daniel Croll (2); Martina Peter (1)

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Abstract

Transposable elements (TEs) are selfish genetic elements that proliferate by exploiting host replication machinery, often triggering evolutionary arms races with genome defense systems. We assembled a telomere-to-telomere reference genome for *Cenococcum geophilum* strain 1.58, the most widespread ectomycorrhizal fungus in boreal and temperate forests. Using PacBio HiFi and Illumina Hi-C sequencing, we generated a 178.54 Mbp assembly comprising seven contiguous chromosomes. Remarkably, over 78% of the genome consists of TEs, with three families (Ty3, Ty1, Tad1) contributing over 60% of genome size. Critically, 94% of TEs show repeat-induced point mutation (RIP) signatures, revealing pervasive antagonistic coevolution between TEs and this genome defense mechanism that operates during sexual reproduction. This extensive RIP activity provides molecular evidence for cryptic sexual reproduction in this putatively asexual species. Comparative analysis of 15 strains revealed lineage-specific TE expansions and recent activity, demonstrating that several families have escaped RIP suppression and continue to drive genome evolution. Differential expression analysis across ectomycorrhizal tissues, free-living mycelium, and stress-resistant sclerotia identified 56 TEs regulated during symbiosis and 66 TEs altered in sclerotia, suggesting these selfish elements may be co-opted for host adaptive functions. Our findings reveal ongoing genetic conflict in *C. geophilum*, where massive TE proliferation is counterbalanced by RIP-mediated suppression, yet escapee elements continue shaping genome architecture and potentially contributing to ecological adaptation.

Poster 14 | **Chromosomal inversions accelerate genetic evolution and drive ecological speciation across an island gradient**

Gómez-Ramos, I (1); Sánchez-Villegas, R (2); Mohan, AV (3); Lavergne, C (4); Cerca, J (5,6,7); Márquez-Corro, JI (2); Marques, A (8); Martín-Bravo, S (2); Luceño, M (2); Lucek, K (3); Escudero, M (1)

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Abstract

The hyperdiverse sedge genus *Carex* represents a fascinating system for studying plant genome evolution, particularly regarding their characteristic holocentric chromosomes, which drive rapid karyotypic evolution and speciation. However, high-quality genomic resources remain limited for key insular lineages. Here, we present the first highly contiguous, chromosome-level reference genome assemblies for two endemic species from the island of Réunion: *Carex borbonica* and *Carex boryana*. We employed a state-of-the-art sequencing strategy combining deep PacBio HiFi long reads with Hi-C proximity ligation and Illumina short-read data. This approach allowed us to successfully scaffold both genomes into pseudochromosomes, accurately capturing their complex holocentric architecture. Our comparative genomic analyses highlight the extent of structural variation, genome synteny, and sequence divergence between these two closely related insular sedges. By comparing these highly contiguous assemblies, we identify chromosomal rearrangements and repetitive element dynamics that likely play a central role in their evolutionary divergence and ecological adaptation. Ultimately, these robust new genomic resources provide a critical foundation for unravelling the mechanisms driving speciation, chromosomal evolution, and biogeographic history within *Carex*, offering valuable insights into how holocentric genome architectures influence plant diversification in isolated oceanic island ecosystems.

Poster 15 | **Exploring the relationship between DNA methylation and genomic rearrangements in Lepidoptera**

Escuer, P (1)

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Abstract

Holocentric chromosomes are defined by lacking a single centromere region, instead, they present multiple centromere-like structures, and have independently evolved in multiple lineages of plants and invertebrates. Due to this structure, chromosomal rearrangements like fusions or fissions are common in holocentric species, which can act as reproductive barriers and promote speciation. Groups presenting holocentrism as Lepidoptera, the order comprising moths and butterflies, displays high diversity in karyotypes, which is not equally distributed among and even within genera. This diversity may be due to the impact of large-scale rearrangements as a barrier to gene flow at different evolutionary scales. Former studies suggest that fusion and fission sites are enriched for repetitive elements, which often have unique methylation patterns. However, the methylation landscape in Lepidoptera has remained largely unknown. Here, we characterise the methylation landscape in Lepidoptera and their association with genomic breakpoints underlying chromosomal fusions or fissions. For that, we used Bisulfite sequencing across 60 species of butterflies and moths to analyze genome-wide methylation patterns across the genome and in rearrangements breakpoints. Our results will uncover the relationship between the methylome and chromosomal rearrangements, shedding light on the epigenetic mechanisms associated with holocentric speciation.

Poster 16 | **The Dynamic Genome: Chromosome Evolution Across the Animal Tree of Life**

Price, C (1); Burden, F (1); Quigley, S (1); Kirkland, C (1); Farré, M (1,2)

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Abstract

Chromosomes are dynamic structures that evolve through large-scale rearrangements such as fusions, fissions, inversions and translocations. These structural changes reshape genome architecture, influence recombination landscapes, and can ultimately contribute to species divergence. The rapid expansion of chromosome-level genome assemblies, enabled by cutting-edge sequencing technologies such as long-read sequencing and Hi-C, now provides unprecedented opportunities to study chromosome evolution across the animal tree of life. In this talk, I will present work from our group investigating the mechanisms and consequences of chromosome evolution using comparative genomics approaches. By identifying conserved syntenic blocks—the preserved order of genes inherited from common ancestors—we reconstruct ancestral karyotypes and trace lineage-specific rearrangements across diverse taxa. These analyses allow us to infer when and where chromosomal changes occurred and to investigate whether particular genomic regions are more prone to breakage and rearrangement. Integrating genome assemblies, cytogenetic data, and computational tools for synteny visualization and ancestral reconstruction enables us to explore both the mechanisms that generate chromosomal variation and the evolutionary consequences of these events. Together, our work illustrates how large-scale genome architecture evolves across animals and demonstrate how modern genomics is transforming our understanding of chromosome evolution.

Poster 17 | **Genomic Structural Variation as a Basis for Ecological Divergence and Local Adaptation in a Wing-Polymorphic Beetle**

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Abstract

Structural variation plays a central role in shaping evolutionary trajectories yet remains poorly characterized in many natural systems. Inversions can affect the organization of adaptive variation, making them drivers of divergence and local adaptation. Understanding how these arise, persist, and shape genome architecture is essential for understanding evolutionary patterns in natural populations. Here, I use the saltmarsh beetle Pogonus chalceus to explore how structural variation contributes to adaptive divergence. This species consists of short- and long winged ecotypes that occupy contrasting habitats and repeatedly evolve in geographic proximity. To investigate the genomic basis of this divergence, I generated two chromosome level genome assemblies, one for each ecotype, using a combination of long read sequencing, Hi C scaffolding, and linkage mapping. Comparative genomics reveal multiple large scale rearrangements between ecotypes, including several Mb inversions. These inversions encompass most of the genomic differentiation between ecotypes and coincide with regions previously associated with adaptive traits such as wing morphology. Genome-wide association analyses using over 300 individuals from two highly admixed populations identified loci significantly associated with wing size that fall within these structurally rearranged regions, further supporting their functional relevance. Moreover, epistatic interactions between inversion loci provide a mechanism by which alternatively selected alleles can become masked from natural selection, providing an explanation of how repeated adaptation occurs from inversion polymorphisms that are maintained as standing genetic variation in alternative populations. Overall, this study highlights the importance of genome architecture in adaptive evolution and demonstrates how integrating genome assembly, GWAS, and comparative genomics can uncover the evolutionary significance of structural variants in natural populations.

Poster 18 | **Structural genetic diversity across the Tree of Life: how can we access evolutionary patterns and processes?**

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Abstract

A significant fraction of genetic diversity lies in structural genomic variation (SV), e.g. chromosomal rearrangements or copy-number variants. Recent technologies coupled with new high-quality reference assemblies provide unprecedent access into SVs, showing their prevalence and their implication in adaptation or diversification. This is opening new prospects in the study of genetic variation and transforming our understanding of the genetic basis of evolutionary changes. Here, we will reflect on the role of SVs in the evolution of biodiversity and adaptation, with insights from experimental and ecological studies, and ask how the new genome resources may help to more systematically investigate SVs. In particular, we have developed a pipeline leveraging long-reads and genome assemblies from the Darwin Tree of Life project to address patterns of intra-specific structural variation across a broad range of taxa. We'll discuss how such type of datasets provides opportunities to investigate the role of species' life-history and ecology in shaping the architecture of genetic diversity and architecture.

Poster 19 | **Drivers of sex chromosome turnover in Lepidoptera**

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Abstract

Lepidoptera possess holocentric chromosomes and are therefore presumed to tolerate chromosomal rearrangements more readily. Nevertheless, their karyotypes are remarkably conserved, with the main exceptions occurring in the sex chromosomes, which frequently fuse with autosomes. We investigated whether sexually antagonistic selection drives sex chromosome turnover in butterflies by analyzing the genomic distribution of sex-biased genes, used as a proxy for sexually antagonistic selection. We focused on butterflies of the tribe Danaini, which experienced repeated sex chromosome–autosome fusions >10 My ago, and on the common blue butterfly, Polyommatus icarus, which harbors a recent neo-sex chromosome system. In danains, autosomes involved in the fusions were significantly enriched in female-biased male-biased genes expressed in gonads, which may have facilitated fixation of the neo-sex chromosomes. In P. icarus, expression profiling revealed significant enrichment of male-biased genes on the ancestral Z chromosome (Zanc) in both gonads and somatic tissues. Regulatory changes between larvae and sexually dimorphic adults further supported gonadal enrichment of Zanc in genes neutral in females but beneficial in males, consistent with sexually antagonistic selection. In contrast, the newly added Z segment (Znew) was not enriched in sex-biased genes expressed in gonads but contained significantly more female-biased genes expressed in soma. Interestingly, autosomal transcription was feminized in soma as well, suggesting that sex linkage of Znew genes may have resolved sexual conflict by shifting expression toward a female optimum. Yet, limited co-expression between Znew-linked and autosomal female-biased genes indicates that this feminization may instead result from W-linked gene duplicates. We identified independently evolved neo-sex chromosomes also in other P. icarus populations and hypothesize that evolution of their gene content contribute to reproductive isolation.

Poster 20 | **A Scalable Comparative Genomics Framework Reveals Diversity in Microbial Sulfur Metabolism**

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Abstract

Sulfur is a ubiquitous element across the hydrosphere, lithosphere, atmosphere, and biosphere. Bacteria and Archaea are the primary microbial drivers of the sulfur biogeochemical cycle, mediating transformations of both inorganic and organic sulfur compounds across oxidation states ranging from −2 to +6 for assimilation and energy conservation. This continuous turnover prevents the accumulation of toxic sulfur species, maintains redox balance, and contributes to climate regulation and ecosystem functioning. Despite recent advances in understanding microbial sulfur cycling, the metabolic potential of many newly described lineages—particularly uncultivated archaeal groups—remains poorly characterized. Here, we developed a large-scale comparative genomics workflow that includes similarity search, fusion and fission aware clustering and functional annotation. Systematic approach allowed to identify genes involved in organic and inorganic sulfur metabolism across archaeal and bacterial genomes. Our analysis, spanning nearly 80,000 genomes, reveals the broad distribution and diversity of sulfur metabolic pathways across both domains. Within archaea, members of the Thermoproteota are particularly enriched in sulfur metabolism genes, exhibiting diverse mechanisms for both assimilatory and dissimilatory sulfur transformations. In contrast, methanogenic lineages predominantly encode distinct pathways for assimilatory sulfur metabolism. We further infer potential mechanisms for the metabolism of diverse sulfur compounds across both established and newly described methanogenic groups. These findings highlight lineage- and environment-specific adaptations in cellular sulfur cycling. Finally, insights from archaeal metabolism shed light on organosulfur degradation pathways, uncovering alternative variants of previously characterized pathways in marine microbes, that may underpin yet unknown metabolic flexibility in sulfur utilization.

Poster 21 | **Genomic signatures of host-parasite coevolution in the bank vole - nematode system**

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Abstract

Parasites play a crucial role in the evolution of their hosts. Variation in parasite prevalence, genetic diversity, and community composition among host populations can generate spatially heterogeneous selection pressures, potentially promoting local adaptation and genomic differentiation in their hosts. On the other hand, host populations are equally diverse, leading to local, host-parasite arms race visible at the genetic level. This co-evolution has been comprehensively described from the host perspective, yet little is known about the parasite adaptations to the host defense. Moreover, all studies up to date focused on SNP variance, neglecting structural variation which is an underexplored yet potentially critical component of adaptive evolution. In the project, aim to fill this gap using bank vole *Myodes glareolus* - nematode *Heligmosomum mixtum* system to study the role of structural variants, in particular inversions, in host-parasite evolutionary interplay. Using samples collected along a geographical cline (Finland-Poland-Czech Republic) and a temporal cline (2005-2025), this study aims to detect structural variants from RAD-seq data using window PCA, with the goal of distinguishing recent mutations linked to ongoing climate change from those that arose during the last glaciation.

Poster 22 | **Identifying the genomic footprint of Robertsonian translocations and their possible effects on speciation in a marine snail**

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Abstract

Chromosomal rearrangements play a key role in evolutionary biology establishing barriers to gene flow and promoting speciation. Among them, chromosomal inversions have been widely studied due to their ability to suppress recombination and isolate genomic regions, linking structural variation to adaptation. Robertsonian translocations (Rbs) involve the fusion of the long arms of two acrocentric chromosomes into a single metacentric chromosome, causing major genomic reorganization. These rearrangements give rise to chromosomal races, characterized by certain acrocentric and metacentric chromosomes. Recent studies show that Rbs reduce recombination, affect nuclear organization, and may be linked to adaptive traits. However, population genomic studies assessing their genome-wide impact and role in shaping population structure remain limited. The marine intertidal snail *Nucella lapillus* presents two chromosomal races across Northeast Atlantic populations, inhabiting different intertidal environments, sometimes within the same shore with partially overlapping distributions. These races differ in karyotype due to Robertsonian translocations across five chromosome pairs. In the lower intertidal zone, exposed to wave action, individuals have thinner shells, wider apertures, and a karyotype of 2n=26. In contrast, upper intertidal individuals, exposed to crab predation, exhibit thicker shells, smaller apertures, and variable chromosome numbers (2n=27–36) resulting from multiple Robertsonian translocations. While these races are phenotypically distinct, little is known about the genomic architecture or barriers between them, especially in rearranged regions. Here we present progress on identifying genome-wide patterns of differentiation using a recent reference genome and WGS data from natural populations with both ecotypes (n=114). The results provide a first view of genomic variation between chromosomal races, offering insights into chromosomal evolution and speciation.

Poster 23 | **Understanding the role of inversions in adaptation and speciation across *Littorina* marine snails**

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Abstract

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. We will present the collective efforts of the Littorina Research Community to understand the role of inversions in adaptation and speciation in *Littorina* marine snails, an emerging model system to study the mechanisms of adaptation and how reproductive isolation accumulates during divergence in the presence of gene flow. By combining whole-genome re-sequencing and phenotypic information from multiple populations and species, we argue that: i) polymorphic inversions are relatively abundant across *Littorina* species, ii) SNPs showing strong differentiation between ecotypes as well as divergently adaptive traits often map to inversions; iii) many inversions in different species show a clinal distribution across different environmental gradients; and iv) the evolutionary history of some inversions is complex and inference is complicated by gene flux and/or multiple origins.

Poster 24 | **How does genome structure shape adaptation to climate in a seaweed fly?**

Mérot, C (1);

(1) ECOBIO - CNRS UMR 6553, University Rennes 1, Rennes, France

Abstract

Tba

Poster 25 | **Structural genomic variation and the evolution of wing dimorphism in *Bembidion properans***

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Abstract

Structural genomic variations (SVs) are increasingly recognized not as rare anomalies, but as powerful drivers of evolutionary innovation and adaptation. While single nucleotide polymorphisms (SNPs) have long dominated studies of genetic diversity, SVs can have far-reaching effects by reshaping gene content and regulatory landscapes. This project explores the evolutionary role of SVs through the lens of wing dimorphism in the ground beetle *Bembidion properans*. Wing dimorphism represents a classic evolutionary trade-off between dispersal and reproduction, yet its genomic basis remains largely unresolved. In *B. properans*, individuals occur as either flight-capable long-winged or flightless short-winged morphs, a polymorphism controlled by a single Mendelian locus. However, preliminary analyses reveal that this genetic architecture is underpinned by a complex structural variant at the wing locus. This variant consists of a large 200 kb insertion present only in the short-wing allele and embedded within a highly repeat-rich region, suggesting a role for transposable element associated variation in shaping this trait. This project aims to understand how these structural variant influences wing development across key developmental stages, spanning larval, pupal, and adult transitions and specifically, it will test whether the variant acts as a coordinated regulatory module such as a supergene or major cis-regulatory element modulating multiple developmental pathways underlying dispersal-related phenotypes. To address this, high-quality haplotype-resolved genomes will be generated using PacBio HiFi and Omni-C data, complemented by Iso-seq based annotation. Population resequencing and pan-genome analyses will characterize SV diversity, while RNA-seq and ATAC-seq across developmental stages will link structural variation to gene expression dynamics and chromatin accessibility.

Poster 26 | **Modeling the evolutionary dynamics of transposable elements and the emergence of host regulatory strategies**

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Abstract

The ubiquity of Transposable Elements (TEs) across the tree of life presents a complex puzzle for evolutionary biology. Traditionally characterized as genomic parasites, TEs are increasingly recognized for their potential to generate adaptive genetic variation. However, the conditions under which a host genome might evolve to strategically regulate TE activity—balancing the risk of deleterious mutations against the potential for beneficial innovation—remain poorly understood from a theoretical perspective. In this study, we develop a comprehensive multilocus population genetics model to track the dynamics of TE accumulation and distribution within a host genome. Our framework incorporates a heterogeneous genomic landscape, accounting for both the pervasive costs of genomic instability and the rare occurrence of adaptive insertions. Central to our analysis is the introduction of a modifier locus that allows for the evolution of host-encoded transposition and excision rates. We derive the analytical conditions that govern the invasion of novel regulatory strategies.Our model provides new insights into the fundamental principles of TE evolution, revealing how the distribution of fitness effects of TEs shapes the evolution of host control. By characterizing the formal relationship between host fitness and TE activity, this study offers a robust theoretical basis for understanding the transition between genomic conflict and cooperation, and provides a general framework for investigating the maintenance of TE activity in diverse biological systems.

Poster 27 | **Optimizing the characterization of chromosomal inversions to better understand their role in local adaptation**

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Abstract

Chromosomal inversions have aroused a growing interest as they play a critical role in evolutionary processes. By limiting recombination between an inverted and standard arrangement, inversions are a particular genetic architecture that are predicted to be involved in local adaptation and speciation. This is supported by empirical cases in which a few adaptive inversions were indirectly detected when contrasting phenotypes or finding blocks of genetic differentiation. However, the recent availability of entire genome assemblies reveal that even a few individuals may vary in multiple inversions. To understand the genetic architecture of adaptation and the importance of inversions, it is therefore important to characterize the full range of inversions across individuals and populations accurately and in a cost-efficient way. We address this objective by comparing the effectiveness of characterizing inversions at population-scale using two sequencing methods: long reads and linked reads (Haplotagging) in two species, *Coelopa frigida* and *Ciona intestinalis*. Analysing long-read data is the most exhaustive approach to detect and genotype inversions of all lengths. It has proven to be very efficient to refine the breakpoints of adaptive inversions previously detected by an indirect method. Yet, long-reads cannot scale-up to population-wide studies in a cost-efficient manner. Analysing linked-reads data thus has provided a relevant alternative to assess the position and frequency of inversions across many more individuals. Overall, the combination of both datasets has given valuable insights into the distribution of inversions across the genomes of *C. frigida* and *C. intestinalis* and across several populations. By scaling up inversion characterization to the population level, our study thus represents a crucial step toward a better general comprehension of the role and dynamics of inversions in population genetics and evolutionary ecology.

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