

ABSTRACTS

AsiaEvo 2023

Singapore



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Abstracts are sorted by the last name of the presenter, in alphabetical order. The numbering corresponds to the numbers in the schedule (above) and the list of attendees (at the end).

Talk by **Gembu Abe**:

(1) Understanding the evolutionary development mechanism of bilateral form of vertebrate appendages using twin-tail morphology

Early evolution of vertebrates from evo-devo and paleontological perspectives

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Vertebrates have well-organized locomotor appendages (fins and limbs) crucial for environmental adaptation and prosperity. Those locomotor appendages are categorized into two groups based on their location: paired fins (e.g., pectoral, pelvic fins, and limbs) on the bilateral trunk region and unpaired median fins (e.g., caudal, anal, and dorsal fins) along the midline. While median fins are evolutionarily ancestral, it is thought that paired fins evolved by coopting their developmental mechanism to the lateral regions of the body trunk. However, the question of how a single midline structure was transformed into bilaterally paired structures on the lateral sides remains unanswered. To address this question, we focused on the "Twin-tail morphology" observed in certain strains of goldfish and mutant zebrafish. The Twin-tail morphology represents the bilateral duplication of caudal and anal fins, providing a model for analyzing the mechanisms behind the evolutionally developmental transition from midline to bilateral form. In the previous studies, we and other groups found the genetic factors contributing to Twin-tail phenotypes associated with early embryonic ventralization. However, how the ventralization linked to the duplication of the median fins remains unclear. Hence, our study aimed to elucidate the developmental mechanisms responsible for the manifestation of the Twin-tail phenotype by conducting analyses and experiments using zebrafish Twin-tail mutants. First, we analyzed how the developmental process of the median fin primordia, median fin fold, is altered in Twin-tail embryos through reporter gene expression and cell lineage tracing. Our results revealed that presumptive median fin fold cells in normal embryos expressed broadly and then closed to form a midline single structure. In contrast, in Twin-tail embryos, these cells were more widely distributed and did not close completely. Therefore, it was suggested that the bifurcation of the ventral median fin fold in twin-tail embryos is caused by the movement of the presumptive ventral fin fold cells not closing in the midline due to the influence of early embryonic ventralization. Furthermore, at this time, analysis of the expression of the fin fold marker genes and the functional molecules of fin development revealed that the area capable of fin fold forming expanded from the presumptive ventral fin fold region of the tail to the ventral trunk region. Therefore, it is suggested that the embryonic origin may be shared between the ventral fin fold and the paired fins, at least in the epithelial tissues. Taken together, our findings suggest that the developmental process of the ventral fin fold intrinsically possesses left-right axis information, and the bilaterality of the ventral fin fold in Twin-tail embryos arises from a failure in the transition from lateral to midline direction. Furthermore, there is a competence field for fin-formation on the ventral side, and it may be that paired fins evolved by directly modifying the developmental mechanism of such a competence shared with median fins.

Talk by **BV Aditi**:

(2) Beyond neutral loci: Understanding immune gene variation in an endangered big cat

Genomic diversity in nonequilibrium populations

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Habitat fragmentation is a significant threat to wild populations worldwide, leading to increased isolation and inbreeding, loss of genetic diversity and increased extinction risk. Carnivores, owing to their ecology, are particularly susceptible to the consequences of habitat fragmentation. While previous studies have focused on neutral loci to assess genetic diversity, such loci may not provide an accurate prediction of a population's adaptive potential. In contrast, loci known to be involved in fitness can offer insights into the adaptive potential of isolated carnivore populations. We assess genetic diversity and possible selection acting on non-MHC immune genes, which are known to be involved in immunity, but are less studied than MHC loci. Using tigers as a model system for wild, endangered carnivores with low neutral genetic variation, we mine whole genome resequencing data from 120 range-wide genomes to examine patterns of genetic variation for non-MHC immune genes. We identified variants in five families of innate and adaptive immune genes. Our findings contrast immune gene diversity at receptor and signaling genes with neutral loci and in populations of different sizes and connectivity. We find that Toll-Like Receptor genes have the highest diversity amongst the gene families examined. Amur tigers have the lowest diversity at adaptive loci whereas South China and Indo Chinese tigers have the highest diversity. We also identified mutations that could be deleterious and highlight populations that carry a high frequency of such mutations, results of potential significance to management.

Talk by **Aneil Agrawal**:

(3) Genomic response to release from sexual constraint

Open category

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Under standard inheritance, autosomal genes can be constrained in responding to divergent selection between the sexes. Using *Drosophila melanogaster*, we used an experimental manipulation to evolve populations in which ~50% of the autosomal genome was largely released from the constraints imposed by being part of a gene pool equally shared across the sexes. Instead, the experimental manipulation resulted in two gene pools: one that experienced selection only through males and the other that experienced selection primarily through females. Here we examine divergence between these gene pools with respect to genetic properties putatively believed to be related to sexual dimorphism and sexual conflict.

Talk by **Neetika Ahlawat**:

(4) How does resource presentation change adaptive trajectories?

Open category

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Adaptive trajectories of populations are dictated by the make-up of the environment in which they evolve. For instance, the adaptive trajectory in a glucose-limiting environment is distinct from when adaptation takes place in presence of glycerol. However, how do adaptive trajectories of a population change when the same resource is presented to the population in different packaging? To answer this question, we evolve *E. coli* in three similar but non-identical environments where glucose and galactose were presented in the form of lactose, or melibiose, or as a mixture of glucose and galactose. Six lines of *E. coli* were evolved in each of the three environments for 300 generations. Phenotypic characterization of the evolved lines shows that melibiose evolved lines behave qualitatively differently than the lactose- and glucose-galactose evolved lines. Specifically, melibiose-evolved lines have a higher fitness in not only melibiose, but also in non-native environments (lactose and glucose-galactose). Thus, from the context of phenotypic adaptive response, resource packaging and presentation dictates adaptive trajectories. Genome sequencing of evolved lines shows that adaptation in glucose-galactose, in each of the six lines, happens via mutation in either RpoB or RpoC, thus exhibiting convergent adaptation. On the other hand, all melibiose-evolved lines exhibit mutations in distinct genes, leading to adaptation. This genetic diversity provides insights into challenges associated with predictability of evolutionary processes. More importantly, we report a novel phenomenon, that the nature of resource packaging might alter the evolutionary trajectories of evolving populations.

Talk by **Per E. Ahlberg**:

(5) New light on Devonian tetrapod braincases and middle ears

Early evolution of vertebrates from evo-devo and paleontological perspectives

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The otoccipital region of the braincase underwent dramatic changes over the course of the fish-tetrapod transition. In fish members of the tetrapod stem group, such as *Eusthenopteron* and *Gogonasus*, the otoccipital region is demarcated anteriorly by an intracranial joint. The basioccipital forms a tunnel for the notochord, opening anteriorly into a basicranial fenestra. The dorsal part of the hyoid arch is a hyomandibula, which articulates against a lateral commissure straddling the jugular vein. The lateral otic fissure ends ventrally in a vestibular fontanelle, but this opening into the inner ear space has no direct connection with the hyomandibula. This architecture persists into the elpistostegals *Panderichthys* and *Tiktaalik*. By contrast, at the tetrapod crown group node, the intracranial joint and basicranial fenestra have disappeared, the basioccipital is no longer notochordal, the lateral commissure has been lost, and the dorsal part of the hyoid arch is now a stapes with its footplate lodged in a fenestra vestibuli, in direct contact with the inner ear. The transition between these endpoints is documented by braincases of Devonian stem tetrapods. Only two are known in their entirety: those of *Acanthostega* and *Ichthyostega*. They both have persistent notochordal tunnels, and lack basicranial fenestrae and lateral commissures, but in other respects they are quite dissimilar. The braincase of *Ichthyostega* is proportionately longer than that of *Acanthostega* and narrower relative to the

skull roof; its fenestra vestibuli is smaller; and its stapes is a delicate paddle-like bone whereas that of *Acanthostega* is more robust. Uncertainty is introduced by the fact that *Acanthostega* has been reconstructed from partially flattened specimens whereas *Ichthyostega* is known from a relatively poor CT scan. Here we present two informative new otoccipital braincases of Devonian tetrapods: one from *Ventastega* (late Famennian, Latvia), the other from an undescribed tetrapod (latest Famennian, East Greenland). The latter, which comes from a new locality yielding a unique fossil assemblage with partial soft-tissue preservation, is preserved with both stapes in position. *Ventastega* has been imaged from a high-resolution CT scan, the Greenland braincase using synchrotron microtomography. Both braincases are notochordal and lack a basicranial fenestra. The occipital regions are short and relatively tall, similar to that in *Acanthostega*. The fenestra vestibuli is very large in both braincases, much bigger than would be required just to accommodate the footplate of the stapes. The major differences between them are that the Greenland braincase is narrower dorsally, creating flanking spaces underneath the wide skull roof in a manner similar to *Ichthyostega*, and that it has incipient paired basioccipital condyles which are absent in *Ventastega*. The stapes of the Greenland braincase, like that of *Ichthyostega*, is a thin, subcircular paddle with robust dorsal and ventral feet, but its orientation is more vertical and it is concave anterolaterally rather than posteromesially. We interpret it as part of an auditory but non-tympanic ear. Preserved soft tissues include a ligament or muscle connecting the stapes to the skull roof, and part of the mesial wall of the middle ear cavity.

Talk by **John S. Ascher**:

(6) How can biogeography, life history, and community science inform conservation of Asian bee species?

An evolutionary perspective on pollinator biodiversity, systematics, and conservation

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Thousands of bee species occur across Asia and this continent is a global hotspot for radiations of honey bees (*Apis*), bumble bees (*Bombus*), stingless bees (*Meliponini*), carpenter bees (*Xylocopa*), and myriad less conspicuous groups. Regional species include charismatic megafauna such as giant honey bees that provide important ecosystem services and economic benefits. However, a large proportion of Asian bee species are known only from inadequate primary descriptions, often unillustrated, for a single sex, and from one or a few localities. Workers across much of Asia, especially the tropics, find it difficult to identify most of the regional species in part because most types and other reference material resides elsewhere, especially in Europe. This talk will first describe progress made in identifying regional bees and determining their geographic ranges. In particular, it will showcase the emergence of iNaturalist as an important resource to improve and share taxonomic and biogeographic data across Asia, a region with a paucity of digitized historical specimens and facing serious impediments to ongoing collecting. Data accumulating daily online has expanded the ranges of many species, improved species distribution models, and demonstrated persistence of key bee pollinators across the region. Nonetheless, a large proportion of Asian bee species have zero records from any source in public databases (GBIF+) if represented there are at all (many are lacking even from the taxonomic backbone) so are unlikely to be assignable to a threat status (other than Data Deficient) in conservation assessments planned by the IUCN Wild Bee Specialist Group for Asia. to describing how a synthetic approach combining insights from phylogenies (still highly incomplete for Asian bee taxa), biogeographic and modeling studies, life history studies, and trait databases can inform bee conservation despite fragmentary species-specific information, modeled after a recent application of this approach by P. Williams to better-studied bumble bees.

Poster by Eapsa Berry:

(7) Spatial distribution of species hotspots in the Himalaya – identifying relationships between the salient geobotanic features

Paleo- and macro- ecology in tropical Asia

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Phytogeographic insularity through heterogeneity in landforms is the key for evolution and functional distinctiveness of land plants on the earth. Classically, biogeography as a discipline started about 200 years ago primarily with the study of taxon rarity by naturalists through the concepts of biological insularity in oceanic islands. A little later in time, scientists started drawing analogies of rich biodiversity in mountains with oceanic islands; they called these mountain systems “sky islands” or “edaphic islands” or simply “montane islands” as naturalists discovered a large part of this taxon rarity, technically called endemism, on these mountains. The question is what physical landscape in a mountain system is congenial for a rich endemic flora to flourish? In other words, what are the factors that govern insular biogeography of mountain systems? Invariably, unfortunately and misleadingly, these islands are referred to either as mountaintops or else there is no clear definition of what makes these islands. To understand the factors we need to identify the features of geobotanic similarity/dissimilarity, and homogeneity/heterogeneity. In this study, we compare 15 sites of rich plant biodiversity, identified by us through the use of literature, across the Himalaya, and we have tried to gain insights about the geobotanic similarity and related features, and arrived at emergent relationships between these sites.

Talk by Joy Bose:

(8) Chronic adaptation to malnutrition in the pre-adult stage mitigates infection costs at the expense of disease transmission risk in *Drosophila* adults: a novel trade-off in immunity.

Open category

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Malnutrition is a global concern, and many populations are experiencing malnutrition for generations in many parts of the world. Restricted resource availability under malnutrition leads to impaired body metabolism, which in turn affects various life-history traits. It has been indicated that reduced immunity and therefore, susceptibility to infection is one major consequence of malnutrition. However, to date, it is unclear how it affects immunity & infection response in populations under chronic malnutrition. In this study, we have addressed this question using *Drosophila melanogaster* populations adapted against chronic malnutrition in the larval stages. To test that, we have used *Providencia rettgeri* infection both at pre-adult and adult life stages, followed by assessing their immune-competence and disease- transmission risk. This result aligns with the elevated pathogen clearance in maladapted larvae compared to controls. Moreover, we have identified that underpinning immune mechanisms attributed to insect cellular & humoral immunity, such as crystal cell number, Phenol oxidase activity, and consistently display an elevated level irrespective of identity (i.e., pathogen-infected vs. mock-infected) suggesting a basal increase of immune traits associated with larval-maladaptation. We furthermore evaluated the plausible ecological connection associated with larval

maladaptation to adult traits upon infection using the same pathogen. As expected, here we identified a substantial fitness loss followed by elevated pathogen load across infection doses, suggesting an antagonistic pleiotropic response across *Drosophila* life stages. As the fitness loss indicates an immune-compromised body condition, we, therefore, continued to test the disease transmission risk of these evolved lines as an ecological approach. Surprisingly, here we have identified these larval-maladapted adults shedding a substantially more pathogen compared to controls while passing through their body. The passaged pathogen through malnutrition lines also induced a significant fecundity loss compared to control counterparts while inhabiting a common uninfected fly line; WSO118, suggesting either (a) higher shedding or (b) increased virulence in passaged pathogen facilitates disease transmission risk to the surrounding susceptible population. Now to disentangle the effect of higher shedding or increased virulence we have adjusted to a fixed dose to control and maladapted passaged pathogens & introduced the secondary infection to a common host genotype, i.e., control flies. Surprisingly, here we have identified substantially higher mortality for maladapted-fly passaged pathogen compared to control passaged, suggesting that maladapted fly physiology facilitates enhanced virulence. To check whether such enhanced virulence shows consistency against other fly genotypes, we have used those passaged pathogens to infect other fly lines i.e., WSO118, Oregon R & the results remain the same as mentioned previously. Finally, the enhanced virulence in pathogen passaged through maladapted fly lines was confirmed by identifying different SNPs-related virulence factors' expression by whole genome sequencing. Taken together, this study suggests, that maladaptation leads to general stress response and is therefore beneficial against infection. However, that is restricted to certain life stages in fruit flies as it also facilitates disease transmission risk to uninfected individuals.

Poster by Joy Bose:

(9) The Evolution of Antibiotic Resistance in *Bacillus thuringiensis* hitchhikes the pathogenicity: A silent threat

Open category

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The discovery of antibiotics has substantial Implications and revolutionized global health in the 20th Century. The successful uses of antibiotics are not only limited to the treatment of bacterial, fungal, and parasitic infections but also to the treatment of chronic & life-threatening diseases such as cancer, diabetes, etc. Most importantly, antibiotics can be applied not only to treat humans rather to treat nearly all living entities on this earth. However, the other side of this successful story is indeed alarming. Precisely saying, extensive & unauthorized uses of antibiotics in human therapy, aquaculture, animal husbandry, and farming have imputed the emergence of antibiotic resistance in pathogens globally. Unfortunately, this scenario is not only limited to the uncontrolled use of antibiotics per se, raising demand for antibiotics resulting in substantial industrial production of diverse antibiotics, which in turn thrive mutation or horizontal gene transfer in pathogens to develop multiple mechanisms of resistance against each & every antibiotic used in practice. To date, various attempts have been made to develop strategies that encompass assessing molecular epidemiology, and biogeographical patterns, or introducing mathematical modeling to develop 'evolution-proof antibiotic'. However, to complete the restoration of therapeutic applications of antibiotics, there is a need to understand, under antibiotic selection how pathogens enhance their fitness, which is often mediated by modulating virulence levels to exploit host resources efficiently. In this study, we have merely explored (a) antibiotic resistance evolution & its underlying costs and (b) virulence hitchhiking, as one of the prime consequences of antibiotic resistance using the experimental evolution approach. To perform experimental evolution, we exposed *Bacillus thuringiensis* (Bt); ID:18246; against streptomycin antibiotic over 30 serial transfers across 8 independent lines. Respective control lines were maintained in parallel without antibiotic throughout the serial transfers (i.e., two regimes: control & antibiotic selected). As expected, we did identify a direct response to selection in the presence of antibiotic in terms of bacterial growth dynamics and colony number at the expense of fitness trade-offs for the same traits in the absence of antibiotic. Interestingly, evolved Bt lines demonstrated elevated virulence by exacerbating host fitness against *Caenorhabditis elegans* & *Drosophila*

melanogaster infections. Such elevated virulence of antibiotic-resistant in Bt lines across two distantly related phylum postulates a robust hitchhiking of virulence alleles that is contiguous to antibiotic resistance evolution. Taken together, our findings elucidate that in addition to epidemiological, molecular, & theoretical approaches in drug development, the evolutionary underpinning of pathogens' fitness needs to be appraised on a serious note to reverse the frightening trend of antibiotic resistance.

Talk by **Charles Cannon**:

(10) Quantifying the potential for future introgressive hybridization at continental and community scales among suites of interfertile species

Impact of introgressive hybridization on tropical diversification

Charles Cannon¹

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Introgressive hybridization (IH), where small fractions of the entire genome are shared among interfertile species through initial F1 hybridization and subsequent integration through backcrosses, is increasingly being detected in many different organisms. This natural process has played a significant role in the diversification of many major tropical lineages. Given the ecological and environmental settings of tropical forests, particularly for trees, the potential for IH is quite large. In species rich forests, where numerous interfertile species are sympatric in any one location, IH also creates a complex network of potential pathways for adaptive genes to be shared. One of the most likely ways isolated species become maladaptive is through the loss of critical function, through genetic drift, particularly if that function is only required sporadically over very long periods of time. Here, I discuss how existing geospatial data about species distributions can be used to explore and quantify the potential for IH among suites of interfertile species. These estimates and descriptors can be applied at various spatial scales using different approaches to characterize species distribution. Additionally, I discuss how the network properties of the syngameon (the suite of interfertile species) facilitates sharing of adaptive alleles and has synergistic effects of diversification capacity of a group. Given the rapid change in environmental conditions and the emergence of novel ecosystems, species will need to greatly accelerate their adaptive processes, precisely at a moment when most of these processes are being disrupted by human activity. The likelihood of IH will probably substantially increase during the Anthropocene, due to declining population sizes in each species, increased mobility among sites, and the increasing adaptiveness of transgressive or novel phenotypes in novel environments. Understanding the potential future dynamics of IH and the probable outcomes from the process given different assumptions are important questions for biodiversity conservation. Enabling the natural potential in IH may be one of the most effective means to sustain their adaptive capacity of threatened species.

Talk by **Tom Carney**:

(11) Identification of an intermediate fin in the median to paired fin transition

Early evolution of vertebrates from evo-devo and paleontological perspectives

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Paired appendages are considered to have evolved either from the gill arch or from paired lateral fin folds. Evidence for the latter has been derived from the shared structural and molecular features of the unpaired and paired fins, suggesting that the developmental program generating paired fins was co-opted from median fins during evolution. It is hypothesised that a lateral fin fold would have been an intermediate state between the two, but there is scant evidence for this in the fossil record or extant species. Furthermore, despite commonalities in development, median fins and paired fins derive strictly from distinct mesodermal compartments, namely paraxial and lateral plate mesoderm respectively. Thus, the fin developmental program must have been copied from the paraxial to lateral plate at some unknown point. Using a combination of RNA

in situ staining and transgenic cell lineage tracing methods we here show that fish surprisingly possess a lateral plate derived median fin and suggest that this fin is an intermediate in the median to paired fin transition. We show that this is conserved through evolution from cyclostomes to tetrapods, and further show by gene knockdown that it possesses latent and conserved capacity for being bifurcated into paired structures. Our work thus provides support for the lateral fin fold hypothesis.

Talk by **Carlos Manuel Herrera Castillo**:

(12) Investigating the causes of adaptation in three-spined sticklebacks (a spiny subject)

Genetics of adaptation and evolution of novel traits

Carlos Manuel Herrera Castillo¹

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The three-spine stickleback (*Gasterosteus aculeatus*) has been the focus of numerous studies exploring its response to changing environments. Phenotypic changes have been linked to its adjustments to diverse habitats. We specifically study two populations thriving in marine and acidic freshwater environments. The dominant marine phenotype possesses three dorsal spines and a fully developed pelvic girdle formed by pelvic spines, pelvic processes, and pelvic plates. In contrast, the most frequent acidic freshwater phenotype exhibits merely two dorsal spines and lacks pelvic structures. Our study's primary aim is to discern the loci accountable for these dual phenotypic traits and unravel the underlying developmental mechanisms. To achieve this, we execute a genome-wide association study to pinpoint the most distinct genomic regions in spined versus spineless fish. Our investigation uncovers two profoundly dissimilar regions: chromosome VI governing dorsal spines and chromosome XIV overseeing pelvic spines. Employing whole-mount skeletal and cartilage staining, we identify the developmental stages where the ontogeny of these two phenotypes diverges. Building on this knowledge, we analyse the RNA expression profiles of the regions of interest. As we refine our understanding of the causative loci and the developmental stages at which the divergence in the ontogeny of the distinct phenotypes occurs, we intend to conduct in-situ hybridisation experiments. Additionally, we will endeavour to induce changes using CRISPR-Cas9 to corroborate our findings within the framework of established protocols.

Poster by **Joshua Kevin Chang**:

(13) Mapping the sequence function relationship of UP and Dis promoter elements in bacteria promoters

Fitness landscapes bridge evolution and molecular biology

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Promoters are DNA sequences located upstream of genes, and their sequence composition influences their binding affinity with RNA polymerase, which determines the transcription rate. I aim to elucidate the sequence-function relationship of bacterial promoter elements, with particular interest on the upstream (UP) region and discriminator (Dis). The quantitative impact of both elements on promoter strength is poorly understood. I apply saturated mutagenesis and massively parallel reporter assays to characterize UP and Dis at high degree of resolution. I have successfully conducted a high-throughput characterization of the Dis element. Preliminary analysis shows that GC is more enriched in weaker variants while for stronger variants AT is more enriched. I have also performed in silico analyses on various bacterial species, such as *Escherichia coli*, and found that the same rules apply to most genes. This indicates that Dis element is optimized for high expression in *E. coli* genes. The insights gained from these experiments can be used to construct an in silico model for predicting and designing promoter functions

Talk by **Nontawat Chatthanabun**:

(14) Species and evolutionary relationships in the diverse bee genus of *Megachile*, Latreille, 1802 (*Megachilidae*: *Megachilini*) in Thailand

An evolutionary perspective on pollinator biodiversity, systematics, and conservation

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The evolutionary and phylogenetic relationships of the diverse and important crop-pollinated bees in the genus *Megachile* (*Anthophila*; *Megachilidae*) in Southeast Asia have never been explored, despite the abundant presence and wide distribution of the genus in the region. This study focuses on using the integrative taxonomic approach to resolve some evolutionary questions relating to the *Megachile* found in Thailand. 315 Thai *Megachile* specimens were examined, whereas 103 were used for molecular analyses. The initial COI phylogeny obtained from this study shows that most *Megachile* putative species are grouped within monophyletic clades suggesting congruence between the morphological and molecular evidence, whereas the relationships among the subgenera are unresolved due to low supporting values. The color patterns of the mesothoracic and metathoracic hairs overlapping among the subgenera are usually found in many sympatric species. This may suggest that the color patterns in Thai and possibly Southeast Asian *Megachile* may be driven by convergent evolution. Further studies using more genetic markers are expected to resolve other questions relating to sexual dimorphism and genetic variations among the wide spread species in *Megachile*.

Talk by **Balaji Chattopadhyay**:

(15) Diversification and complex patterns of introgression in Old World fruit bat

The genomics of adaptation and speciation

Balaji Chattopadhyay¹

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Bats are the second most specious group of mammals with a high cryptic diversity. Next-generation sequencing has revolutionized our understating of speciation and diversification patterns, especially in species complexes with rapid radiation. In this talk, I will discuss the diversification and speciation patterns of the widely distributed Old World fruit bat genus *Cynopterus*. This genus has undergone a recent radiation giving rise to multiple species which share broad sympatric zones across South and Southeast Asia. For this study, we generated about 1.5 MB of genome-wide DNA sequence data from close to 1000 loci from multiple species of *Cynopterus* bats across their distribution using sequence capture method. Phylogenetic reconstructions and tests for introgression revealed potential new species level lineages and rampant introgression between various sympatric lineages. This study highlights the role of gene flow in diversification and speciation.

Talk by **Nandita Chaturvedi**:

(16) Evolution of Populations in Heterogeneous and Dynamic Environments

Open category

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The question of adaptation to environmental change at long time scales remains an important area of theoretical investigation, but has been treated mainly in the context of single environments. However, organisms almost always deal with multiple environments and trade offs arising from them, in addition to the possibility of long term change. Here we combine the idea of repeated variation, heterogeneity, like seasonal

shifts, with long term and directional dynamics. To address this complex situation, we extend the framework of fitness sets and study how the optimal phenotype in this situation can itself change with long term shifts. We consider selection from two distinct environments. We find that the behavior of a population under such a system is qualitatively different and more complex than that of a population responding to long term change in a single environment. The chance of survival or extinction depends crucially on the relative frequency of the two environments, the strength and asymmetry of their selection pressure in addition to population size, phenotypic diversity, fecundity and the rate of change of the environment. We study characteristics of the population under selection such as its phenotypic lag behind the optimal phenotype and the mean time to extinction.

Talk by **Chhaya Chaudhary**:

(17) Marine species diversity in the recent past, present and future

Paleo- and macro- ecology in tropical Asia

Chhaya Chaudhary¹

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The literature has widely discussed latitudinal patterns in marine species richness and their origins, i.e., the richness peaks at low latitudes and declines with increasing latitude. The tropics have always accommodated the highest biodiversity and harbours maximum unique bioregions at present. The deviation from unimodality to bimodality in richness, with a dip at the equator and peaks in sub-tropics, under climate warming has been recently reported. This talk discusses the change in the bimodal pattern resulting from the widening of the equatorial dip and northward shift (richness) in the northern hemisphere since the 1980s. The shift is in line with the increasing temperature over time, suggesting that the tropics are too warm for species to survive, and species are tracing their habitat in cooler waters. Species richness across latitudinal bands was sensitive to temperature, reached a plateau or declined above a mean annual sea surface temperature of 20 °C for most taxa. The paleo data also observed the equatorial dip during mass extinction under extremely high temperatures. Using species-specific global climate suitability models (of corals, molluscs, fish, crustaceans, and polychaetes- representing coral reef ecosystem), the potential coherence and differences and their cumulative impact on the ecosystem under present and future climate scenarios (RCP 4.5 and 8.5) were assessed. Under a warming future, nearly 90% of 30 warm-water species would coherently lose their suitability in the parts of the Indo-west Pacific, the Coast of Northern Australia, the South China Sea, the Caribbean Sea, and the Gulf of Mexico. Irrespective of their taxonomic group, the species with wider distribution ranges (thermal and geographic) will gain higher suitability than their stenothermal counterparts, suggesting an increase of generalist species and a decline of specialist (endemic) species of the ecosystem. This indicates local mass extinction risk in native habitats and a high species turnover across the ecosystem. Such changes may destabilise predator–prey dynamics in the ecosystem, especially if foraging specialists dominate coral food webs and adversely affect the associated countries. As the prediction models plays a crucial part in the strategic planning of marine biodiversity resources, they must be improved to assess the risk more accurately. One important aspect of the improvement is the inclusion of life stage bottlenecks. Tropical fish spawners, comparably vulnerable life stage than adults, are already facing temperatures closer to their thermal maxima, coinciding with the equatorial dip. Another bottleneck is the younger life stages, which serve as a primary diet component in marine ecosystems, are more sensitive to extreme temperatures than adults. Such life stage bottlenecks would restrict species' overall thermal and geographical range. One crucial part that is currently missing in the prediction models is the inclusion of life-stage bottlenecks, including this information in the models is expected to improve their robustness.

Talk by **Jing Che**:

(18) Adaptive evolution of amphibians and reptiles on the Qinghai-Tibetan Plateau (QTP)

Behavioral evolution in vertebrates: diversity, genomics and mechanisms

Wei Gao¹ and Jing Che²

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The Qinghai-Tibetan Plateau (QTP) is known as the Roof of the World, with an average altitude of 4,000 meters. Compared with low-elevation taxa, those species occurring on such high elevation experience extreme environmental conditions such as hypoxia, low temperatures and strong ultraviolet (UV) radiation. How these organisms adapt to the extreme environment of QTP has received great interests worldwide. Herein, we show that how the frogs (Amphibia, Dicroglossidae, Nanorana) and lizards (Reptilia, Agamidae, Phrynocephalus) have evolved a series of phenotypic, physiological and behavioral adaptations to counter the harsh condition on the QTP, i.e., the transition from oviparity to viviparity along the altitudes rises and the UV defense. By integrating omics data with functional validation research, we discovered genes related to UV defense and a corresponding temporal expression pattern in *N. parkeri*. Multiple defense genes (i.e., TYR for melanogenesis) exhibit positive selection with function-enhancing substitutions. By comparing differences in gene expression during the reproductive cycle, we revealed that the genetic basis of the evolution in reproductive behavior from oviparity to viviparity involved temporal and spatial changes in expression of appropriate genes (i.e., ESR1, PTGS2) that account for eggshell reduction or degeneration, placental development, delayed oviposition. Our work offers an improved understanding of evolution of organisms on the Roof of the world.

Poster by **Bingjie Chen**:

(19) Contribution of pks+ E. coli mutations to colorectal cancer evolution

Open category

Bingjie Chen¹

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The dominant mutational signature in colorectal cancer genomes is C>T deamination (COSMIC Signature 1) and, in a small subgroup, mismatch repair signature (COSMIC signatures 6 and 44). Mutations in common colorectal cancer driver genes are often not consistent with those signatures. Here we performed whole-genome sequencing of normal colon crypts from cancer patients, matched to a previous multi-omic tumour dataset. We analysed normal crypts that were distant vs adjacent to the cancer. In contrast to healthy individuals, normal crypts of colon cancer patients have a high incidence of pks+ (polyketide synthases) E.colimutational and indel signatures, and this is confirmed by metagenomics. These signatures are compatible with many clonal driver mutations detected in the corresponding cancer samples, including in chromatin modifier genes, supporting their role in early tumourigenesis. These results provide evidence that pks+ E.coli is a significant driving force of carcinogenesis in the human gut evolution. dominant mutational signature in colorectal cancer genomes is C>T deamination (COSMIC Signature 1) and, in a small subgroup, mismatch repair signature (COSMIC signatures 6 and 44). Mutations in common colorectal cancer driver genes are often not consistent with those signatures. Here we performed whole-genome sequencing of normal colon crypts from cancer patients, matched to a previous multi-omic tumour dataset. We analysed normal crypts that were distant vs adjacent to the cancer. In contrast to healthy individuals, normal crypts of colon cancer patients have a high incidence of pks+ (polyketide synthases) E.colimutational and indel signatures, and this is confirmed by metagenomics. These signatures are compatible with many clonal driver mutations detected in the corresponding cancer samples, including in chromatin modifier genes, supporting their role in early tumourigenesis. These results provide evidence that pks+ E.coli is a significant driving force of carcinogenesis in the human gut evolution.

Poster by **Baohua Chen**:

(20) Genomic Signatures of Selection Reveal the Impact of Climate Change on Large Yellow Croaker Populations in the South China Sea

Fitness landscapes bridge evolution and molecular biology

Baohua Chen¹ and Peng Xu²

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The large yellow croaker (*Larimichthys crocea*) is one of China's most economically valuable marine fish. Its stock division and distribution have been debated since the 1960s due to their implications for ecological protection, germplasm recovery, and fishery resource management. In this study, we aimed to investigate the current population structure and habitat division of large yellow croaker populations living in the South China Sea using genomic signatures of selection. We built a fine-scale genetic structure of large yellow croaker populations distributed along the eastern and southern Chinese coastline based on 7.64 million SNP markers. Compared with the previous Daiqu-Minyuedong-Naozhou division system proposed in the 1960s, our results revealed a climate-driven habitat change probably occurred between the Naozhou (Nanhai) Stock and the Min-yuedong (Mindong) Stock. The boundary between these two stocks' habitats might have shifted northwards from the Pearl River Estuary to the northern area of the Taiwan Strait, accompanied by highly asymmetric introgressions. In addition, we found two divergent landscapes of natural selection existed in different stocks living in north and south areas. The northern population suffered highly-gathered and strong natural selection around developmental-process-related genes, which may help them exploit the rare growing periods efficiently. Meanwhile, we detected moderate and interspersed selective signatures from the southern populations. Moreover, many immune-related genes were associated with these signals, which aid in the adaptation to a high-pathogen-density warm environment. Our results provide new insights into the evolutionary history and adaptation of this species and have implications for its conservation and management. We hope that our findings will contribute to a better understanding of large yellow croaker populations living in the South China Sea and inform future research on this important species.

Talk by **Donglei Chen**:

(21) The first record of structurally preserved Devonian tetrapod skin.

Early evolution of vertebrates from evo-devo and paleontological perspectives

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Although the timing and speed of terrestrialization within the broader process of the fish-tetrapod transition is debated, it eventually produced fully terrestrial vertebrates. This placed new functional requirements on the skin, and it is self-evident that the transformation of the skin must have been a very important part of the fish-tetrapod transition. However, until now there has been no direct evidence at all for the condition of the skin in stem tetrapods or related fossil fishes such as elpistostegians. A comparison between extant bony fish and tetrapods shows that all tetrapods have a keratinous outer layer on the epidermis, which is absent in fish; conversely, mucous and granular glands are present in fish and amphibians, but not in amniotes. This indicates that a keratinous layer must have evolved within the tetrapod stem group, while mucous and granular glands were retained. However, this phylogenetic bracket does not predict the character of stem tetrapod skin very precisely. In particular, it cannot answer whether it resembled the thin and well-vascularized skin of modern lissamphibians, which is adapted for cutaneous respiration. We present here the first example of three-dimensionally and structurally preserved skin from a Palaeozoic tetrapod. It derives from a new locality in the latest Famennian (latest Devonian) of East Greenland, yielding a unique fossil assemblage with exceptional

preservation including, in some cases, cellular-resolution soft-tissue preservation. The preserved skin comes from an essentially articulated but somewhat disturbed area of tetrapod belly scales and tail lepidotrichia, representing the ventral surface of the abdomen of a stem tetrapod. Apparently, the skin adhered to the mud, remaining while most of the body washed away. During collection the blocks split just above (=internal to) the level of the scales, leaving the skin preserved on the surface of thin counterslabs. These have been imaged with synchrotron microtomography at ESRF, with a voxel size of 1.72 μm . The skin is strikingly thick: the layer external to the squamation is up to 600 μm in thickness. For comparison, in a frog the entire skin is typically only 40-200 μm thick. The external surface carries robust papillae, about 2 mm long and spaced approximately the same distance apart. The interior of the skin contains preserved cellular-scale histology, including aligned 3D spaces of columnar or cuboidal secretory cells that may have formed lumens or acini of glands, as well as associated muscle fibres and probable capillaries. This glandular level must be part of the dermis, but the overall interpretation of the skin hinges on whether the epidermis is preserved. If it is preserved, the aforementioned papillae are features of the skin surface; if it is lost, it could have been quite thick, and the papillae may have been sub-surface structures like the papillate dermis-epidermis boundary of mammals. Further scans at sub- μm resolutions, which will reveal more of the cellular architecture, should allow us to answer this question. However, it is already clear that the skin was much thicker than modern amphibian skin, which must reflect functional differences.

Poster by **Guangji Chen**:

(22) Adaptive expansion of ERVK solo-LTRs in accompanying with Passeriformes speciation

The genomics of adaptation and speciation

Guangji Chen¹, Dan Yu², Yu Yang³, Xiang Li⁴, Xiaojing Wang⁵, Danyang Sun⁶, Yanlin Lu⁷, Rongqin Ke⁸, Jie Cui⁹, Guojie Zhang¹⁰, and Shaohong Feng¹¹

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Endogenous retroviruses (ERVs) are residues of ancient viral infections in host genomes. In the absence of selection pressures to maintain their components intact, ERVs are commonly deleted through unequal homologous recombination between two flanking long terminal repeats (LTRs). This process leaves residues of solitary LTRs (solo-LTRs) in a host's genome. We detected and compared the composition of solo-LTRs in 362 bird species and their outgroups in reptiles and mammals. We discovered a substantially higher frequency of solo-LTRs in bird genomes than in mammals and reptiles, indicating strong selective pressures to purge ERVs from bird genomes. Most strikingly, in the diverse bird order Passeriformes, and especially in the parvorder Passerida, endogenous retrovirus-K (ERVK) family solo-LTRs showed bursts of formation and recurrent accumulation that corresponded to speciation events during the past 22 million years. Moreover, our results indicate that the continuous expansion of ERVK solo-LTRs is still an ongoing process in these bird species in confronting the high transcriptional activity of ERVK retroviral genes in their reproductive organs, resulting in high variation of solo-LTRs between individuals of zebra finches, a representative species under Passerida. Interestingly, we found that specific ERVK solo-LTRs contain cis-elements with potential regulatory functions. We experimentally demonstrated that the promoter activity of recently evolved ERVK solo-LTRs in the zebra finch leads to significantly higher expression of the ITGA2 gene in the high vocal center (HVC) and robust nucleus of the arcopallium (RA) regions of this species compared to an ortholog in chicken. These findings suggest that the expansion of solo-LTRs may introduce novel genomic sequences that serve as cis-regulatory elements to host genomes and enhance regulatory networks, contributing to adaptive evolution. These

findings underscore that the residual sequences of ancient viruses can influence the adaptive diversification of species by regulating gene expression.

Talk by **Sean Chun-Chang Chen**:

(23) Comparative Genomics of the Arthropoda

Novel insights regarding genome architecture evolution in the arthropoda

Sean Chun-Chang Chen¹ and Carol Eunmi Lee²

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The phylum Arthropoda is the largest and most diverse group of animals on the planet, representing about 80% of all known animal species, encompassing spiders, crustaceans, insects, and numerous other species. However, comparative genomic studies within the subphylum Pancrustacea have focused predominately on the insect clade (Hexapoda). As such, we lack a clear understanding of what constitutes an “insect” versus a “crustacean” genome relative to other arthropod subphyla. Here, we present our preliminary analyses on the characteristics of arthropod genomes. We analyzed 75 Arthropod genomes (15 Chelicerates, nine Myriapods, and 51 Pancrustacean genomes), along with two Tardigrade outgroups. We found intriguing differences in genomic characteristics among arthropods. First, high AT-richness across all arthropod subphyla was found. While insect genomes had been noted for being AT-rich, we found that genomes of chelicerates (minus the parasitiforms) were even more AT-rich, and crustaceans significantly less so. This pattern was particularly true for non-coding DNA sequences, but much less so for coding sequences. The fact that non-coding sequences tended to be far more AT-rich than coding sequences for all arthropod subphyla suggests that neutral processes drive the AT-richness in arthropod genomes, while purifying selection suppresses the AT-richness in coding sequences. Second, chelicerates showed an inverse relation between genome size and AT-richness of the 3rd codon. In contrast, crustaceans and insects exhibited positive relationships. AT-richness and genome size have been found to be negatively correlated in some taxa, including in specific bacterial phyla, but the pattern varies considerably in animals. Third, gene families specific to insects alone include odorant binding proteins and odorant receptors, potentially related to terrestrial colonization by insects. We also annotated previously unknown crustacean gene families and elucidated evolutionary patterns of several gene families related to environmental adaptation. Our results are a first step toward revealing the evolutionary forces that shape the genome architectures of arthropod lineages and uncovering the association with ecological factors.

Talk by **Ying Chen**:

(24) Variation in deleterious mutation load in nine-spined stickleback (*Pungitius pungitius*) populations

Open category

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The theory predicts that natural selection is effective in removing deleterious mutations from large outbred populations whereas small population isolates may accumulate them due to increased genetic drift and/or inbreeding. We assessed the frequency and genomic distribution of deleterious mutations in 17 wild nine-spined stickleback (*Pungitius pungitius*) populations differing in their effective population sizes. Using whole-genome resequencing data (10-20X) for 363 individuals and the program SnpEff we annotated SNP variants and predicted their effects on protein-coding sequences, categorizing mutations as putative high, moderate, or low-level deleterious mutations. We compared the frequency of putative deleterious alleles between populations and investigated the influence of demographic history and population isolation on the accumulation of putative deleterious mutations. Preliminary results indicate a significantly lower frequency of putative

deleterious mutations in populations with high contemporary effective population sizes both for homozygous and heterozygous mutations, suggesting that deleterious mutations have been efficiently removed by purifying selection from larger populations. As expected, drift load (fixed homozygous mutations) was higher in pond (smaller N_e) than marine populations. The majority of putative deleterious mutations were unique to given pond population, indicating that the accumulation of deleterious mutations has occurred independently in each population rather than in their common ancestor.

Talk by **Charleston Chiang**:

(25) A genealogy-based framework to estimate population structure and demographic history

Genomic diversity in nonequilibrium populations

Charleston Chiang¹

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Learning the demographic histories of nonequilibrium populations helps us understand the causes of population structure, the pattern of genetic variation, and the evolution of traits. Many existing methods to infer population structure or demographic history from genetic data use relatively low-dimensional summaries, such as the allele frequency spectra, which often ignore the linkage information between markers. In principle, much more information is available from the sequence of gene-genealogical trees, known as the ancestral recombination graph (ARG), that describes the history of sampled alleles. As a step toward capturing all the available genomic information, we introduce two methods that leverage the ARG to infer population structure and demographic histories. First, we describe a framework to infer the expected relatedness between pairs of individuals given an ARG of the sample, which we call the eGRM. We show that the eGRM better captures the structure of a population than the canonical Genetic Relationship Matrix (GRM), even when using limited genetic information found on a genotyping array. Moreover, the eGRM can reveal the time-varying nature of population structure in a sample. Second, we devised a method called gLike that derives the full likelihood of a genealogical tree under any hypothesized demographic history. Employing a graph-based structure, gLike summarizes the relationships among all lineages in a tree with all possible trajectories of population memberships through time and efficiently computes the exact marginal probability under a parameterized demographic model. Through extensive simulations of multiple admixtures, we showed that gLike accurately estimates dozens of demographic parameters, including ancestral population sizes, admixture timing, and admixture proportions, and outperforms conventional demographic inference methods that leverage only the allele frequency spectrum. We applied both methods to real-world human genomic data from Finnish, Latino American, and Native Hawaiian cohorts to gain further insights into the patterns of population structure and to estimate parameters of the admixture histories. Taken together, our studies demonstrate the power of leveraging the genealogical trees for downstream population genetic inferences.

Talk by **Lars Chittka**:

(26) The Mind of a Bee

The evolution of invertebrate sensory ecology and behaviours

Lars Chittka¹

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Most of us are aware of the hive mind—the power of bees as an amazing collective. But do we know how uniquely intelligent bees are as individuals? I argue that they have remarkable navigational abilities, can recognize not just flowers but also human faces, exhibit basic emotions, count, use simple tools, solve problems, and learn by observing others. They may even possess consciousness. I illustrate how bee brains are unparalleled in the animal kingdom in terms of how much computing power is packed into their tiny nervous systems. I examine the psychological differences between individual bees and the ethical dilemmas that arise in conservation and laboratory settings because bees might feel and think.

Talk by **Hugo Darras**:

(29) Crazy reproduction in crazy ants

Why sex? insights from asexual genomes

Hugo Darras¹

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Ant societies are characterized by a reproductive division of labor and haplodiploid sex determination mechanism. In most species, females are produced by sexual reproduction and develop into queens or workers depending on environmental factors, while males develop from unfertilized, haploid eggs. The combination of eusociality and haplodiploidy has, however, led to the emergence of unusual reproductive strategies in several ant taxa. In the longhorn crazy ant, *Paratrechina longicornis*, our analyses revealed that all queens and males around the globe belong to two separate, non-recombining clonal lineages. Queens are clones of their mothers, while males are clones of their fathers. By contrast, workers are all first-generation inter-lineage hybrids. This unusual genetic system may have pre-adapted this invasive ant for global colonization by maintaining heterozygosity in the worker force, thus alleviating genetic bottlenecks. We recently discovered another unique reproductive system in the yellow crazy ant, *Anoplolepis gracilipes*. Males of this species are all chimera of haploid cells from divergent lineages. Chimerism occurs when parental nuclei bypass syngamy and divide separately within the same egg. When syngamy occurs, the diploid offspring either develops into queen or worker females depending on the genotype of the sperm. Genetic analyses suggest that this unusual mode of reproduction is probably the result of a genetic conflict between a bisexual lineage and an androgenetic lineage.

Poster by **Tong Deng**:

(30) Ultra-micro evolution against the backdrop of macro-evolution, a perspective from positive selected sites.

Open category

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Tumorigenesis has been widely recognized as an evolutionary process, with distinct characteristics and attributes compared to species evolution. With the extensive tumor sequencing data, we are now able to explore the genomic features of cancer populations site by site. Recently, we have discovered some mutations that recurrently appear in cancer populations and cannot be explained by natural mutation rates alone. We refer to these mutations as cancer driving nucleotides (CDNs), which may be positive selected and play a significant role in tumorigenesis. Simultaneously, we analyzed the CDNs in the context of species evolution, and found that these CDNs (sites), especially those with ultra-high mutation hits in cancer populations, are quite conservative in vertebrates, implying their involvement in crucial biological functions.

Poster by **Guohua Ding**:

(31) Female preference for size-matched males in an assortative mating frog: evidence from acoustic playback experiments

Behavioral evolution in vertebrates: diversity, genomics and mechanisms

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Abstract: Amplexus is a distinctive mating strategy in the reproductive life cycle of amphibians, encompassing both assortative and random mating strategies. Prior to amplexus, male frogs commonly emit acoustic signals to attract females, emphasizing the significant role of acoustic communication in the anuran reproductive process. However, it has remained unclear whether males' acoustic signals significantly affect the female choice of male size. In our study, we examined the mating strategy of a paddy frog, *Fejervarya multistriata*, and whether females can use acoustic signals to locate appropriately sized males. This investigation entailed an examination of the relationships between amplexus pairs' sizes, the acoustic properties of male frogs, and phonotaxis experiments. The results showed that: (1) *F. multistriata* employed size-assortative mating as a reproductive strategy. (2) The first frequency band and note interval in male advertisement calls can serve as key indicators of individual male size. (3) Through phonotaxis experiments, female frogs preferred acoustic signals that matched male size. Therefore, we suggested that *F. multistriata* females can use acoustic signals to select size-matched males, thus achieving assortative mating. **Keywords:** acoustic properties; assortative mating; *Fejervarya multistriata*; female mate-choice; male size

Talk by **Bing Dong**:

(32) Kin selection as a modulator of human handedness: sex-specific, parental and parent-of-origin effects

Open category

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The frequency of left-handedness in humans is ~10% worldwide and is slightly higher in males than females. Twin and family studies estimate the heritability of human handedness at around 25%. The low but substantial frequency of left-handedness has been suggested to imply negative frequency-dependent selection, e.g. owing to a “surprise” advantage of left-handers in combat against opponents more used to fighting right-handers. Because such game-theoretic hypotheses involve social interaction, here, we perform an analysis of the evolution of handedness based on kin-selection, which is understood to play a major role in the evolution of social behaviour generally. We show that: (1) relatedness modulates the balance of right-handedness versus left-handedness, according to whether left-handedness is marginally selfish versus marginally altruistic; (2) sex differences in relatedness to social partners may drive sex differences in handedness; (3) differential relatedness of parents and offspring may generate parent-offspring conflict and sexual conflict leading to the evolution of maternal and paternal genetic effects in relation to handedness; and (4) differential relatedness of maternal-origin versus paternal-origin genes may generate intragenomic conflict leading to the evolution of parent-of-origin-specific gene effects—such as “genomic imprinting”—and associated maladaptation.

Talk by **Bo Dong**:

(33) Spatially-resolved single-cell atlas of ascidian endostyle provides insights into the origin of vertebrate pharyngeal organs

Marine evo-devo: new frontiers from emerging marine model organisms

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The pharyngeal endoderm, an innovation in deuterostome ancestors, functions as a pharyngeal developmental major player that orchestrate the formation of different germ layers and multiple pharyngeal derivatives in vertebrates. However, the evolutionary origin of multiple pharynx organs in vertebrates remains largely unknown. The endostyle, a distinct pharyngeal organ exclusively presents in basal chordates, represent a good model in understanding the origin of pharyngeal organs. Here, utilizing cutting-edged Stereo-seq and single-cell RNA-seq, we constructed the first spatially-resolved single-cell atlas in the endostyle of ascidian, *Styela clava*. The spatial location of Stereo-seq and high capture efficiency of single-cell RNA-seq complement each other to ensure the high quality of the atlas. We comprehensively resolved the cellular composition of hemolymphoid region (HLR), which harbors immune and blood cell lineages, illuminating a mixed ancestral structure for blood and lymphoid system. Additionally, we discovered a hair cell-like cell (HCLC) cluster in zone 3, which shares homologous features with vertebrate acoustico-lateralis system hair cells, and the results were further validated by in situ hybridization of cell-specific markers, electronic microscopy and cross-species comparison. These findings reshape the understanding of the pharynx of basal chordate and provide clues for the evolutionary origin of multiplexed pharyngeal organs.

Talk by **Philip Donoghue**:

(34) Origin and early evolution of vertebrates

Early evolution of vertebrates from evo-devo and paleontological perspectives

Philip Donoghue¹

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The question of which group of spineless relatives the ancestry of the vertebrates is to be found within has been a popular scientific parlour game since the formalization of evolutionary theory. Scope for controversy has narrowed dramatically with the availability of molecular data for phylogenetic analysis in genomic depth and taxonomic breadth, as well as the discovery and reinterpretation of key fossils that evidence the origin of the fundamental bodyplans of vertebrates. It now appears impossible to recover anything other than tunicates as the sibling lineage of the vertebrates and cyclostome monophyly. However, despite widespread perception to the contrary, the interrelationships of fossil invertebrate chordates, early vertebrates and their living relatives, remain poorly resolved or supported. This is of consequence since understanding of the relationship between phenotypic, developmental and genome evolution depends critically upon how knowledge of the timing and sequence of assembly of bodyplan characteristics preserved in the fossil record. Recent work, stimulated by annotation of a hagfish genome, has allowed us to constrain not only the timing and tempo of early vertebrate evolution, but also that of the whole genome duplication events that characterize this formative episode in our own evolutionary history. Integrating evidence from living and fossil vertebrates it is clear that not all such genomic events are imbued with the same evolutionary potential and we explore why the evolution of jawed vertebrates has been so different from their jawless and spineless kin.

Talk by **Mark Elgar**:

(35) Natural and sexual selection pressures influencing chemical sensory morphology in insects

The evolution of invertebrate sensory ecology and behaviours

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Many animals, but especially insects, monitor their environment through the perception of chemical signals and cues, which can provide vital information, including the location of food resources, oviposition sites or reproductive partners. This form of communication differs from other modalities in a crucial way: detection of the signal or cue requires a physical interaction between the odorant molecule and the odour receptor. The

receptors used to detect these odours are mostly located on sensilla that are supported by the antennae. The diverse morphologies of insect antennae and the sensilla they support are both astonishing and puzzling: what selective pressures are responsible for these morphologically different solutions to the same problem — to perceive signals and cues? Here, I discuss the natural and sexual selection pressures that act on the number of sensilla supported by the antennae. These pressures are likely balanced against the costs of producing and receiving chemical signals. While these questions address fundamental issues, there are more practical insights: air pollution dramatically compromises the capacity of insects to detect odours, and so perhaps contributes to their global population decline.

Poster by **Takako Fujichika**:

(36) Geographical variation of reproductive diapause in *Drosophila triauraria* populations from Japan

Open category

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Seasonal adaptation is essential for insects to expand their habitat. Some insects that overwinter in the temperate zone to the subarctic zone induce a physiological state called reproductive diapause to adapt to the winter season. The insects that induce reproductive diapause for overwintering suppress the development of eggs or sperm in their reproductive organs. These insects are likely to be sensing the changes in temperature and day length as signals to determine the timing of diapause induction. Short-day conditions could allow insects to predict seasonal changes and induce diapause at optimal timing, depending on the latitude. In general, temperature affects photoperiodic responses. Thus, it is likely to interact with day length to determine the timing of diapause. *Drosophila triauraria*, as well as some other species of *Drosophila*, has been observed to induce reproductive diapause for overwintering in the field. A previous study reported that the isofemale strain of *D. triauraria* from a high-latitude locality (42.0°N, 140.4°E) in northern Japan induced reproductive diapause in a short-day condition. However, two strains from southern Japanese islands (27.2°N, 128.3°E and 26.2°N, 126.5°E) did not. These results have suggested that *D. triauraria* is adapted to the regional climate. However, comparing the diapause conditions of only those strains does not tell us how this species has genetically adapted to winter in a wide range of latitudes. Therefore, it is necessary to examine the diapause conditions and to perform genomic analyses using strains from various localities of the Japanese archipelago. In this study, we first investigated the diapause phenotype in the females of 21 strains originating from various localities under long- and short-day photoperiod at 12°C, which is just above the critical temperature for growth. The strains originated from mid-latitude localities (36.1°N, 140.1°E to 31.5°N, 131.3°E) induced reproductive diapause regardless of the day length. In contrast, the strains from southern islands did not induce reproductive diapause regardless of the day length. Interestingly, the strains from high-latitude localities (42.6°N, 141.6°E to 42.0°N, 140.4°E) went into reproductive mode under the long-day photoperiod, while they induced diapause under the short-day condition. These results indicate that the response of this species to low temperature and day length differs significantly among regional populations. The strains from northern Japan may be adapted to take an opportunity to reproduce even at a low temperature if the day length is long. Thus, the critical photoperiod to induce reproductive diapause at a given temperature may vary among the regional populations. Next, we compared the genomes of all strains to investigate the genomic regions involved in geographical variation in reproductive diapause. The analyses revealed that the degree of divergence between regional populations is small even though the genetic variation for the diapause trait is differentiated. We also found that some genomic regions are highly differentiated between the strains from low-latitude island populations that did not induce diapause and those from the rest that induced diapause at 12°C.

Talk by **Zhikun Gai**:

(37) The origin of the gnathostome body plan: how the Evo-Devo models intersect with ostracoderm fossils

Early evolution of vertebrates from evo-devo and paleontological perspectives

Zhikun Gai¹ and Philip Donoghue²

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The assembly of the gnathostome body plan has been interpreted as a serial sequence of evolutionary and developmental innovations over the fundamental vertebrate body plan shared with cyclostomes. However, divining their evolutionary origins is more challenging because the fundamental lineages of living vertebrates, the gnathostomes (jawed vertebrates) and cyclostomes (jawless vertebrates) are extremely divergent, relying heavily on insights from developmental models, such as through comparative analyses of craniofacial development from hagfishes, lampreys and jawed vertebrates. Nevertheless, there is a rich fossil record of jawless vertebrates known as the ostracoderms, from the Ordovician to Devonian periods (from 538 to 365 million years ago). The ostracoderms are related by degree to the living jawed vertebrates that effectively record the sequential evolution of the gnathostome bodyplan. In the past twelve years, some major morphological transitions from jawless to jawed vertebrates have been revealed by discoveries of extinct galeaspid ostracoderms from China, which have provided corroborative evidence for models of developmental evolution. For example, using synchrotron radiation X-ray tomographic microscopy, we have shown that the paired nasal sacs and hypophyseal duct in galeaspid Shuyu are independent of each other, as in gnathostomes but cyclostomes or the osteostracan ostracoderms, which is the condition that current developmental models regard as a pre-requisite for the development of jaws. The first articulated galeaspid remains of *Tujiaaspis* from the Silurian of China, reveal a pair of skeletal ventrolateral fins, which are compatible with aspects of the fin-fold hypothesis for the origin of vertebrate paired appendages. Here, we further show that the prechordal cranium and all of the gill arches (splanchnocranium) including mandibular and hyoid arches in galeaspid are incorporated medially into the parachordal cranium to form a single massive endoskeletal ossification. This pattern is compatible with aspects of the intermediate stage of branchiomere development in gnathostomes in which neural crest cells have a specific median relocation to form a cylindrical wall surrounding a mesodermal core. A hollowed cylinder-shaped branchial chamber enclosing gills and their associated musculature and vessels are widely seen in Silurian-Devonian armored ostracoderms (e.g. osteostracans, heterostracans). Therefore, the cylindrical branchial chamber in jawless ostracoderms probably represents an intermediate condition between the lateral in lampreys and medial location of gill arches in jawed vertebrates.

Talk by **Jiansi Gao**:

(38) Quantifying and improving Bayesian phylogenetic inference of large viral dataset

Virus evolution: from basic research to public health applications

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Phylogenetic analysis of large genomic dataset has been key for elucidating the evolutionary and transmission dynamics of pathogens. The results of such phylodynamic analysis have featured prominently in the decision-making process during the pandemic, leading to the dynamic enactment of effective surveillance and intervention strategies in real time. Bayesian phylodynamic methods stand out thanks to their capability of employing complex models, expressing uncertainties, and incorporating various sources of information. However, the computational complexity of these methods often hinders their application on analyzing modern large-scale viral dataset. Here, we provide empirical evidence demonstrating that: 1) the computational difficulties largely stem from inefficient exploration of the phylogenetic tree space; 2) despite good performance in estimating the continuous parameters, convergence and mixing issues are widespread in tree inference; 3) these striking tree-inference issues are frequently caused by a small number of clades that are challenging to sample under the conventional scheme; 4) a limited number of sites in the genome alignment,

which frequently exhibit conflicting phylogenetic signal, can significantly exacerbate the tree-inference issues, and fortunately; 5) the inferred molecular evolutionary and demographic processes are minimally affected by the poor exploration of tree space, whereas impacts on the estimated origin time and introduction history of particular clades appear to be more pronounced. We offer theoretical explanations underlying the observed difficulties in exploring tree space, identify specific biological properties of viral datasets that may impede the exploration, and propose new sampling mechanisms targeting these properties to improve the performance.

Talk by **Kritika M. Garg**:

(39) Impact of Quaternary glacial cycles on avifauna in Southeast Asia

Impact of introgressive hybridization on tropical diversification

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The past 2.6 million years, earth has undergone periodic cycles of cooling and warming. Known as the Quaternary glacial cycles, these periodic fluctuations in global climate have been responsible for biotic diversification across the globe. During the cooling phase of the glacial cycles, water is locked up as ice at the poles, leading to a drop in sea levels and the formation of land bridges across islands. These land bridges allow for gene flow between isolated island populations and can have a varied impact on demography and speciation patterns, depending on the species biology. In this talk, I will discuss the impacts of the Quaternary glacial cycles on gene flow and divergence of two understory babblers commonly found across the forests of Southeast Asia. We leverage the important museum collections of these babblers from remote islands in Southeast Asia to understand the genomic affinity of these isolated populations. Our analyses suggest that Quaternary land bridges and paleo-rivers shape the population structure of birds on the remote islands in Southeast Asia.

Poster by **Zanke Gong**:

(40) An epidemiological model of SARS-CoV-2 give us insight into a previously unseen pattern of evolution

Virus evolution: from basic research to public health applications

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SARS-CoV-2 has caused a worldwide pandemic since January 2020. Through the huge amounts of genomic data generated by the sequencing of SARS-CoV-2, we are seeing several astonishing and puzzling evolutionary phenomena, including the continual replacement of dominant variants. This phenomenon hints at a new pattern of evolution that we have not been able to see in traditional evolutionary studies due to sample size limitations, namely, that a set of mutations which has been successful in the past can eventually fail. But the prevalence of variants prior to Omicron was low (Delta was about 1%), why can't the population accommodate more than one variants at the same time? Given the consistency of this pattern throughout the evolution of SARS-CoV-2, a general driving force is likely to exist. We focus on population exposure, a factor inherent in the spread of the virus, and model the transmission dynamics. We assume two variants with different infectivities circulating in a naive population. We find that when the number of exposures of susceptible population is greater than 1, these two variants compete with each other and cause substitution to occur. Though outnumbered, the strong variant may eventually beat the increasing dominant weak variant due to its high probability of infection in a single exposure. The exposure times of susceptible individuals actually reflect the overlap of the two transmission chains in the population. As exposure increases, person-to-person contact

increases, the two variants become more disruptive to each other's transmission, and competition between them becomes more intense. The overall low prevalence is only indication of the number of people infected, in this scenario, many uninfected individuals have also been exposed to the virus and provide an implicit platform for virus substitution. The results suggest that the exposure process shapes the current evolutionary pattern of SARS-CoV-2 in some way. Different sets of mutations lead to the gap in the selection advantage of different variants, and variants with greater transmission advantages are constantly selected. Understanding this fundamental phenomenon of variants substitution can give us insight into other doubts about the evolution of SARS-CoV-2 and other species. Beyond that, an emphasis on viral exposure allows us to better optimize our public health policy to respond to such serious emergencies in future.

Talk by **Zhen Gong**:

(41) The origin and evolution of a plant resistosome

Open category

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The NLR protein ZAR1 interacts with ZRKs and PBLs to form a pentameric resistosome, triggering immune responses. Here, we show that ZAR1 emerged through gene duplication and ZRKs derived from cell surface immune receptors WAKs through losing extracellular domain before the split of eudicots and monocots in the Jurassic. Many angiosperm ZAR1 orthologs, but not ZAR1 paralogs, are capable of oligomerization in the presence of AtZRKs and triggering cell death, indicating the functional ZAR1 resistosome might have originated during the early evolution of angiosperms. Surprisingly, inter-specific pairing of ZAR1 and AtZRKs often results in the formation of resistosome in the absence of pathogen stimulation, suggesting a with-in-species compatibility between ZAR1 and ZRKs as a result of co-evolution. Numerous concerted losses of ZAR1 and ZRKs occurred in angiosperms, further supporting the ancient co-evolution between ZAR1 and ZRKs. Our findings provide insights into the origin of new plant immune surveillance networks.

Talk by **Toni Gossmann**:

(42) Long-term selection on mitocoding genes buried in mammalian and avian nuclear genomes

The genomics of adaptation and speciation

Toni Gossmann¹

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Sporadically genetic material that originates from an organelle genome integrates into the nuclear genome. However it is unclear what processes maintain such an integration over longer evolutionary time. Recently it was shown that nuclear DNA of mitochondrial origin (NUMTs) may harbour genes with intact mitochondrial reading frames despite the fact that they are highly divergent to the host's mitochondrial genome. Two major hypotheses have been put forward to explain the existence of such mitocoding nuclear genes: (A) recent introgression from another species and (B) long-term selection. To address whether these intriguing possibilities we conducted a large-scale analysis which we phrase "phylonumtomics" of more than 1,000 avian and mammalian species. We indeed identified that the subclass of divergent NUMTs harbouring mitogenes with intact reading frames are widespread across mammals and birds. We can show that for these NUMTs signatures of cross-species introgression are widespread in birds, but not mammals with the exception of ungulates. We can also show that a substantial fraction of deeply divergent NUMTs are maintained by selection. For a small number of NUMT genes we identify an evolutionary signature that is consistent with adaptive evolution including one human NUMT that is shared among seven ape species. This highlights the intriguing possibility that NUMT insertions occasionally may contribute to adaptation.

Talk by **Shubha Govindarajan**:

(43) Impact of foundress context on adaptation to a novel habitat

Open category

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Factors affecting adaptation of populations to heterogeneous environments is a core question in evolutionary biology. Broadly, fitness related traits should also affect adaptation in addition to population genetics and demography. Female contexts such as age and density have been shown to impact fecundity and the speed of offspring development. This, in turn, can have downstream effects on subsequent generations through distribution of eggs across resources, hence influencing adaptation. To test this prediction, I used experimental evolution in a full factorial design, with populations founded by young or old females that experienced either low or high density. Interestingly, foundress context did not alter population dynamics, but affected the change in fecundity and oviposition resource choice within ten generations. Thus, these long lasting maternal effects are not mediated through population demography. In ongoing work, I am trying to understand the physiological and biochemical basis of these context-dependent effects.

Talk by **Yuanting Guo**:

(44) Adaptations to a cold climate promoted social evolution in Asian colobine primates

Behavioral evolution in vertebrates: diversity, genomics and mechanisms

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The biological mechanisms that underpin primate social evolution remain poorly understood. Asian colobines display a range of social organizations, which makes them good models for investigating social evolution. By integrating ecological, geological, fossil, behavioral, and genomic analyses, we found that colobine primates that inhabit colder environments tend to live in larger, more complex groups. Specifically, glacial periods during the past 6 million years promoted the selection of genes involved in cold-related energy metabolism and neurohormonal regulation. More-efficient dopamine and oxytocin pathways developed in odd-nosed monkeys, which may have favored the prolongation of maternal care and lactation, increasing infant survival in cold environments. These adaptive changes appear to have strengthened interindividual affiliation, increased male-male tolerance, and facilitated the stepwise aggregation from independent one-male groups to large multilevel societies.

Poster by **Yuanting Guo**:

(45) Study based on molecular convergence offer insight into adaptation to folivorous diet in primate subfamily Colobinae

Behavioral evolution in vertebrates: diversity, genomics and mechanisms

Yuanting Guo¹

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The dietary adaptation of animals is a powerful driving force for species niche differentiation and speciation, and the genetic mechanisms underlying adaptive evolution have been a research hotspot. Among primates, although there are many species that feed on high-fiber foods such as leaves, only the colobine primates (Colobinae), similar to herbivorous ruminants, have evolved a pattern of foregut fermentation. The

evolutionary strategy of phenotypic convergence between the two clades provides an opportunity to explore the genetic mechanism of folivorous or herbivorous diet adaptation in mammals. We explored the molecular convergence of colobine primates and ruminants in the host genomes and host-associated microbiomes. Analysis of host genomic convergence revealed several convergent amino acid substitution sites, including PLA2G4E and PLA2G4F related to lipid metabolism, RPP25 as a component of ribonucleases, and TACR2 involved in positive regulation of gastric smooth muscle differentiation and contraction. Additionally, based on the genome-wide functional convergence test, genes under positive selection and rapidly evolving genes in both groups were significantly enriched in immune action, microbial regulation, energy metabolism, epithelial development, and other pathways. Analysis of 16S data showed high similarity between foregut samples of colobines and ruminants, while this phenomenon was not observed in hindgut samples. We also identified six highly expressed bacterial genera in both colobines and ruminants associated with cellulose and lignin degradation. These findings contribute to our understanding of the genetic basis of foregut fermentation in primate evolution and shed light on theories concerning adaptation to the environment and dietary transitions during primate radiation.

Poster by **Tomoko Hamabata**:

(46) Exploring the adaptation of green turtles: Genetic signatures of the Northernmost population

The genomics of adaptation and speciation

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Green turtles (*Chelonia mydas*) exhibit a global distribution that spans tropical and subtropical regions. Japan serves as the northernmost breeding site and foraging habitat for this species. Previous studies have clarified that there is a distinct distribution boundary of foraging habitats in Japanese waters depending on the turtles' natal origins: The coastal seagrass beds south of Japan's Ryukyu Islands are utilized by populations from low latitudes and the northernmost nesting sites. In contrast, the coastal waters surrounding Japan's main islands are almost exclusively used by the population from the northernmost nesting sites. Since the coastal waters around Japan's main islands are temperate, the water temperature seasonally varies. Especially in winter, it substantially drops compared to the tropical and subtropical waters. In addition, the types of food resources for green turtles also differ in these two waters due to the differences in environments. Thus, the distribution boundary suggests differences in adaptation between turtles that can live in this temperate water and those that cannot, such as tolerance to low water temperatures in winter. However, the differences in adaptive traits in individuals from low latitudes and northernmost natal origins have yet to be clarified due to the challenges in understanding the in-water ecology of such highly mobile marine animals. In addition, seawater temperatures along the coast of Japan's main islands have been increasing due to climate change, which may cause changes in their future distribution. Understanding the genetic signatures related to adaptation can provide insights into how species respond to this global challenge and may be useful for future monitoring. This study seeks adaptive traits from identifying regions that underwent natural selection using population genomic methods. Whole-genome sequencing data from 17 individuals from the northernmost nesting populations (Ogasawara, Japan) and the low-latitude nesting populations (Southeast Asia and the western Pacific islands) were collected, and their variants were analyzed. The regions under selective pressures were estimated for each population. Based on the genetic loci related to the regions extracted, the adaptive traits of the Northernmost population will be estimated and discussed.

Talk by **Yan Hao**:

(47) Comparative genomics reveals the genetic basis of adaptation in ground jays endemic to deserts

Open category

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Species inhabiting extreme desert environments have undergone intense selective pressures, resulting in the evolution of striking adaptations. While extensive research has focused on phenotypic characteristics associated with desert adaptation, the genetic basis underlying these adaptations remains elusive, particularly in a monophyletic avian group. Here we investigate this within a remarkable lineage Podoces, comprising four ground jays that are exclusively found in desert habitats. We constructed genome assemblies for these species, which included two representative chromosomal-level genomes, and identified the evolutionary mechanisms driving desert adaptations through comparative genomics. Our findings revealed distinctive and widespread accelerated selection in ground jays across protein-coding genes, gene families, and conserved nonexonic elements linked to energy metabolism and the maintenance of water balance. Notably, gene families and noncoding regions with high evolutionary flexibility may be involved in morphological adaptations, such as the morphogenesis of the ureteric bud branching structure in ground jays. Furthermore, we found that structural variations also contribute to the important evolutionary forces driving desert adaptation in ground jays. Collectively, our study suggests that desert adaptation patterns are shaped by the co-evolution of genetic variation at multiple scales. Our results have implications for comprehending the historical processes of desertification and shed light on the intricate genetic mechanisms underlying adaptations to extreme desert environments. Key words: adaptive evolution; deserts; positive selection; accelerated evolution; Podoces

Poster by **Yaoxi He**:

(48) Polygenic adaptation leads to a higher reproductive fitness of native Tibetans at high altitude

Genetics of adaptation and evolution of novel traits

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The adaptation of Tibetans to high-altitude environments has been studied extensively. However, the direct assessment of evolutionary adaptation, i.e. the reproductive fitness of Tibetans and its genetic basis remain elusive. Here, we conduct systematic phenotyping and genome-wide association analysis of 2,252 mother-newborn pairs of indigenous Tibetans, covering 12 reproductive traits and 76 maternal physiological traits. Compared to the lowland immigrants living at high altitudes, indigenous Tibetans show better reproductive outcomes, reflected by their lower abortion rate, higher birth weight, and better fetal development. The results of genome-wide association analyses indicate a polygenic adaptation of reproduction in Tibetans, attributed to the genomic backgrounds of both the mothers and the newborns. Furthermore, the EPAS1-edited mice display higher reproductive fitness under chronic hypoxia, mirroring the situation in Tibetans. Collectively, these results shed new light on the phenotypic pattern and the genetic mechanism of human reproductive fitness under extreme environments.

Talk by **Tatsuya Hirasawa**:

(49) Unveiling the enigmatic Middle Devonian vertebrate, Palaeospondylus

Early evolution of vertebrates from evo-devo and paleontological perspectives

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There are still unknowns in the phylogenetic relationships and morphological evolution of the early evolution of vertebrates. Palaeospondylus gunni from the Middle Devonian represents one such enigma, whose phylogenetic position has remained unknown for the past 120 years. Homologies of skeletal elements in Palaeospondylus cranium was not well understood, since the interpretation of the skeletal homologies depends on the higher taxon being compared. Until recently, data about the morphotypes of the extant vertebrates had been incomplete, and the precise morphology of Palaeospondylus cranium itself was not observable. In the past decade, progress has been made in developmental biology of extant vertebrates, in particular the hagfish and coelacanth embryos. Interestingly, there is a morphological similarity between Palaeospondylus and the hagfish embryo at a certain developmental stage, and we once proposed that Palaeospondylus was a stem-hagfish. However, the proof was not conclusive, and we decided to conduct a detailed observation of Palaeospondylus fossils. To observe the complete cranial skeleton of Palaeospondylus, we searched for specimens in which the entire cranium was still embedded within the matrix and only the tail was exposed on the rock. We found two hopeful specimens and observed them using synchrotron radiation X-ray micro-computed tomography, eventually showing complete cranial skeletons in both specimens with their microstructures. Based on the skeletal histology, including the distribution of cell lacunae, and the pattern of displacement of skeletal elements observed so far, we were able to identify the skeletal boundaries in Palaeospondylus cranium. The cranial morphology of Palaeospondylus corresponds to the morphotype of tetrapodomorph crania, in particular the combination of the intracranial joint, basicranial fenestra, distinct basiptyergoid process and lateral commissure carrying a hyomandibular articulation. The skeletal element articulated with the caudal end of the Palaeospondylus cranium, which had been particularly enigmatic, was found to be the hyomandibula. While the hyomandibula is large relative to the Meckel's cartilage, the proportional length of the hyomandibula relative to the other cranial skeletal elements in Palaeospondylus is not necessarily unusual for tetrapodomorphs. The strangeness of the cranial morphology of Palaeospondylus is attributable largely to the unusually small size of the Meckel's cartilage. The homology correspondences enabled us to perform cladistic analyses for the first time, showing the inference that Palaeospondylus is closely related to stem-tetrapods such as Acanthostega and 'elpistostegals'. The absence of teeth, dermal bones, and skeletal elements of paired appendages in Palaeospondylus indicates that there was a heterochronic evolution in which these did not develop concurrently with other organs of the body. Palaeospondylus fossils tend to be preserved in specific layers, where Palaeospondylus and Mesacanthus of approximately the same body size were accumulated. It is possible that the same body size may have sorted during transportation before burial. Therefore, it is difficult to conclude whether the bodies hitherto found as Palaeospondylus reflect the entire ontogenetic stages of this animal. Palaeospondylus may have been a larval form, with teeth, dermal bones, and paired appendages appearing as it grew, or the form preserved as Palaeospondylus fossils may have been an adult.

Poster by **Mei Hou**:

(50) Intra- vs. inter-host evolution of SARS-CoV-2 driven by uncorrelated selection - The evolution thwarted

Virus evolution: from basic research to public health applications

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In viral evolution, a new mutation has to proliferate within the host (Stage I) in order to be transmitted and then compete in the host population (Stage II). We now analyze the intra-host single nucleotide variants (iSNVs) in a set of 79 SARS-CoV-2 infected patients with most transmissions tracked. Here, every mutation has two measures: i) iSNV frequency within each individual host in Stage I; ii) occurrence among individuals ranging from 1 (private), 2-78 (public) to 79 (global) occurrences in Stage II. In Stage I, a small fraction of non-synonymous iSNVs are sufficiently advantageous to rise to a high frequency, often 100%. However, such iSNVs usually fail to become public mutations. Thus, the selective forces in the two stages of evolution are uncorrelated and, possibly, antagonistic. For that reason, successful mutants, including many VOCs (variants of concern), have to avoid being eliminated in Stage I when they first emerge. As a result, they may not have the transmission advantage to outcompete the dominant strains and, hence, are rare in the host population. Few of them could manage to slowly accumulate advantageous mutations to compete in Stage II. When they do, they would appear suddenly as in each of the 6 successive waves of SARS-CoV-2 strains. In conclusion, Stage I evolution, the gate-keeper, may contravene the long-term viral evolution and should be heeded in viral studies.

Poster by **Naina Hu**:

(51) Establishing a promising bivalve model and functional tools for understanding molluscan biology and evolution

Marine evo-devo: new frontiers from emerging marine model organisms

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Model organisms are irreplaceable tools of fundamental biological research by boosting many major scientific breakthroughs in life science. However, less efforts have been devoted to establishing animal models for species-rich and highly diverse marine invertebrates such as molluscs. Especially, with many marine molluscs have entered into the post-genome era, there is an urgent need for developing mollusc models for functional genetic studies. Our group has been focusing on the dwarf surf clam (*Mulinia lateralis*), a promising bivalve model with many appealing features such as small body size, rapid development, ease of raising or breeding, etc. We have established the standardized aquatic facilities for artificial breeding and culture of *M. lateralis* in the laboratory, with attainable capacity of five generations per year. We generated abundant multi-omics resources, including haplotype-resolved genome, the full sets of transcriptomes covering all developmental stages and adult tissues, as well as single-cell sequencing data. The transgenic, CRISPR-based gene editing as well as flow cytometric based-cell sorting and in vitro cell culture have been preliminarily applied in *M. lateralis*, laying the foundation for decoding the function of interested genes. The successful application of these techniques makes *M. lateralis* a promising bivalve model and provides powerful functional tools for understanding the biology and evolution of molluscs.

Talk by **Christian Huber**:

(52) Beyond Static Selection: The Genomic Footprints of Temporally Oscillating Alleles

Genomic diversity in nonequilibrium populations

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In recent years, a surge in genetic evidence has illuminated the phenomenon of fluctuating selection in *Drosophila* and other species. This has been identified by observing temporal oscillations in thousands of alleles. However, we currently lack an understanding of the effect of fluctuating selection on population genetic statistics and its influence on genome-wide genetic diversity. The ages of these fluctuating alleles also remain ambiguous, as their oscillations are observed over merely short time scales. In this study, we use forward simulations to produce seasonally fluctuating selection. We then characterize the resulting genomic patterns across various time scales, employing a wide range of population genetic summary statistics. These patterns were compared against those arising from classical forms of positive and balancing selection. Further, we evaluated the capability of different summary statistics in pinpointing loci influenced by fluctuating selection. Our findings reveal that while long-term fluctuating selection is distinct from positive selection, it exhibits considerable parallels with genomic patterns characteristic of balancing selection. Diversity and site frequency spectrum based statistics face challenges in pinpointing fluctuating selection, but haplotype-based approaches present promising avenues. In conclusion, fluctuating selection can substantially influence genome-wide genetic diversity, suggesting a pivotal role in determining genetic diversity in many species.

Talk by **Alice Hughes**:

(53) Mapping the distribution of key pollinator groups and pollination service provision across landscapes

An evolutionary perspective on pollinator biodiversity, systematics, and conservation

Alice Hughes¹

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The vast majority of studies on pollination focus on bees, but a tremendous variety of pollinators come from other groups. Many of these other pollinators provide unique and indispensable ecosystem services, including to crops. Bats are a useful example, with many plants such as durian, agave, baobab, and other key species heavily reliant on them. I will discuss several case studies, with focus on tropical Asia, and more broadly explore the global distribution of bat pollination services. Furthermore, given the growing recognition of the need to map and prioritise the protection of ecosystem services, new methods to better map and quantify these are needed if they are to be factored into spatial planning approaches. Here we explore new ways to map these services across the landscape, to add additional dimensions to existing approaches of mapping and conserving ecosystem service provision. We also explore a landscape based approach to integrating conservation approaches to maintain pollination provision and services in agricultural landscapes, and to thereby ensure that we can maintain both biodiversity and key services in these landscapes. Additionally we discuss the use of new tools and approaches for mapping and prioritizing species with scant distributions, including both insect pollinators and our bat-cave vulnerability index, to demonstrate how data can be integrated to enable more effective prioritization, which both recognizes the vulnerability and diversity of species, as well as the services they provide; thus providing a more holistic mechanism for developing and implementing priorities at the landscape scale.

Talk by **Jerome Hui**:

(54) Insights from the understudied non-insect arthropod genomes

Novel insights regarding genome architecture evolution in the arthropoda

Jerome Hui¹

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The Arthropoda is the phylum that contains most of the described living animal species in the world, including insects, crustaceans (e.g. shrimps/crabs/lobsters), chelicerates (e.g. mites/ticks/scorpions/spiders), and myriapods (e.g. centipedes/millipedes). Due to historical and various practical reasons, most of our understanding on the biology of arthropods mainly come from the insects and some lineages in the crustaceans and chelicerates. In terms of arthropod genomics, the situation is even more skewed or biased towards the insects. Collaborating with worldwide researchers, our team is fortunate to study the non-insect arthropod genomics since the last decade or so. In this talk, I would summarise some key and unexpected findings that we have and can learn from these understudied hidden gems, and argue the situation is just the tip of the iceberg.

Poster by **Naoto Inui**:

(55) Development and evolution of air-breathing organs in terrestrial isopods (Crustacea, Oniscidea)

Open category

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Functional differentiation of appendages is one of the factors contributing to the success of arthropods. During evolution, many arthropod lineages have colonized on land and independently acquired air-breathing organs, such as book lungs in chelicerates and tracheae in myriapods and insects. The location of the organs and some gene expression patterns suggest that these respiratory organs are derived from the appendages of ancestors. However, the processes or mechanisms of the evolution remain unclear because the morphologies of these respiratory organs have been largely modified from the normal appendages. Among arthropods, terrestrial isopods (Malacostraca, Isopoda, Oniscidea) are known to have specialized structures for air breathing in their abdominal appendages (pleopods), called pleopodal lungs or pseudotrachea. Depending on habitats, the structure of respiratory surface area on the pleopods varies. These can be categorized into three types, i.e., covered lungs, uncovered lungs, and dorsal respiratory fields. These diverse isopod lungs allow us to study the evolutionary processes of respiratory organs associated with terrestrialization. To date, comparative morphological studies have been the primary approach to elucidating lung evolution, while less is known about the detailed developmental processes of lungs. In this study, we compared the developmental process of respiratory organs among terrestrial isopods to identify novel developmental mechanisms that contribute to the acquisition of lungs. We performed morphological and histological observations on three species with three different types of respiratory organs (covered lungs: *Porcellio scaber*, uncovered lungs: *Nagurus okinawaensis*, and dorsal respiratory fields: *Alloniscus balssi*) and one species without lungs (*Armadilloniscus ellipticus*). The results revealed that in *P. scaber*, the epithelial tissue near the base of the pleopods invaginated during the postembryonic manca stages and developed the lung structure. In *N. okinawaensis*, the respiratory region appeared after the manca stages through the formation of wrinkled epithelium. In addition, in *A. balssi*, the respiratory region appeared near the base of the pleopods immediately after hatching and gradually expanded. In contrast, *A. ellipticus* did not develop any specialized structure in their pleopods. The lungs of these isopod species generally developed by modification of the region near the base of the pleopods. On the other hand, the formation timings the epithelial transition of respiratory regions were different among species. These results suggest that the specific region of pleopods that becomes the lungs in derived lineage was already present in the ancestral pleopods, and lung-bearing lineage acquired the novel developmental mechanisms that transformed the region into a complex lung structure.

Talk by **Naoki Irie**:

(56) Intrinsically embedded inertial force in phenotypic evolution?

Evolvability: a common currency of evolution, ecology and development

Naoki Irie¹, Yui Uchida², Masahiro Uesaka³, Haiyang Hu⁴, Philipp Khaitovich⁵, Guojie Zhang⁶, Wen Wang⁷, Jr-Kai Yu⁸, and Shigeru Kuratani⁹

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What makes certain phenotypes, such as the basic anatomical patterns of animals (body plans), remain strictly conserved even after hundreds of millions of years of evolution? Potential explanations include purifying selection, the influence of genetic drift, or merely the result of coincidence. In the meantime, I would like to discuss the contribution of less evolvability, which results from having less potential to generate phenotypic variation within a generation. We initially discovered that the body plan development phase, known as the phylotypic period, is rather robust against mutations and environmental perturbations. This suggests that the conservation of the body plan cannot be solely attributed to the higher lethality of the phylotypic period. Subsequently, we conducted comparative transcriptomic analyses of chordate embryos and found that the phylotypic period is enriched with genes expressed in various stages and tissues. This implies that pleiotropic gene expression itself could contribute to the conservation of the phylotypic period and, by extension, the body plan. While the reuse of existing genes has long been known to facilitate evolutionary diversification (e.g., by creating novel traits), our findings suggest that gene re-utilization has a double-edged sword effect on evolution, limiting diversification. Finally, the phylotypic period exhibited smaller inter-individual variations than the early and later developmental stages. These results suggest that the period responsible for establishing the body plan has a reduced potential to generate phenotypic variations, making it less likely to diversify even under the pressures of positive selections. In other words, these intrinsic factors could have played a role in contributing to the conservation of strictly conserved features, such as the body plan.

Talk by **Kavita Jain**:

(57) Joint effect of changing selection and demography on site frequency spectrum

Genomic diversity in nonequilibrium populations

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I will summarize our theoretical results on the effect of periodically varying selection and population size on the site frequency spectrum and associated measures of genetic diversity.

Talk by **Dong-Yan Jin**:

(58) Origin and evolution of SARS-CoV-2

Virus evolution: from basic research to public health applications

Dong-Yan Jin¹

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In this brief overview of the origin and evolution of SARS-CoV-2, existing evidence in support of the zoonotic origin of human coronaviruses will be reviewed from the perspective of an experimental virologist, with a brief analysis of the anecdotal support for a past pandemic caused by human coronavirus OC43. The timeline for the separation of SARS-CoV-2 from SARS-CoV and for the split of SARS-CoV-2 and RaTG13 or BANAL-20-52 Laos will be estimated. Adaptive mutations in S protein found during the passage of SARS-CoV-2 in cultured cells as well as their prevalence in circulating strains in human population will be discussed. Comparison with the origin of HIV as a human pathogen will also be made. Other topics to be covered include ancestral, intermediate and reservoir hosts of SARS-CoV-2; asymptomatic coronavirus infection in bats and humans, as well as evolution and variant biology of SARS-CoV-2. Supported by HKRGC (C7142-20GF and T11-709/21-N).

Talk by **Philip Johns**:

(59) Group behaviours in Singapore's smooth-coated otters and the evolution of cooperative breeding

Behavioral evolution in vertebrates: diversity, genomics and mechanisms

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The cause of the evolution of cooperative breeding, where adult offspring remain with family groups as helpers, is not fully resolved. In smooth-coated otters (*Lutrogale perspicillata*), adult offspring remain with family groups, sometimes for years. Smooth-coated otters have repopulated and thrived in urban Singapore, which allows for careful observation of their behaviors. Here we present recent findings of group living in Singapore's otters, including active teaching in groups, coordinated foraging in groups, group defense against heterospecific threats, and group territorial defense. We pose questions about the inheritance of group resources between generations and describe the possibility that the genomic background of Singapore's otters influences their sociality. We outline future research that would help resolve how cooperative breeding evolved in otters.

Talk by **Parul Johri**:

(60) Limitations of the inference of the distribution of fitness effects of new mutations in partially-selfing populations with linkage

Genomic diversity in nonequilibrium populations

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The accurate estimation of the distribution of fitness effects (DFE) of new mutations is critical for population genetic inference but remains a challenging task. While various methods have been developed for DFE inference using the site frequency spectrum of putatively neutral and selected sites, their applicability in species with diverse life history traits and complex demographic scenarios is not well understood. Selfing is

common among eukaryotic species and can lead to decreased effective recombination rates in such populations, increasing Hill-Robertson interference between selected mutations. We employ forward simulations to investigate the limitations of current DFE estimation approaches in the presence of selfing and linked effects of selection. We find that distortions of the site frequency spectrum due to Hill-Robertson interference in highly selfing populations lead to an overestimation of the proportion of mildly deleterious mutations. In addition, the proportion of adaptive substitutions estimated at high rates of selfing is overestimated. Our results better clarify the parameter space where current DFE methods might be problematic and where they remain robust in the presence of selfing and other model violations like departures from semi-dominance, population structure, and uneven sampling.

Talk by **Jingliang Kang**:

(61) Gene losses, parallel evolution and heightened expression confer adaptations to dedicated cleaning behaviour

The genomics of adaptation and speciation

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Cleaning symbioses are captivating interspecific interactions in which a cleaner fish removes ectoparasites from its client, contributing to the health and diversity of natural fish communities and aquaculture systems. However, the genetic signatures underlying this specialized behaviour remain poorly explored. To shed light on this, we generated a high-quality chromosome-scale genome of the bluestreak cleaner wrasse *Labroides dimidiatus*, a dedicated cleaner with cleaning as primary feeding mechanism throughout its life. Compared with facultative and non-cleaner wrasses, *L. dimidiatus* was found with notable contractions in olfactory receptors implying their limited importance in dedicated cleaning. Instead, given its distinct tactile pre-conflict strategies, *L. dimidiatus* may rely more heavily on touch sensory perception, with heightened gene expression in the brain in anticipation of cleaning. Additionally, a reduction in NLR family CARD domain-containing protein 3 might enhance innate immunity of *L. dimidiatus*, probably assisting to reduce the impacts from parasite infections. In addition, convergent substitutions for a taste receptor and bone development genes across cleaners (*L. dimidiatus* and facultative cleaners) may provide them with evolved food discrimination abilities and jaw morphology that differentiate them from non-cleaners. Moreover, *L. dimidiatus* may exhibit specialized neural signal transductions for cleaning, as evidenced by positive selection in genes related to the glutamatergic synapse pathway. Interestingly, numerous glutamate receptors also demonstrated significantly higher expression in *L. dimidiatus* not engaged in cleaning, as compared to those involved in cleaning. Besides, apparent contractions in *L. dimidiatus* for protocadherins, which are responsible for neuronal development, may further promote specialised neural signal transductions in this species. This study reveals that *L. dimidiatus* harbours substantial losses in specific gene families, convergent evolutions across cleaners, and a large-scale high gene expression in preparation for cleaning, allowing for adaptation to the dedicated cleaning behaviour.

Talk by **Petri Kempainen**:

(62) Boundary effects cause false signals of range expansions in population genomic data

Genomic diversity in nonequilibrium populations

Petri Kempainen¹ and Paolo Momigliano²

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Studying range expansions (REs) is central for understanding genetic variation through space and time as well as for identifying refugia and biological invasions. Range expansions are characterized by serial founder events causing clines of decreasing diversity away from the center of origin and asymmetries in the two-dimensional allele frequency spectra. These asymmetries, summarized by the directionality index (ψ), are sensitive to REs and persist for longer than clines in genetic diversity. In continuous and finite meta-populations, genetic drift tends to be stronger at the edges of the species distribution. Such boundary effects (BEs) are expected to affect geographic patterns in ψ as well as genetic diversity. With simulations we show that BEs consistently cause high false positive rates in equilibrium meta-populations when testing for REs. In the simulations, the absolute value of ψ ($|\psi|$) in equilibrium data sets was proportional to the fixation index (F_{st}). By fitting signatures of REs as a function of $\epsilon = |\psi|/F_{st}$ and geographic clines in ψ , strong evidence for REs could be detected in data from a recent rapid invasion of the cane toad, *Rhinella marina*, in Australia, but not in 28 previously published empirical data sets from Australian scincid lizards that were significant for the standard RE tests. Thus, while clinal variation in ψ is still the most sensitive statistic to REs, in order to detect true signatures of REs in natural populations, its magnitude needs to be considered in relation to the overall levels of genetic structuring in the data.

Talk by **Hie Lim Kim**:

(63) Prehistoric human migration between Sundaland and South Asia was driven by sea-level rise

Open category

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Rapid sea-level rise between the Last Glacial Maximum (LGM) and the mid-Holocene dramatically transformed the Southeast Asian coastal landscape and the landmass was reduced to half. However, the impact on human demography remains unclear. Here, we create a paleogeographic map that focuses on sea-level changes during the period spanning the LGM to the present day, and we infer the human population history in Southeast and South Asia using 763 high-coverage whole-genome sequencing datasets from 59 ethnic groups. We show that sea-level rise, particularly meltwater pulses 1A (MWP1A, ~14,500–14,000 years ago) and 1B (MWP1B, ~11,500–11,000 years ago), resulted in the fragmentation of the landmass and promoted segregation of the Sundaland populations, contributing to the diversity of Southeast Asians. As a result of the rapid sea-level rises, the increase in population density drove the migration of Malaysian Negritos into South Asia, as we found genetic evidence of common ancestry between the populations. Integrated paleogeographic and population genomic analysis demonstrates the earliest documented instance of forced human migration driven by sea-level rise.

Talk by **Akira R. Kinjo**:

(64) Plasticity-led evolution as an intrinsic property of developmental gene regulatory networks

Open category

Eden Tian Hwa Ng¹ and Akira R. Kinjo²

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The Modern Evolutionary Synthesis seemingly fails to explain how a population can survive a large environmental change. That is, the pre-existence of heritable variants adapted to the novel environment is too opportunistic, whereas the search for new adaptive mutations after the environmental change is too slow. Plasticity-led evolution, the initial environmental induction of a novel adaptive phenotype followed by genetic accommodation, has been proposed to solve this problem. However, the mechanism enabling plasticity-led evolution is unclear. Here, we present computational models that exhibit behaviors compatible with plasticity-led evolution by extending the Wagner model of gene regulatory networks. The models exhibit adaptive plastic response and uncovering of cryptic mutations under significant environmental changes, followed by genetic accommodation. Moreover, these behaviors are consistently observed over distinct novel environments. We further show that environmental cues, developmental processes, and hierarchical regulation cooperatively amplify the above behaviors and accelerate evolution. These observations suggest plasticity-led evolution is a universal property of complex developmental regulation independent of particular mutations. Preprint is available at <https://www.biorxiv.org/content/10.1101/2023.05.25.542372v1>

Talk by **Fyodor Kondrashov**:

(65) Diversity of fitness peak shapes in the Green Fluorescent Protein

Fitness landscapes bridge evolution and molecular biology

Fyodor Kondrashov¹

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How genotypes are manifested into phenotypes, known as fitness landscapes, remains one of the most important unanswered questions in biology. However, deep mutational scans - empirical assays of the fitness landscapes - are increasingly being used to shape our understanding of the complex nature of interaction of changes on the genetic level. In my talk I will outline what we have learned from our study of the empirical assays of different orthologues of the Green Fluorescent Protein. We find that the fitness peak associated with each orthologue is unique, demonstrating different overall shape but also showing interactions between different amino acid sites. We have also been able to utilize these data and make generalized models of the fitness landscapes that are fairly accurate at genetic distances vastly beyond what has been assayed experimentally. The uniqueness of the shape of each fitness peak, however, leads to an inherent limitation of predicting the shape of one fitness peak based on the information contained in another fitness peak. To create better and more general models of fitness landscapes different empirical and theoretical approaches will be needed.

Talk by **Samantha Kreling**:

(66) So overt its covert: Wildlife coloration in the city

Open category

Samantha Kreling¹

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With novel human–wildlife interaction, predation regimes, and environmental conditions, in addition to often fragmented and smaller populations, urban areas present wildlife with altered natural selection parameters and genetic drift potential compared with nonurban regions. Plumage and pelage coloration in birds and mammals has evolved as a balance between avoiding detection by predator or prey, sexual selection, and thermoregulation. However, with altered mutation rates, reduced predation risk, increased temperatures, strong genetic drift, and increased interaction with people, the evolutionary contexts in which these colorations arose are radically different from what is present in urban areas. Regionally alternative color morphs or leucistic or melanistic individuals that aren't typical of most avian or mammalian populations may become more frequent as a result of adaptive or neutral evolution. Therefore, I conceptualize that, in urban areas, conspicuous color morphologies may persist, leading to an increase in the frequency of regionally atypical pelage coloration. In the present article, I discuss the potential for conspicuous color morphs to arise and persist in urban mammalian and avian populations, as well as the mechanisms for such persistence, as a result of altered environmental conditions and natural selection pressures.

<https://academic.oup.com/bioscience/article-abstract/73/5/333/7095303>

Talk by **Shigeru Kuratani**:

(67) Development of cyclostomes and early evolution of vertebrates

Early evolution of vertebrates from evo-devo and paleontological perspectives

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Modern jawless vertebrates, including lampreys and hagfish, belong to a monophyletic group called cyclostomes. This group is closely related to its sister group, gnathostomes. While we previously knew little about the embryonic development of hagfish, we can now observe their embryos using histological and gene expression techniques. One interesting aspect of cyclostome development is that the embryos of lampreys and hagfish resemble each other during the middle stages of development. This similarity allows us to compare the structures of these two animals. At a specific stage of development unique to cyclostomes, the craniofacial region of the embryo consists of anterior and posterior processes adjacent to the median nasohypophyseal placode, as well as the mandibular arch. For example, the upper lip of the ammocoete (lamprey larva) is derived from the posterior process, like the oro-nasal septum of the hagfish, and also similar to a skeletal element called trabecula cranii in jawed vertebrates. In hagfish, the root of the posterior process undergoes degeneration, connecting the nasohypophyseal duct and the oral cavity. This trait once distinguished hagfishes from lampreys, but this difference only emerges in the later stages of development, confirming their close evolutionary relationship. Primarily, the craniofacial features of cyclostomes include having a single nasohypophyseal duct that does not directly open into the oral cavity, a trait also found in the stem group of jawed vertebrates known as ostracoderms. This suggests that cyclostomes retain an ancient craniofacial developmental program. On the other hand, possessing structures like the lingual apparatus and velum, which derive from the mandibular arch, can possibly be considered defining features of cyclostomes. Among the cyclostomes, hagfishes seem to have undergone more changes in craniofacial morphology compared to lampreys, which show a pattern more similar to the embryonic state of cyclostomes. However, lampreys also display unique traits that may have arisen during their larval stage or metamorphosis. For instance, the position of the lamprey esophagus shifts as they undergo metamorphosis, and their brain development differs from that of hagfishes and jawed vertebrates: larval lamprey brain does not differentiate a rhombic lip (at the morphological level) as in the hagfish and gnathostomes. The appearance of an exocrine organ, endostyle, in lamprey larvae is also puzzling. Although the ammocoete endostyle was regarded to

recapitulate an ancestral, pre-vertebrate state of evolution, recent findings suggest that the larval stage of lampreys might have evolved relatively recently (Miyashita et al., 2021), challenging the previously accepted idea that lamprey and protochordate endostyles are homologous. Thus, embryonic development and craniofacial features of cyclostomes provide insights into mechanisms behind morphological diversity in early evolution of vertebrates.

Talk by **Buntarou Kusumoto**:

(68) Geographical patterns of global woody plant diversity: their contemporary and historical environmental drivers

Paleo- and macro- ecology in tropical Asia

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Sampling bias in species observation has challenged biogeographers for many years to precisely quantify macro-scale biodiversity patterns. Based on sample completeness-based standardization, we generated a bias-corrected global species diversity map for woody angiosperms using > 10 million occurrence records. The highest woody species diversity was identified in central South America followed by western tropical Africa and Indomalayan-Australasian region including the mid latitudinal zone of East Asia. The bias-corrected diversity demonstrated heterogeneous, non-linear latitudinal and longitudinal gradients. The latitudinal diversity gradient in the Americas showed a typical symmetric shape with a peak at the equator and decline toward both poles. The latitudinal diversity gradient in the Africa-Europe region showed a peak at the equator and decline toward higher latitude in the Northern Hemisphere and up to middle latitude in the Southern Hemisphere. The latitudinal diversity gradient in the Asia-Oceania region showed a peak at northern central latitudes. Current climate coupled with paleoclimatic/topographic factors emerged as fundamental drivers in the generation of highly complex biodiversity patterns for woody angiosperms. Notably, at the global scale actual evapotranspiration (AET) was the most important predictor across a range of spatial resolutions. At the regional levels, the latitudinal and longitudinal diversity gradients had region-specific links to different environmental variables. Temperature seasonality exhibited a negative correlation with species diversity and outperformed AET in the Americas and the Africa-Europe region, but not in Asia-Oceania. Historical temperature change since the Last Glacial Maximum contributed substantially to shaping the latitudinal diversity gradient in the Americas, but not in the Asia-Oceania region. Older historical imprints (e.g., those of the Paleo- and Neogene) might have played a pivotal role in shaping the high species richness in the subtropical zone in East Asia.

Talk by **Carol Eunmi Lee**:

(69) Genome Architecture Evolution in the Copepod *Eurytemora affinis* Species Complex

Novel insights regarding genome architecture evolution in the arthropoda

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Copepods are among the most abundant organisms on the planet and play critical functions in aquatic ecosystems. Populations of the copepod *Eurytemora affinis* species complex are numerically dominant and highly invasive, with the extraordinary capacity to rapidly invade novel salinities. Prior studies from my laboratory revealed parallel selection acting on the same sets of ion transporter genes during independent saline to freshwater invasions by populations from genetically distinct clades. Our chromosome-level genomes of three genetically divergent clades of this species complex revealed peculiar genome architectures that might contribute to their remarkable capacity to acclimate and evolve during salinity invasions. The genomes, assembled using high-coverage PacBio and Hi-C sequencing of inbred lines (10-30 generations of full-sib

mating), consisted of 521-671 Mb anchored onto variable numbers of chromosomes. Remarkably, we found striking patterns of chromosome fusions in the *E. affinis* complex, with the Europe clade (*E. affinis* proper) having 15 chromosomes, fusing independently into 7 chromosomes in the Gulf clade (*E. gulfia*) and 4 chromosomes in the Atlantic clade (*E. carolleeae*). We explored signatures of selection at the chromosomal fusion sites. Crossing between these clades resulted in varying levels of reproductive isolation, with asymmetric hybrid inviability or sterility between reciprocal crosses. Of the predicted ~20-24K protein-coding genes, we found an extraordinary expansion of ion transporter gene families in the *E. affinis* complex based on comparative analyses of 13 arthropod genomes. Notably, we found genome-wide signatures of extremely high historical methylation levels of the ion transporter gene bodies, suggesting transcriptional robustness of these genes. These high-quality genomes provide an invaluable resource that could help yield fundamental insights into the capacity of populations to expand their ranges into novel habitats.

Talk by **Daehan Lee**:

(70) Single-cell and single-gene dissection of nervous system evolution in the ecological specialist *Drosophila sechellia*

Genetics of adaptation and evolution of novel traits

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Nervous systems display remarkable adaptability, rapidly evolving in response to environmental changes. The three closely-related drosophilids: *D. melanogaster* (Dmel), *D. simulans* (Dsim), and *D. sechellia* (Dsec) offer an ideal model for examining how ecological adaptations shape nervous system evolution. This drosophilid trio species exhibit distinct ecologies: Dmel and Dsim are cosmopolitan generalists, while the island endemic Dsec exhibits extreme niche specialism for ripe *Morinda citrifolia* (noni) fruit, providing an evolutionary context for their differences. To systematically investigate interspecific variability in nervous system cell types and gene expression, we applied single-nucleus RNA-sequencing (snRNA-seq) to the central brains, antennae, and developing antennal discs of this trio of species. With this dataset, we are addressing following questions: Is there interspecific variation in the composition and organization among drosophilid nervous systems (e.g., species-specific gain, loss or modification of neuronal populations)? How does gene expression evolve in conserved cell types (e.g., conservation or diversification of cell-type specific gene expression profiles)? What are the molecular and developmental mechanisms of species-specific remodeling of the nervous system (e.g., how genetic variants modify GRNs or that control neurodevelopment or functional properties of mature neurons)? How do changes in cell types and gene expression impact the neural circuits and behaviors of the species? The discovery of evolving neuronal and non-neuronal populations in this drosophilid trio will provide an entry point to more broadly study the evolvability of nervous systems across and beyond the *Drosophila* genus.

Poster by **Jason Cheok Kuan Leong**:

(71) Are echinoderm embryos more evolutionarily derived than chordate embryos? – Let's distinguish "conservation" and "derivedness"

Evolvability: a common currency of evolution, ecology and development

Jason Cheok Kuan Leong¹, Masahiro Uesaka², Echinoderm Genomes Sequencing Consortium³, and Naoki Irie⁴

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Which embryo of which species evolved more from the common ancestor? For example, echinoderms achieved an exceptional five-fold symmetrical body plan despite being bilaterian animals – are their embryos

more evolutionary derived than the sister group (chordates), i.e., did the way how they form their bodies accumulate much more evolutionary changes than chordates since the divergence from their common ancestor? In order to answer this, methods to properly evaluate their “evolutionary derivedness” have to be devised. Previous approaches mainly list up individual traits while comparing their embryonic phenotypes, but this can be highly arbitrary, and no consensus has been made to address this issue. Importantly, to evaluate “derivedness”, a conceptual ambiguity with the concept of “evolutionary conservation” has hindered biologists from using proper methods to tackle this question. Here we discuss the essential differences between “conservation” and “derivedness”, and highlight the necessity for the development of more derivedness-oriented molecular methods in the genomics era. In brief, “conservation” represents information retained during evolution while “derivedness” represents evolutionary changes, which additionally cover information that is not shared among the species being compared. As an application of the concept, we devised a method to estimate the degree of derivedness of embryos to evaluate whether echinoderms are more derived than chordates or not. We found consistent tendencies with the current understanding that the stages in echinoderms developing their characteristic penta-radial structures indeed tend to be more derived than the bilateral stages. However, the results surprisingly showed that the echinoderm embryos as a whole may not show higher derivedness than the chordate embryos. Through developing this method, we propose that the distinction between “conservation” and “derivedness” is a key to more properly understanding phenotypic evolution and evolvability.

Talk by **Jun Ying Lim**:

(72) The Cenozoic history of palms: diversification and biogeography

Paleo- and macro- ecology in tropical Asia

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Tropical rain forests and mangroves are much smaller in extent today than in the early Cenozoic, primarily owing to global cooling and drying trends since the Eocene–Oligocene transition. The general reduction of these biomes is hypothesized to shape the diversity and biogeographical history of tropical plant clades. However, this has rarely been examined owing to a paucity of good fossil records of tropical taxa and the difficulty in assigning them to modern clades. Here, we evaluate the role that Cenozoic climate change might have played in shaping the diversity and biogeography of tropical plants through time, by examining the exquisite fossil pollen record for an iconic and ubiquitous component of tropical forests globally: the palms.

Poster by **Wei-Han Lin**:

(73) The Histone Deacetylase Hos2 Regulates Protein Expression Noise by Modulating Protein Translation Machinery

Open category

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Non-genetic variations may contribute to expression noise at the transcript or protein levels, resulting in cell-to-cell heterogeneity within an isogenic population. While cells have developed strategies to reduce noise in some cellular functions, this heterogeneity can also facilitate different levels of regulation and provide evolutionary benefits in fluctuating environments. Although several general characteristics of cellular noise have been revealed, detailed molecular pathways underlying noise regulation remained elusive. Here, we established a dual-fluorescent reporter system in *Saccharomyces cerevisiae* and performed experimental evolution to search for mutations increasing the protein noise. By analyzing evolved cells using bulk segregant analysis coupled with whole-genome sequencing, we identified the histone deacetylase, Hos2, as a negative

noise regulator. *hos2* mutants down-regulated multiple ribosomal protein genes, leading to compromised protein translation. It suggests that Hos2 may regulate noise by modulating translation machinery. Consistently, treating cells with translation inhibitors as well as mutations in several Hos2 targets, RPS9A, RPS28B and RPL42A, led to increased noise. Our study provides an effective strategy for identifying noise regulators and also sheds light on how cells regulate non-genetic variation through protein translation.

Talk by **Richard Ron Litan**:

(74) Evolvability of a nonfunctionally binding transcription factor

Open category

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The initiation of transcriptional rewiring is influenced by changes in both the cis- and trans-regulatory elements. However, the process on how perturbations in trans-acting elements instigate transcriptional rewiring remains elusive. Previous report showed that Sef1 in *Lachancea kluyveri* (LkSef1) facilitates non-functional binding to its major target genes. On the other hand, fusing LkSef1 with the transcriptional activator VP16 not only increased its basal activation but also conferred control to other genes originally unaffected by it. Thus, changes such as in the form of mutations that can improve the activity of a transcription factor may mediate new target genes and consequently elicit rewiring. Here, we combined random mutagenesis in LkSef1 and iterative fluorescence-based sorting to select for mutations that can readily enhance its transcriptional activity. Using an LkSef1-enhanced GFP reporter system, gain-of-function mutants were selected, and point mutations were found to increase its transcriptional activity. Also, all mutations are concentrated outside the conserved domains suggesting undefined regions responsible for its activity. Once reconstituted in the genome, these high activity LkSef1 can potentially create novel networks and may ultimately provide mechanisms for transcriptional rewiring.

Talk by **Liang Liu**:

(75) TSH β 2-producing cell: A key orchestrator of reproductive seasonality in sticklebacks

Behavioral evolution in vertebrates: diversity, genomics and mechanisms

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Reproductive seasonality serves as a critical life-history strategy, that significantly influences the fitness of organisms in nature. While some species adapt to seasonal cues such as photoperiods, others change or even lose their seasonality. Understanding the evolutionary mechanisms of reproductive seasonality is crucial for predicting the ecological impacts of climate change and assessing extinction risks for biodiversity conservation. Despite its importance, the molecular genetic mechanisms that facilitate the diversification of reproductive seasonality remain largely unexplored. To address this gap, we used the three-spined stickleback, a model organism known for its diverse photoperiodic responses in reproduction across different ecotypes. Using RNAseq and functional analyses, we found that thyroid-stimulating hormone- β 2 (TSH β 2) dynamically modulates its expression in response to day length, thereby controlling a range of downstream physiological and behavioral traits. Moreover, the pituitary gland, which is responsible for TSH β 2 production, exhibits substantial heterogeneity in both transcriptional regulations and epigenetic modifications. To delve deeper into the TSH β 2 regulatory network, we performed single-cell transcriptomic and epigenetic profiling of the pituitary gland. Our results revealed a novel cell type that uniquely produces TSH β 2. Furthermore, these TSH β 2 producing cells showed increased chromatin accessibility in the region approximately 3kb upstream of the TSH β 2 gene under short-day conditions, suggesting transcriptional and epigenetic modifications in response to photoperiodic changes. Overall, our work highlights the pivotal role of TSH β 2-producing cells in

the evolutionary adaptation of reproductive seasonality. These findings suggest that the TSH β 2-producing cell functions as a pleiotropic hub, coordinating the onset of various reproductive activities.

Talk by Penghui Liu:

(76) Construction of comprehensive and comparative multi-omics database for animal evo-devo (EDomics) and cross-species analysis

Marine evo-devo: new frontiers from emerging marine model organisms

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Construction of comprehensive and comparative multi-omics database for animal evo-devo (EDomics) and cross-species analysis Penghui Liu#, Jiankai Wei#, Fuyun Liu#, Yuli Li*, Shi Wang*, Bo Dong* Abstract: Despite the rapid accumulation of omics data provides unprecedented opportunities to answer many interesting but unresolved evo-devo questions, the access and utilization of these resources are hindered by challenges particularly in non-model animals. Here, we established the first comparative multi-omics database for animal evo-devo (EDomics, <http://edomics.qnlm.ac>) containing comprehensive genomes, bulk transcriptomes, and single-cell data across 40 representative species, many of which are generally used as model organisms for animal evo-devo study. EDomics provides a systematic view of genomic/transcriptomic information from various aspects, including genome assembly statistics, gene features and families, transcription factors, transposable elements, and gene expressional profiles/networks. It also exhibits spatiotemporal gene expression profiles at a single-cell level, such as cell atlas, cell markers, and spatial-map information. Moreover, we conducted cross-species analysis at genomic, transcriptomic and single-cell transcriptomic levels. 34 species were analyzed for the gene family expansion/contraction and pan-gene set. In the macrosynteny analysis module, the genomes of 40 species are analyzed by comparing with bilaterian ALGs represented by three ancient animal genomes. Comparative transcriptomic analysis was also displayed. The developmental correlation provided analysis of developmental transcriptome correlations between two species. By comparing the single cell RNA sequencing data of 9 species with 84 major cell types, we demonstrate the conservation and divergence of cell types. EDomics represents a comprehensive and comparative multi-omics platform for animal evo-devo community to decipher the whole history of developmental evolution across the tree of life. Our results provide a useful tool for the evolutionary development of important species at the molecular and cellular levels respectively.

Poster by Yongjian Liu:

(77) Parallel evolution of a convergent locus underlying lepidopteran melanism

Genetics of adaptation and evolution of novel traits

Yongjian Liu¹

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Color polymorphism is one of the most diverse phenotypes in nature that plays widespread roles in local adaptation, speciation, and hybridization. In Lepidoptera, despite great efforts in addressing mimicry and introgression in butterflies, characterizing the mutational events underlying color variation and associated evolutionary history are still lacking in moths. Here, we focus on geometrid moths which exhibited black and grey body color polymorphism in natural populations. Based on bulked pooling-resequencing of backcross progeny, we characterize a candidate 700-kb locus on chromosome that underlies the color variation. Interestingly, this region is homologous to the targets for controlling wing pattern polymorphisms and mimicry in many butterflies, but pinpoints to a different gene that encodes poly(a)-specific ribonuclease. Functional

studies in geometrids and the lepidopteran model, *Bombyx mori*, support the role of target genes in causing melanism in moths. We further sample and analyze genome-wide variations in additional wild-caught populations and find a divergent sub-pattern within this candidate region, along with strong signal of selection. Based on the wild distribution pattern, we last discuss the potential ecological fitness of this color variation in geometrid moths. Taken together, our study shows the parallel evolved color variation in lepidopterans is controlled by a convergent hotspot region.

Talk by **David J. Lohman**:

(78) Adaptive radiation of Batesian mimics: Rapid divergent phenotypic evolution within and between species

Evolvability: a common currency of evolution, ecology and development

David J. Lohman¹

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Batesian mimicry, in which an undefended species resembles an unpalatable or otherwise undesirable prey item, is found throughout the tree of life. Mimicry is arguably best studied in butterflies, perhaps because it is relatively common, especially in the tropics, and because the earliest concepts of mimicry were based on lepidopteran examples. A handful of lepidopteran lineages have closely related mimetic species (and populations within species) with striking phenotypic differences between them. These apparently evolved because the prevalence of different potential “model” species in different areas selects for resemblance to the locally abundant model. Conversely, distantly related species can mimic the same widespread model and therefore resemble each other despite their geographic and phylogenetic distance. The butterfly genus *Elymnias* (Nymphalidae: Satyrinae) is a monophyletic group of Old World Butterflies that exemplifies an adaptive radiation of highly evolvable Batesian mimics. I will discuss the evolutionary history of this group as inferred with a robust molecular phylogeny and demonstrate remarkable phenotypic convergence and divergence. The most common and widespread species, *Elymnias hypermnestra*, is a facultative dual mimic. Males always mimic melanic *Euploea* species, but females can mimic melanic *Euploea* or orange *Danaus* depending on their locale. GWAS suggests that *WntA* may act as a genetic switch enabling females to mimic one model or the other. I speculate that the tremendous phenotypic variability in this group may result from deploying existing developmental pathways of wing pigments and pattern elements in novel combinations to produce rapid evolution of divergent mimetic phenotypes.

Poster by **Tan Kian Long**:

(79) The role of yellow family genes in *Pieris canidia* wing spots

Open category

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The lepidopterans display a remarkable diversity of colors and patterns that contribute to the success of these animals. The yellow family genes are among some of the known genes responsible for pigmentation and other pleiotropic developmental functions in insects. Here, we characterise the expression of some of the yellow family genes in the wings of *Pieris canidia* and provide functional proof for the role of yellow-y in *Pieris canidia* simple forewing spot formation.

Poster by **Guang-An Lu**:

(80) Canalization of Phenotypes—When the Transcriptome is Constantly but Weakly Perturbed

Open category

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Recent studies have increasingly pointed to microRNAs (miRNAs) as the agent of gene regulatory network (GRN) stabilization as well as developmental canalization against constant but small environmental perturbations. To analyze mild perturbations, we construct a Dicer-1 knockdown line (dcr-1 KD) in *Drosophila* that modestly reduces all miRNAs by, on average, ~20%. The defining characteristic of stabilizers is that, when their capacity is compromised, GRNs do not change their short-term behaviors. Indeed, even with such broad reductions across all miRNAs, the changes in the transcriptome are very modest during development in stable environment. By comparison, broad knockdowns of other regulatory genes (esp. transcription factors) by the same method should lead to drastic changes in the GRNs. The consequence of destabilization may thus be in long-term development as postulated by the theory of canalization. Flies with modest miRNA reductions may gradually deviate from the developmental norm, resulting in late-stage failures such as shortened longevity. In the optimal culture condition, the survival to adulthood is indeed normal in the dcr-1 KD line but, importantly, adult longevity is reduced by ~90%. When flies are stressed by high temperature, dcr-1 KD induces lethality earlier in late pupation and, as the perturbations are shifted earlier, the affected stages are shifted correspondingly. Hence, in late stages of development with deviations piling up, GRN would be increasingly in need of stabilization. In conclusion, miRNAs appear to be a solution to weak but constant environmental perturbations.

Talk by **Jian Lu**:

(81) Evolutionary dynamics of SARS-CoV-2

Virus evolution: from basic research to public health applications

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Coronavirus disease 2019 (COVID-19), caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), has escalated into a global pandemic, profoundly affecting public health and the global economy. Since the release of the first SARS-CoV-2 genome, thousands of genetic variants have emerged from patient samples worldwide. Our study categorizes SARS-CoV-2 genomes in the early outbreak into two primary lineages, L and S, based on variants at positions 8782 and 28144. Evolutionary analysis indicates that the S lineage is ancestral, with the L lineage subsequently evolving from it. By analyzing 271 COVID-19 patients from the early outbreak, we observed significant differences in clinical severity between the L and S lineages, suggesting that lineage tracking can offer insights into disease management. Our research also identified extensive epistasis and advantageous compensatory mutations among closely linked variants in SARS-CoV-2. Notably, the rising number of infections has accelerated the virus's evolution. The S gene, especially the S1 region, displays signs of positive selection in both SARS-CoV-2 and other coronaviruses. While the S1 N-terminal domain shows positive selection signals across all coronavirus genera, it's the S1 C-terminal domain (receptor-binding domain) that primarily undergoes positive selection in SARS-CoV-2. Furthermore, we observed that SARS-CoV-2 favors codons less preferred by humans. This codon deoptimization might attenuate protein expression as the virus evolves. Our findings underscore the significance of codon usage in viral evolution and shed light on optimizing codons for mRNA and DNA vaccine development.

Talk by **Jing Lu**:

(82) The rise of bony vertebrate body plan

Early evolution of vertebrates from evo-devo and paleontological perspectives

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Osteichthyans, or bony vertebrates, gave rise to two primary branches: one excelled in aquatic environments, while the other, approximately 380 million years ago, evolved into tetrapods, including humans. However, our understanding of Silurian bony fishes was limited to isolated scales and bone fragments. Such scarcity posed challenges in comprehending their overall body structure, phylogenetic status, and crucial features like feeding morphology. Here we present a remarkably preserved specimen of *Megamastax amblyodus*, the largest Silurian vertebrate and potentially the earliest apex predator among vertebrates. The specimen was recovered from the Kuantu Formation, dating back to the Late Ludlow period, approximately 423 million years ago, in Yunnan, China. High-resolution computed tomography (HRCT) scanning has unveiled intricate details of various anatomical components, including the neurocranium, palatoquadrate, dermal skull roof, cheek bones, operculum, and dentition. Notably, the inner dentition comprises a series of structures called "tooth cushions," a distinctive form of osteichthyan dentition previously documented only in isolated micro remains of *Lophosteus* from the Silurian Baltic region. The braincase, remarkably, lacks an intracranial joint and features enclosed aortic canals reminiscent of chondrichthyans. However, the dermal cheek bones of *Megamastax* exhibit similarities to those of primitive osteichthyans like *Psarolepis* and basal actinopterygians. Such pattern of the skull roof diverges significantly from known osteichthyans and instead shares similarities with the "maxillate placoderm" *Entelognathus*. This unique combination of chondrichthyan, osteichthyan, and "maxillate placoderm" features suggests that *Megamastax* occupies a position proximate to the origin of the gnathostome crown group. The new discovery offers new insights into the evolutionary pathways through which early osteichthyans developed their body plan.

Talk by **Wenji Luo**:

(83) The last stand: genomes reveal terminal endangerment of tropical species in Southwest China

The genomics of adaptation and speciation

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Modern genomic approaches allow for the detection of cryptic speciation in which species pairs with a conservative morphology have actually separated into deeply diverged lineages. Such discoveries have important ramifications for the conservation of endemic and endangered species. *Vatica guangxiensis* is an endangered species of the family Dipterocarpaceae endemic to southwest China. The species is restricted to three known natural populations and faces the severe threat of extinction. We sequenced more than 80% of known individuals (229), including all available adults and saplings, of *V. guangxiensis* across the three sites of occurrence using over 10,000 genome-wide SNPs to explore the population genomic status of *V. guangxiensis* and potential cryptic speciation. We detected deep genomic differentiation between populations from Guangxi and Yunnan provinces with an estimated divergence at ~3.5 Mya and a lack of subsequent gene flow. Our results support the historic taxonomical treatment that populations in Yunnan and Guangxi constitute two distinct taxa. All populations exhibit a loss of genetic diversity and excess of low frequency alleles, suggesting recent bottlenecks. Forward simulations suggest imminent crashes in the genetic diversity of populations and a need for immediate conservation. Our study unravels the historical differentiation of two species that had

been overlooked for decades because of their morphological conservatism. It highlights the terminal endangerment and the urgent need for conservation of extremely small tropical or subtropical populations of plant species with a strong signal of genomic vulnerability akin to *V. guangxiensis*.

Poster by **Chandrakanth M:**

(84) Breaking Canonical Life-History Trait Correlations: A Study on *Drosophila melanogaster*

Evolvability: a common currency of evolution, ecology and development

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Organisms often encounter varying environments which prompt them to exhibit phenotypic plasticity as a adaptive mechanism. This phenotypic plasticity allows the modification of plastic traits to enhance organismal fitness within a given environment, thus altering correlations between various phenotypic traits. Life-history traits are one of many traits which show plasticity in the face of a changing environment. Body size, lifespan, fertility, and stress resistance such as starvation and desiccation resistance are among the most important life-history traits. These traits show phenotypic, physiological and genetic correlations often manifesting as trade-offs, but can also lead to positive correlations under certain conditions. Previously, studies have shown a trade-off between lifespan and reproduction, and positive correlations in body size and fertility, body size and lifespan, and in body size and stress resistance under different nutritional environments. A key aspect of organismal life-history evolution is to acquire and allocate the energy derived from nutrients across different life stages which are necessary for growth, development and maintenance of vital functions. This distribution of energy primarily dictates the extent and direction of trait correlations including trade-offs. Prior research has primarily investigated the influence of nutrition in regulating trait correlations, by manipulating macronutrient composition in the diet at a specific organismal life stage. However, the impact of such dietary manipulation in conjunction with their nutrient availability at different life stages on these trait correlations is not very well understood. In our study, we aim to address the cross-talk of stage specific dietary manipulation on trait correlations using the holometabolous insect model, *Drosophila melanogaster*. We have measured adult traits such as body size, fertility, lifespan, starvation resistance and desiccation resistance under four distinct nutritional regimes consisting of two isocaloric diets (protein-rich and carbohydrate-rich) for each of the larval and adult stages in a full-factorial experimental design. Our findings shows the disruption of canonical correlations between life-history traits. Firstly, a carbohydrate rich larval diet promotes increased body size but fails to correspondingly enhance the fertility. Secondly, the classic trade-off between lifespan and reproduction is disrupted in flies fed with protein-rich adult diet. Finally, the trade-off between body size and lifespan is broken in flies fed with protein-rich adult diet. This study contributes valuable insights into the complex interaction between stage-specific diet and life-history traits. In conclusion, the exploration of correlations among life-history traits and the influence of stage-specific dietary manipulation on these correlations, highlights the complexity of biological systems and emphasizes the need for interdisciplinary approaches to unravel them.

Talk by **Yafei Mao**:

(85) The roles of structurally complex region in primate evolution and human neurological disease

Genetics of adaptation and evolution of novel traits

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Understanding the evolutionary history of genetic loci associated with novel traits is a key objective in evolutionary biology. Numerous traits emerge or disappear over time in primate evolution. However, our knowledge of the roles played by structurally complex regions in primate evolution and their association with traits has been constrained by technological limitations. Here, we used long-read sequencing to generate high-quality genome assemblies for eight primate species. We found 1,607 structurally complex regions wherein recurrent structural variation contributes to creating SV hotspots where genes are recurrently lost (CARDs, ABCD7, OLAH) and new lineage-specific genes are generated (e.g., CKAP2, NEK5) and have become targets of rapid chromosomal diversification and positive selection (e.g., RGPDS). The genes within structurally complex regions or the genetic architecture of these regions are likely associated with primate trait evolution and potentially implicated in human neurological disease. High-fidelity long-read sequencing has made these dynamic regions of the genome accessible for sequence-level analyses within and between primate species for the first time.

Talk by **Joanna Masel**:

(86) High deleterious mutation rates drive non-equilibrium dynamics

Genomic diversity in nonequilibrium populations

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The genome-wide deleterious mutation rate in humans has a lower bound of $U_d > 2.1$. However, detailed balance between deleterious and beneficial alleles is impossible for $U_d > 1$ (Kondrashov 1995). Instead of equilibrium, a smaller number of large effect beneficial fixations compensate for a larger number of small effect deleterious mutations. This can lead to ratcheting complexity in a similar way to the drift barrier hypothesis, but differs in that it requires high U_d but does not require low population size N (Matheson et al. 2023). With high U_d , neutral genetic diversity is depressed more by background selection from unlinked sites than from linked sites (Matheson & Masel 2023). Widespread linkage disequilibrium between unlinked sites can be seen in simulations, as low variance in the number of deleterious mutations per individual, below the mean. This pattern was previously documented empirically, but interpreted as evidence for synergistic epistasis (Sohail et al. 2017). We show it arises due to background selection alone in the non-equilibrium $U_d > 1$ regime. Our finding of such strong background selection also has implications for population genetics in the wake of population bottlenecks, which sample rare deleterious mutations. When recessive, this intensifies already-strong background selection, in populations that are already beyond the limit of purging.

Talk by **Juha Merilä**:

(87) Secondary contact, introgressive hybridization and genome stabilization in sticklebacks

The genomics of adaptation and speciation

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Advances in genomic studies have revealed that hybridization in nature is pervasive and raised questions about the dynamics of different genetic and evolutionary factors following the initial hybridization event. While recent research has proposed that the genomic outcomes of hybridization might be predictable to some extent, many uncertainties remain. With comprehensive whole-genome sequence data, we investigated the genetic introgression between two divergent lineages of nine-spined sticklebacks (*Pungitius pungitius*) in the Baltic Sea. We found that the intensity and direction of selection on the introgressed variation varied across different genomic elements: while functionally important regions had experienced reduced rates of introgression, promoter regions showed enrichment. Despite the general trend of negative selection, we identified specific genomic regions that were enriched for introgressed variants and within these regions, we detected footprints of selection, indicating adaptive introgression. We found the selection against the functional changes to be strongest in the vicinity of the secondary contact zone and weaken as a function of distance from the initial contact. Altogether, the results suggest that the stabilization of introgressed variation in the genomes is a complex, multi-stage process involving both negative and positive selection. In spite of the predominance of negative selection against introgressed variants, we also found evidence for adaptive introgression variants likely associated with adaptation to Baltic Sea environmental conditions.

Poster by **Minato Miyake**:

(88) Insights into the evolutionary origins of neurons from functions of putative neurogenic transcription factors in Ctenophora

Marine evo-devo: new frontiers from emerging marine model organisms

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The arise of the nervous system is a hallmark of animal evolution, yet little is known of the evolutionary origins and characteristics of neurons in ancestral animals. To answer this, Ctenophora are an optimal target of investigation, as they are the earliest-branching extant animal lineage with neurons. However, ctenophores do not seem to possess major neural genes and neurotransmitters known in Cnidaria/Bilateria (1). A recent study also revealed ctenophores to develop a syncytial neural network of subepithelial neurons (2). These data indicate that the ctenophore nervous system consists of, at least in part, unique molecular and structural features which may have evolved independently from other metazoans. Nonetheless, the molecular mechanisms responsible for their neurogenesis remain unclear, making it difficult to reconstruct the initial processes of neuronal evolution. Recently, our lab identified multiple neuropeptides of the new model ctenophore *Bolinopsis mikado*, revealing common genetic features of neurosecretory machinery between ctenophore and cnidarian/bilaterian peptidergic neurons (3). By using these neuropeptides as definitive neural markers of Ctenophora, we found that transcription factors (TFs), such as bHLH, POU, and SOX, which are pivotal for neurogenesis in Cnidaria/Bilateria, are expressed in neural cell clusters of the ctenophore single-cell RNA-seq dataset. Here, we present our recent progress on expressional and functional analyses of these potential neurogenic TFs in *B. mikado* larvae. In particular, morpholino oligo knock-down of target TFs was performed, and downstream genes were investigated using RNA-seq. Ultimately, the results are hoped to help elucidate the extent to which neurogenic mechanisms are conserved across all animal lineages and provide insights to reconstruct the initial processes of neuronal evolution. References: (1) Moroz, L. L., Kocot, K. M., Citarella, M. R. et al. (2014). The ctenophore genome and the evolutionary origins of neural systems.

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Talk by **Kazuhide Miyamoto**:

(89) Morphogenetic mechanism of the spiny ray in acanthomorpha fish and implication for the fin diversification.

Open category

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Fish fins are one of the most diversified organs in the vertebrates. These structures acquire various functions and facilitate adaptations to various habitats. The free parts of teleost fins are commonly supported by bone structures called “fin rays,” which are further divided into “soft rays” and “spiny rays”. Soft rays are flexible, segmented and mostly branching, whereas spiny rays are stiff, unsegmented, fused of two half-segments (hemitrichia), and which terminate in an acute point. They have evolved independently in several teleost lineages. Spiny rays of acanthomorph fishes are called a “true spine,” and these structures extremely modified in several clades. For example, the sucking disc of remoras has “pectinated lamellae,” formed by bilateral extensions of the base of spiny rays. Anglerfish have an “illicium,” in which spiny rays are modified into and serve as a fishing apparatus. The diversity of spiny ray morphology has attracted considerable morphological, and evolutionary interest. Thus, it is important to understand the underlying mechanism(s) by which these spiny rays form and enable their diversification in some Acanthomorpha lineages. Developmental mechanism of spiny ray is unknown. To elucidate the mechanism, we should examine the morphogenesis using laboratory animals at the levels of cellular and molecular developmental biology. However, popular model fish, zebrafish and medaka, lack spiny rays and do not suitable for studies of spiny rays. Thus, we used the dwarf neon rainbowfish *Melanotaenia praecox*, a small freshwater fish within the order atheriniformes native to northern New Guinea, as a new model fish to study the spiny ray ontogeny. This species has spiny rays in their dorsal, anal, pectoral, and pelvic fins. In our previous studies, the post embryonic staging of this species and microinjection procedure for genetic engineering were established. In this report, we examined cell and extracellular matrix dynamics in the process of the spiny rays development of *M. praecox*. Surprisingly, we found that actinotrichia, which is known as an important ECM structure in zebrafish fin ray growth, are not play a role in spiny ray development. Furthermore, we describe the distribution of the mesenchymal cells, ECM structures and gene expressions of spiny rays in detail. We found that there are the aggregation of the mesenchymal cells and thickened ECM, such as Laminin, layer surrounding the tip of the spiny ray. From our results, we conclude that soft and spiny rays have greatly different morphogenetic processes. Taken together, we speculate that this unique morphogenesis of the spiny rays may facilitate their evolvability and diversification.

Talk by **Paolo Momigliano**:

(90) Biases in demographic modelling affect our understanding of recent divergence

The genomics of adaptation and speciation

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Reconstructing the demographic history during the early stages of population divergence is central to understand fundamental processes in evolutionary biology, such as how populations adapt to novel environments and how reproductive isolation between incipient species arises. One popular approach to test evolutionary scenarios and infer demographic parameters is to obtain summary statistics from a set of populations, and compare them to simulated data in order to choose the most likely model and infer its parameters. As models are always extreme simplifications of a complex reality, it is unclear what the effects of ignoring such complexities are on model choice and parameter estimations. Using simulations, we demonstrate that under realistic scenarios of population divergence, failure to account for population size changes in a daughter population or the ancestral population leads to severe biases in both model choice and parameters estimations. Similarly, ignoring metapopulation structure can also severely affect demographic inference. The inference of divergence time and changes in patterns of gene flow through time, some of the parameters of most interest in the study of speciation, can be strongly biased when using oversimplified models. We illustrate these issues reconstructing the demographic history of North Sea and Baltic Sea turbot (*Schophthalmus maximus*) by testing 16 Isolation with Migration (IM) and 16 secondary contact (SC) scenarios, modelling changes in N_e as well as the effects of linked selection and heterogeneous migration rates across the genome. As in the simulated data, failure to account for changes in N_e resulted in selecting SC models with a long period of strict isolation and divergence times preceding the formation of the Baltic Sea. In contrast, models accounting for N_e changes suggest the Baltic Sea turbot population originated from a very recent (<6 kya) invasion and diverged with constant gene flow from the North Sea. The results have implications for the study of speciation, high-lighting the potential effects of ancestral size changes, bottlenecks, and metapopulation structure on choices between competing scenarios. In general, extreme caution should be exercised when interpreting results of demographic model comparisons.

Talk by **Paolo Momigliano**:

(91) Parallel evolution despite low genetic diversity in Europe's ancient sticklebacks

The genomics of adaptation and speciation

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The three-spined stickleback (*Gasterosteus aculeatus*) is a model system to study parallel adaptation due to its repeated evolution of similar phenotypes in numerous independent colonisations of freshwater habitats. Most of this parallelism stems from parallel selection on alleles that are identical by descent and are maintained in low frequencies in marine populations. Recent evidence suggests that degrees of parallel evolution in sticklebacks are geographically heterogeneous and constrained by demographic history. Since previous genetic research on European sticklebacks was biased towards high-latitude regions, we investigated southern populations thought to stem from a lineage which subsequently colonised the rest of Europe after the last glaciation. As southern marine populations are believed to have gone extinct, the spread of alleles between different southern European populations has been highly unlikely, potentially limiting parallel evolution. We compared levels of genetic differentiation and genetic parallelism of 19 Adriatic and Iberian stickleback populations to Pacific, Atlantic and Caspian counterparts, where gene flow between freshwater populations across extant marine populations is still possible. Our results support previous findings that southern

populations are highly differentiated and of low genetic diversity. Linkage disequilibrium network analyses revealed unexpectedly high levels of genetic parallelism in southern European freshwater populations, which is a likely relic of freshwater adaptation prior to the extinction of marine sticklebacks. Weakening parallelism signatures with latitude likely reflect the diversity loss at the frontiers of the last colonisation wave towards northern Europe, highlighting the importance of demographic history in shaping contemporary patterns of parallel adaptation.

Talk by **Antonia Monteiro**:

(92) Prolegs are novel traits, not leg homologs

Genetics of adaptation and evolution of novel traits

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Lepidopteran larvae have both thoracic legs and abdominal prolegs, yet it is unclear whether these are serial homologs. A RNA-seq analysis with various appendages of *Bicyclus anynana* butterfly larvae indicated that the proleg transcriptome resembles the head-horn transcriptome, a novel trait in the lepidoptera, but not a thoracic leg. Under a partial segment abdominal-A knockout, both thoracic leg homologs (pleuropodia) and prolegs developed in the same segment, arguing that both traits are not serial homologs. Further, four coxal marker genes, *homothorax*, *Sp5*, *Sp6-9*, and *araucan*, were absent from prolegs but two endite marker genes, *gooseberry* and *Distal-less*, were expressed in prolegs, suggesting that prolegs may be using a modular endite gene-regulatory network (GRN) for their development. We propose that larval prolegs are novel traits derived from the activation of a pre-existing modular endite GRN in the abdomen, using abdominal-A, the same Hox gene that still represses legs in more lateral positions.

Talk by **Lin Na**:

(93) Latitudinal gradient control on early Paleozoic biodiversity and ecosystem functioning

Paleo- and macro- ecology in tropical Asia

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Marine communities differ in species richness at global and provincial scales. That the diversity declines from equatorial to polar regions (latitudinal diversity gradient, LDG) is the most pervasive pattern in modern ecosystem. Although recognized for more than two centuries, the underlying mechanisms responsible for elevated low-latitude richness are still unclear. Deriving LDG patterns in deep time can help us understand how biodiversity is generated and maintained, as well as how species composition and biodiversity responded to major extinction events. Here we use fossil occurrences data documented in the Paleobiology, Geobiodiversity, and PhytoPal databases, to derive LDG patterns from the Cambrian to the Silurian among different geographic regions and trophic communities to elucidate ecological and environmental drivers of biogeographic changes over the early Paleozoic. To further understand the functional consequences of the changes in diversity and faunal composition along latitudinal gradient, we classified taxa into different functional groups based on their functional traits. By quantifying functional traits of all taxa, we assess the relationship between functional and taxonomic diversities among biogeographic regions. By dissecting diversity dynamics along ecological and latitudinal gradients, we aim to find key controls on variation in geographic distribution of biodiversity in early Paleozoic marine ecosystem. We find that there is no strikingly LDG trend in the early Paleozoic. Regional differences of faunal composition and biodiversity in non-tropics are strongly controlled by sampling bias, and long-term variation in climate and plate tectonics pose strong influences on biogeographic differences in both taxonomic and functional diversities.

Poster by **Chen Siang Ng**:

(94) The density of Z-DNA may be correlated with some phenotypic attributes in birds

The genomics of adaptation and speciation

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Z-DNA is a high-energy alternative conformation of the DNA double helix in which it has potential roles in gene expression, DNA damage and repair, and implications in certain disease processes. Z-DNA forming sequences are not evenly distributed across the genomes, and their density can vary widely among different organisms based on their genomic complexities and evolutionary histories. In avian genomes, which are generally more compact compared to mammals, the information on Z-DNA density has not been well delineated yet. Here, we applied a predictive tool to estimate Z-DNA forming regions in 79 avian genomes and utilized global datasets of the physiological, anatomical, ecological, and geographical characteristics of birds. We showed that the density of Z-DNA is correlated with body mass and flight efficiency. This study may provide insights into the density and biological roles of this alternate DNA structure across different vertebrates.

Talk by **Francis Nge**:

(95) Macroevolution dynamics of tropical Asia, with a focus on the diverse tropical plant lineage Magnoliids and Annonaceae

Paleo- and macro- ecology in tropical Asia

Francis Nge¹

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Tropical Asia is one of the most biodiverse regions on the planet and highly threatened – including four global biodiversity hotspots within the region. With over 10,000 species in four orders (Canellales, Laurales, Magnoliales and Piperales), Magnoliids is the third most diverse clade of Angiosperms, after monocots and eudicots. Within Magnoliids, Annonaceae is one of the largest families with over 2,500 species distributed across the tropics with highest species diversity in South East (SE) Asia. These clades have a mainly pantropical distribution making it an excellent model to investigate how tropical lineages have diversified through time and space, and answer broader questions relating to tropical systems e.g. what are the major drivers of hyperdiversity in tropical rain forests? Here, we present a near-complete genus-level phylogenomic dataset of Magnoliids and near-complete species-level phylogeny of Annonaceae (> 2000 species included), obtained through high-throughput sequencing hybrid capture approaches. We performed a series of diversification analyses to investigate diversification history of these clades at a broad scale across the tropics. Our phylogenomic dataset provides a robust framework for further systematic and macroevolutionary studies of Magnoliids and Annonaceae. In addition, we utilise an inter-disciplinary approach: integrating novel spatial, morphological, and paleo-climatic data with phylogenetics to better understand the evolution and macro-ecological dynamics of Tropical Asian biodiversity at a global level. The key phylogenomic and diversification results from this study, as well as implications, ongoing work, and research prospects will be discussed.

Poster by **Sofie Nilén**:

(96) The effect of assortative mating on colour morphs, body size and population of origin in a polymorphic insect

Open category

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Assortative mating, where individuals mate non-randomly with respect to phenotype or genotype, can have profound evolutionary consequences. However, little is known about the underlying mechanisms and consequences of assortative mating, especially in polymorphic species. The common bluetail damselfly (*Ischnura elegans*) is a polymorphic insect with three heritable female colour morphs, including a male mimic. This polymorphic system is characterized by strong and spatially varying sexual selection. Here, I investigated the mechanisms of assortative mating within and among populations of this species where I quantified the direction and strength of assortative mating on body size and its effect on fitness within populations, including morph specific effects. I used a 22-year data set of mating pairs of *I. elegans*, with known body size and female fecundity of the three colour morphs from multiple field populations in southern Sweden. I have conducted a mate-choice experiments and quantified the direction and strength of assortative mating with respect to both body size and in relation to immigrant status (resident vs. foreign males). This colour polymorphism is sex-limited in expression and only visible in females. Since morph determination is due to a single autosomal locus, males also carry the colour alleles even if they do not phenotypically express the polymorphism. I am currently genotyping males and females with respect to the morph locus. I will use this information to investigate if the morph locus affects assortative mating in both sexes.

Talk by **Yuichi Oba**:

(97) Firefly and its bioluminescent property

Genetics of adaptation and evolution of novel traits

Yuichi Oba¹

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Firefly is a bioluminescent beetle. All species emit light in larval stage for aposematic display, and some also emit in adult stage for sexual communication. The bioluminescent reaction was explained by the oxidation of the substrate luciferin catalyzed by the enzyme luciferase in the presence of O₂ and ATP. To understand the evolutionary process of the bioluminescent property, we performed whole genome analysis of two firefly species; a Japanese aquatic species *Aquatica lateralis*, and North American terrestrial species *Photinus pyralis*. The result revealed that firefly appeared on earth at Cretaceous period by tandem gene duplication and neo-functionalization of acyl-CoA synthetase to give ancestral luciferase. The luminescence color of the ancestral luciferase was green.

Talk by **Michael Orr**:

(98) How has floral specialization influenced bee evolution?

An evolutionary perspective on pollinator biodiversity, systematics, and conservation

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How and why animals specialize on resources are fundamental questions in biology. In the case of bees, the answers to these questions have important consequences cascading throughout ecosystems and crops alike via the invaluable pollination services they provide. Studies have investigated patterns of floral specialization

in small groups of bees previously, but many questions remain. Primary among these are whether specialization or generalization are ancestral, and whether specialization might be associated with accelerated diversification rates. Here, we leverage the largest bee phylogeny to date to explore the diversification dynamics of bee-flower relationships.

Talk by **Qiaowei Pan**:

(99) The lncRNA ANTSTR coordinates complementary sex determination in ants.

Why sex? insights from asexual genomes

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Animals have evolved a variety of mechanisms for sex determination. About 12% of animal species employ haplodiploid sex determination: males develop parthenogenetically from unfertilised eggs and are haploid, and females from fertilised eggs and are diploid. Here we identify a new mechanism of sex determination underlying haplodiploidy in the ant *Linepithema humile*. A multiallelic regulatory region (Lh-CSD) acts as the primary signal of sex determination in a haplodiploid system. Heterozygous embryos at Lh-CSD develop into females while homozygotes and hemizygotes (haploid individuals) develop into males. Heterozygosity at Lh-CSD greatly increases the expression of ANTSTR, an adjacent long non-coding RNA, thereby providing information on the homozygosity/heterozygosity status of Lh-CSD. Knockdown of ANTSTR in female-destined embryos (i.e., Lh-CSD heterozygotes) resulted in the production of a male-specific splicing form of transformer (*tra*). Comparative analyses indicate that ANTSTR is an ancient, yet rapidly evolving gene in Aculeata. In addition to identifying the first lncRNA acting as a master sex determination gene, this study uncovers a new regulatory mechanism based on complementarity among multiple alleles.

Poster by **Rahayu Pertiwi**:

(100) The genetic basis of wing pigmentation pattern evolution in *Drosophila suzukii* and its closely related species

Open category

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Organisms exhibit various color patterns, which evolve through the processes of de novo origination and modification. While both of these modes are essential for the evolution of patterns, less attention has been given to understanding how the latter process takes place. The diverse wing pigmentation patterns in *Drosophila* species, ranging from a single dark spot to a complex mosaic pattern, is a good model system to investigate the genetic basis underlying de novo as well as modification processes. In particular, the male wings of the species of the *suzukii* subgroup, *Drosophila suzukii*, *D. biarmipes*, and *D. subpulchrella*, have a single dark spot at the distal tip that have undergone slight shifts regarding the position and size. The “shift” represents a modification process of the newly formed spot in the lineage leading to these species. In this study, we investigate how this modification process took place by analyzing the association with vein positions and the locations of Quantitative Trait Loci (QTL) using these species. The wing pigmentation pattern in males was quantified as the relative wing spot position and size along the first and second longitudinal veins (L1 and L2). The measurement of multiple strains of these species indicated that the spot position of *D. subpulchrella* is located closer to the proximal direction of the wing and the spot size is significantly larger compared to those of the other two species. These comparisons inferred the wing pigmentation of *D. subpulchrella* is a derived phenotype that has evolved after the split from *D. biarmipes*. The intersection of the L1 and L2 vein,

close to the area where the spot forms, has also shifted towards the proximal direction in *D. subpulchrella*. To identify the genomic regions that are responsible for the shifts in wing spot pigmentation traits between *D. suzukii* and *D. subpulchrella*, we performed a QTL analysis using backcrossed individuals. The result revealed that the genomic regions that are responsible for wing spot size are on chromosome X and the right arm of chromosome 3. These regions consist of large structural rearrangements between the two species. Moreover, the semi-introgression lines using the introduced visible markers on those two genomic regions are being generated to examine the effects of these unique genomic regions at a sub-chromosomal scale.

Talk by **Michal Polak**:

(101) Flight or mite? The evolutionary ecology of costly behavioral resistance to ectoparasitic mites

Open category

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Significant heritability of anti-parasite adaptations is a typical feature of natural host populations, which is paradoxical in light of the theoretical expectation that natural selection should erode additive genetic variation for fitness-related traits. A major hypothesis for the maintenance of genetic variation for parasite resistance invokes trade-offs between resistance and other fitness-conferring traits. The present study demonstrates significant heritability for behavioral resistance against ectoparasitic mites, *Gamasodes queenslandicus* (Parasitidae), in a natural population of the fly, *Drosophila melanogaster* (Drosophilidae). Deployment of energetically expensive bursts of flight was a main mechanism of resistance against mite attack. RNA-seq and functional studies identified candidate host metabolic genes involved in resistance, consistent with the fact that flight is an energetically expensive form of defense. Among adult flies, whole-body lipid and protein reserves were reduced in ectoparasite-resistant lines relative to control lines, and consequently starvation resistance was compromised also. These results suggest antagonistic pleiotropy between host resistance and host nutrient management. We also tested for costs of resistance at the larval stage of the host life cycle under variable levels of environmental stress. Resistant lines expressed significant reductions in larva-to-adult survivorship with increasing toxic (ammonia) stress, identifying an environmentally modulated pre-adult cost of resistance. Thus, ectoparasite resistance in flies is an ecologically important trait with significant evolutionary potential maintained in part by environmentally modulated costs of resistance expressed across the host life cycle. The results shed light on the genetic, physiological and behavioral components of evolutionary relevant trade-offs affecting parasite resistance.

Talk by **Audrey Miranda Prasetya**:

(102) Beyond Endpoints: Islands drive radiation of passerine birds in the Indo-Australian Archipelago

Open category

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Islands are often perceived as endpoints of colonization. However, recent research has highlighted the pivotal role of islands as sources of both speciation and dispersal. In regions of high species turnover such as the Indo-Australian Archipelago, dispersals have typically been treated as a dichotomy between the main continental shelves of Sunda and Sahul. This undermines the role of intervening islands to act not only as sites of insular diversification but also as sources of radiation following upstream colonization events. We aim to explore the substantial role of islands using large-scale ancestral state estimations on passerine birds of the Indo-Australian Archipelago. We tested the effects of historical changes in connectivity, compared within-area

diversifications along with inwards and outwards dispersal between areas, and investigated speciation events occurring post-upstream dispersal. We show that islands such as Wallacea, New Guinea, and the East Melanesian arc disproportionately influence the generation of lineages that further diversify into major clades of the passerine super radiation. These findings support recent perspectives that position islands as catalysts for colonization. Our study underscores the important biogeographical role of islands, highlighting their dual capacity as both sources and sinks. By shedding light on the ability of islands to drive radiations across a region, our research offers insights with broad implications for understanding the dynamics of species diversification and biogeography.

Talk by **Wenfeng Qian**:

(103) Evidence for a mouse origin of the SARS-CoV-2 Omicron variant

Virus evolution: from basic research to public health applications

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The rapid accumulation of mutations in the SARS-CoV-2 Omicron variant that enabled its outbreak raises questions as to whether its proximal origin occurred in humans or another mammalian host. Here, we identified 45 point mutations that Omicron acquired since divergence from the B.1.1 lineage. We found that the Omicron spike protein sequence was subjected to stronger positive selection than that of any reported SARS-CoV-2 variants known to evolve persistently in human hosts, suggesting a possibility of host-jumping. The molecular spectrum of mutations (i.e., the relative frequency of the 12 types of base substitutions) acquired by the progenitor of Omicron was significantly different from the spectrum for viruses that evolved in human patients but resembled the spectra associated with virus evolution in a mouse cellular environment. Furthermore, mutations in the Omicron spike protein significantly overlapped with SARS-CoV-2 mutations known to promote adaptation to mouse hosts, particularly through enhanced spike protein binding affinity for the mouse cell entry receptor. Collectively, our results suggest that the progenitor of Omicron jumped from humans to mice, rapidly accumulated mutations conducive to infecting that host, then jumped back into humans, indicating an inter-species evolutionary trajectory for the Omicron outbreak.

Talk by **Archishman Raju**:

(104) A Theoretical Perspective on Waddington's Genetic Assimilation Experiments

Open category

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Genetic assimilation is the process by which a phenotype that is initially induced by an environmental stimulus becomes stably inherited in the absence of the stimulus after a few generations of selection. While the concept has attracted much debate after being introduced by C. H. Waddington seventy years ago, there have been few experiments to quantitatively characterize the phenomenon. Here, we revisit and organize the results of Waddington's original experiments and follow-up studies that attempted to replicate his results. We then present a theoretical model to illustrate the process of genetic assimilation and highlight several aspects that we think require further quantitative studies, including the gradual increase of penetrance, the statistics of delay in assimilation, and the frequency of unviability during selection. Our model captures Waddington's picture of developmental paths in a canalized landscape using a stochastic dynamical system with alternative trajectories that can be controlled by either external signals or internal variables. Our results provide theoretical insight into the concepts of canalization, phenotypic plasticity, and genetic assimilation.

Talk by **Frank Rheindt**:

(105) The build-up and loss of genetic diversity in Southeast Asian biota

Plenary talk

Frank E. Rheindt¹

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In many respects, Southeast Asia is a singular evolutionary arena. Like the rest of the world, it has been subject to ~20 Quaternary cold epochs ('ice ages'), but more so than any other region, it has undergone extreme fluctuations in the distribution of land across the world's most complex island realm, the Indonesian Archipelago. In modern times, Southeast Asia has become one of the most densely inhabited regions on Earth, highly affected by the modern environmental crisis. In this talk, we will explore the pronounced impact that Southeast Asia's unique history has had on the evolutionary trajectories of its birds and other vertebrate biota, and how the recent anthropogenic change has impacted its species in terms of genetic diversity loss.

Talk by **Kenneth F Rijdsdijk**:

(106) Mapping Coastline Evolution and Sea Depth Dynamics in SE Asia since the last ice age 26 ky ago

Paleo- and macro- ecology in tropical Asia

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We present a global geophysical based coastline and sea depth model to produce accurate reconstructions of coastline positions, shelf seas, and coral seas, covering a time span from the last glacial maximum 26,000 years ago to today. Its precision is achieved by incorporating geological data to account for factors like crustal deformation, gravitational effects from ice sheets, and local uplift and subsidence rates. This flexibility allows for adjustments based on localized variations in sea levels. The model generates raster and polygon outputs at regular intervals of at least 500 years, enabling detailed measurements of coastal changes and sea depth shifts. These reconstructed geographical configurations and rates allow for biogeographic and statistical analyses, offering insights into the impact of spatial dynamics on ecosystems, species migrations and biodiversity. An interactive map of the Sunda-Saharan region is presented, showing how connections between key islands like Borneo, Sulawesi, New Guinea, and satellite islands have evolved since the last ice age. Also the spatial dynamics of shallow seas <40 m is demonstrated. To ensure consistency and ease of use, we integrated our workflow into the Temporal Altitudinal Biomes Shift (TABS) R package. This package provides a user-friendly default setup applicable to islands globally, with the option to include local bathymetric models and geological data, such as uplift and subsidence rates. TABS not only captures the dynamic nature of past terrestrial and marine biomes, but also provides a valuable tool for projecting future sea-level rise scenarios. By integrating geological, climatic and ecological dynamics, we aim to bridge the gap between theoretical models and practical applications, providing a comprehensive framework to better understand and manage the evolving landscapes of our planet's biomes.

Talk by **Keita Saito**:

(107) Developmental noise and phenotypic plasticity are correlated in *Drosophila simulans*

Evolvability: a common currency of evolution, ecology and development

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Non-genetic variation is the phenotypic variation induced by the differential expression of a genotype in response to varying environmental cues and is broadly categorized into two types: phenotypic plasticity and developmental noise. The former is the reaction norm to environmental changes, thus plasticity is caused by external factors. The latter is phenotypic variation caused by random fluctuations in chemical and physical signaling processes during development. However, unlike plasticity developmental noise depends solely on the local conditions of the developing phenotypes. Therefore, these two sources of non-genetic variation are fundamentally different in their causes, where one depends on external causes and the other on internal fluctuations. These variation aspects have been suggested to play an important role in adaptive evolution; however, the mechanisms by which these two types of non-genetic variations influence the evolutionary process are currently poorly understood due to difficulties in independently accessing the two non-genetic variation. Using a machine-learning based phenotyping tool, we independently quantified the phenotypic plasticity and developmental noise in the wing morphological traits of a fruit fly *Drosophila simulans*. Plasticity must be evaluated by multiple reaction norm, although plasticity was evaluated as the reaction norm to a single environmental cue (e.g., temperature) in most case of previous studies. Therefore, we used three environmental cues, temperature, nutrient condition, and light-dark cycle. In addition, to evaluate accurate developmental noise, we measured fluctuation asymmetry. Utilizing a rearing experiment, we demonstrated plastic responses in both wing size and shape as well as non-zero heritability of both phenotypic plasticity and developmental noise, which suggests that adaptive phenotypic plasticity can evolve via genetic accommodation in the wing morphology of *D. simulans*. We found a positive correlation between phenotypic plasticity and developmental noise, while the correlation between the plastic response to three kinds of environmental factors that were examined (nutrient condition, temperature, and light–dark cycle) were poor. These results suggest that phenotypic plasticity and developmental noise contribute to evolvability in a similar manner, however, the mechanisms that underlie the correspondence between these two variation types remains to be elucidated.

Poster by **Saubhik Sarkar**:

(108) Immunity in the context of ageing and evolution

Evolvability: a common currency of evolution, ecology and development

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Evolutionary theory predicts a rapid decline in the strength of natural selection with ageing and it might become negligible after the prime reproductive age is passed. Natural selection that optimizes organismal physiology for development and reproduction early in life can become too weak to effectively regulate the late-life performances in older individuals. This hypothesis is perhaps consistent with our previous studies with insect models, where immune defense against pathogens turned progressively over-reactive and nonspecific with ageing, which in turn increased the immunopathological costs and post-infection mortality. Also, immunopathological costs of early-life immune activation in juveniles are often paid at later life-stages, leading to faster ageing and morbid phenotypes. However, there are no direct experiments to test how age-specific changes in immune responses in populations are associated with their intrinsic rate of ageing and concomitant weakening of selection pressure beyond the reproductive age. To fill this gap, we used replicated populations of the fruit fly *Drosophila melanogaster* with divergent reproductive schedules and thereby evolving different

ageing rates (e.g. ‘early reproduction-faster ageing’ vs ‘late reproduction-delayed ageing’). We tracked the changes in their immunity and post-infection survival throughout their entire lifespan (i.e. starting from the day of eclosion to their reproductive window and then until the 90 percentiles of their total lifespan). We found that populations evolving with an early reproductive schedule and accelerated ageing rate also showed early onset of immune senescence, characterized by less effective immunity with higher bacterial load and post-infection mortality. Interestingly, populations evolving with delayed reproductive schedules and slower ageing rates had lower immunity and higher infection-related mortality at early stages of their adult lifespan. However, their ability to maintain a balanced immunity and post-infection health was maximised at their reproductive window and then declined rapidly thereafter. These results indicate that weaker selection strength post-reproductive prime can indeed be a plausible driver of both development and ageing of immunity at the population level, with strong implications to health and pathogenic infections.

Talk by **Daiki Sato**:

(109) Genes underlying social collectives of flies under visual threat

The evolution of invertebrate sensory ecology and behaviours

Daiki Sato¹ and Yuma Takahashi²

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Many animals form groups or societies that exhibit characteristic group behavior, called collective behavior. Collective behavior is typically seen in the coordinated shoaling behavior of fish or social division of labor of eusocial insects and differs from simple sums or averages of individuals. The principles and parameters of individual behavior that enable collective behavior have been elucidated through mathematical modeling and observational empirical studies. However, genetic substrates underlying collective behavior remain largely unknown. Here, by extending the genome-wide association analysis that has been limited to the individual to the population level, we aimed to reveal the molecular mechanism of collective behavior and gain a detailed understanding of its evolutionary processes. In this study, we focused on the collective freezing behavior of the model organism *Drosophila melanogaster* when exposed to visual stimuli. With a panel of 104 inbred strains with known genomic backgrounds, we tracked flies’ behavior and quantified fear response and social behavior in group experiments. In our experimental setup, flies were subject to looming stimuli for 5 min (20 trials of a black circle expanding within 500 ms on a white background every 15 sec) after a non-stimulating term for 5 min. We confirmed the fear response toward threatening stimuli, as observed in the significant reduction in locomotor activity. We also observed “group effects”, which mitigate the fear response of flies when surrounded by conspecifics, and this effect was likely achieved by the visual response to motion cues of others. The threshold of the visual response varied among strains, and we conducted genome-wide association analysis to detect genetic variants likely associated with the trait. Those hit above the genome-wide significance level included genes involved in the development of eyes and visual neurons. We are now working on the functional studies of the candidate genes, which can further deepen our understanding of the molecular mechanism of flies’ social interaction that improves group performance.

Talk by **Philipp Schiffer**:

(110) Adaptation of asexual and anhydrobiotic nematodes in extreme environments

Genetics of adaptation and evolution of novel traits

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Deserts are among the most hostile environments to life on earth. Yet, some animals have adapted to survive and diversify in such extreme water limited environments. Evolutionary strategies for this include parthenogenesis enabling the exploration of transient ecological opportunities by offspring of a single individual, and cryptobiosis enabling organisms to wait for abiotic conditions to become favourable. Using

biodiversity genomic assays with latest sequencing methods it is now possible to study genomes of single minute invertebrates, as well as population structures in many samples from extreme environments to understand the evolutionary strategies of different species. Here, I will present our genomic, population genetic, and ecological functional analyses of the linked evolution of these traits in nematodes from the hyper arid Atacama in comparison with the younger, more dynamic Namib desert. We find locally diverse species assemblages. In accordance with evolutionary theory these are dominated by sexual species, but heterozygosity through polyploidy appears provide an adaptive advantage to parthenogens. We observe species to employ anhydrobiosis, a mode of cryptobiosis, in different ways, to either revive fast or more slowly upon water availability. We also recently assembled the genome of a triploid parthenogenetic *Panagrolaimus* revived from another extreme environment, the Russian permafrost. Analysing it genetically and biochemically in comparison to *C. elegans* we find resemblances in the genetic mechanisms the model organism's dauer larva and this nematode use for prolonged dormancy. Using the CRISPR/Cas system we are now able to study cryptobiosis in *Panagrolaimus*, allowing us to understand this trait on a genetic level comparing species from different extreme environments.

Talk by **Daniel Schrider**:

(111) Strong Positive Selection in *Aedes aegypti* and the Rapid Evolution of Insecticide Resistance

Novel insights regarding genome architecture evolution in the arthropoda

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Aedes aegypti vectors the pathogens that cause dengue, yellow fever, Zika virus, and chikungunya and is a serious threat to public health in tropical regions. Decades of work has illuminated many aspects of *Ae. aegypti*'s biology and global population structure and has identified insecticide resistance genes; however, the size and repetitive nature of the *Ae. aegypti* genome have limited our ability to detect positive selection in this mosquito. Combining new whole genome sequences from Colombia with publicly available data from Africa and the Americas, we identify multiple strong candidate selective sweeps in *Ae. aegypti*, many of which overlap genes linked to or implicated in insecticide resistance. We examine the voltage-gated sodium channel gene in three American cohorts and find evidence for successive selective sweeps in Colombia. The most recent sweep encompasses an intermediate-frequency haplotype containing four candidate insecticide resistance mutations that are in near-perfect linkage disequilibrium (LD) with one another in the Colombian sample. It is possible that this haplotype may continue to rapidly increase in frequency and perhaps spread geographically in the coming years. However, we do observe an unusual pattern of LD within this region: although the insecticide resistance mutations are in LD with one another, they are interspersed with stretches of polymorphisms that do not exhibit strong LD with any of the resistance mutations. This crenellated pattern of LD with the resistance mutations may suggest the presence of strong epistasis, undetected structural variation, or both—possibilities that we will examine in future work. Overall, our results extend our knowledge of how insecticide resistance has evolved in this species and add to a growing body of evidence suggesting that *Ae. aegypti* has an extensive genomic capacity to rapidly adapt to insecticide-based vector control.

Poster by **Inge Seim**:

(112) Genomic insights into the retransition to fully aquatic life within superorder Afrotheria

Genetics of adaptation and evolution of novel traits

Inge Seim¹

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The geographical isolation of Africa and Eurasia allowed the independent emergence of fully aquatic mammals approximately 55 million years ago. While the molecular evolution of the more than 100 species of extant cetaceans has received considerable research attention, there has been less attention on the four species of

extant sirenians: the dugong and three manatee species whose ancestors diverged ~30 million years ago. Here, I present recent research insights on the molecular evolution of sirenians. By juxtaposing genomes of the dugong and West Indian manatee, we revealed possible solutions to aquatic life by sirenians, including aquatic herbivory and daily activity patterns in shallow waters. Convergent loss of integumentary system genes, mainly those expressed in the outer layers of the skin, by sirenians and cetaceans agrees with the idea that convergent gene loss occurs in species with similar ecological pressures. We propose that sirenian loss of KCNK18 is related to their shift in activity patterns and may render sirenians, particularly manatees in the colder US waters, susceptible to the often-fatal cold stress syndrome (CSS). Finally, we show evidence that the plentiful Australian dugong populations are relatively healthy, but other populations worldwide may follow the Japanese and Chinese dugongs on the fast track toward extinction.

Poster by **Yue Shi**:

(113) Unraveling the dynamic post-mating gene regulatory network in the reproductive roles of *Monomorium Pharaonis*

Why sex? insights from asexual genomes

Yue Shi¹

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Division of labour is a defining characteristic of the eusocial insect. In *Monomorium pharaonis*, the diploid individuals develop as reproductive gynes and workers who lose their reproductive opportunities for a lifetime. Remarkably, only the inseminated gyne assume the role of reproduction while the unmated individuals progressively transform into worker-like roles within the colony. Mating elicits notable physiological and behavioral change in females but our comprehension of the underlying genetic mechanisms remains constrained. Here, we analyzed the post-mating response in the reproductive tissues of *M. pharaonis*. We showed that similar morphological status between young mated queens and virgins. To identify genetic factors responsible for the physiological and behavioural differences, we compared transcriptomic profiles of mated and unmated queens over two months of post-mating, focusing on the gene expression of the ovary and spermatheca. We found that the early distinction was initiated by the act of insemination, notably characterized by the activation of the innate immune system. The subsequent distinction diminished until 30-day after mating when more pronounced disparities appeared in the ovary. Apart from the time-dynamic gene regulatory network (GRN), the expression of a geneset remains consistently associated with the identity, indicating a robust amplification of the reproductive impact on the ovary. These results showed the temporal dynamics of the post-mating GRN, which serves to enhance our comprehensive understanding of the genetic mechanisms driving the divergent trajectories in mated and unmated females, and offer insights into its evolutionary significance in the broader context of reproductive adaptations.

Talk by **Aidan W. Short**:

(114) Ancient hybridization leads to the repeated evolution of red flowers across a monkeyflower radiation

The genomics of adaptation and speciation

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The reuse of old genetic variation can promote rapid diversification in evolutionary radiations, but in most cases, the historical events underlying this divergence are not known. For example, ancient hybridization can generate new combinations of alleles that sort into descendant lineages, potentially providing the raw material to initiate divergence. In the *Mimulus aurantiacus* species complex, there is evidence for widespread gene flow among members of this radiation. In addition, allelic variation in the *MaMyb2* gene is responsible for differences in flower color between the closely related ecotypes of subspecies *puniceus*, contributing to reproductive isolation by pollinators. Previous work suggested that *MaMyb2* was introgressed into the red-

flowered ecotype of puniceus. However, additional taxa within the radiation have independently evolved red flowers from their yellow-flowered ancestors, raising the possibility that this introgression had a more ancient origin. In this study, we used repeated tests of admixture from whole-genome sequence data across this diverse radiation to demonstrate that there has been both ancient and recurrent hybridization in this group. However, most of the signal of this ancient introgression has been removed due to selection, suggesting that widespread barriers to gene flow are in place between taxa. Yet, a roughly 30 kb region that contains the MaMyb2 gene is currently shared only among the red-flow-ered taxa. Patterns of admixture, sequence divergence, and extended haplotype homozygosity across this region confirm a history of ancient hybridization, where functional variants have been preserved due to positive selection in red-flowered taxa but lost in their yellow-flowered counterparts. The results of this study reveal that selection against gene flow can reduce genomic signatures of ancient hybridization, but that historical introgression can provide essential genetic variation that facilitates the repeated evolution of phenotypic traits between lineages.

Talk by **Shivansh Singhal**:

(115) Genomic Parallelism in Pest Beetle Adaptation to Novel Environments

The genomics of adaptation and speciation

Shivansh Singhal¹ and Deepa Agashe²

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Populations that enter a novel environment face strong and novel selection pressures. Adaptation to novel conditions is of interest to evolutionary biologists, conservation biologists, and ecologists in the context of human-associated environmental change on Earth. How often does adaptation occur using the same alleles across populations and environments? Understanding this parallelism in the genomic basis of adaptation may help in predicting the impact of selection in natural populations. Laboratory evolution systems provide an opportunity to study the effect of selection on the extent and degree of genomic parallelism during adaptation. We address this using laboratory adaptation to novel resources in a pest, the red flour beetle *Tribolium castaneum* (Ancestral resource- Wheat, Novel resources- Corn, Finger Millet, and Sorghum; most to least sub-optimal). Specifically, we ask whether parallelism is influenced by the founding population size or the strength of selection (different for different resources). After 35-60 generations of evolution, populations exhibit early stages of adaptation and ecological divergence: increased fitness in the new resources, as well as significant assortative mating across populations, adapted to distinct resources. To determine the genetic basis of adaptation, I sequenced the pooled genomic DNA of 20 adults from ancestral and evolved lines and determined the change in allele frequencies over time (for standing genetic variation), as well as new variants representing mutations during evolution. Overall, we found very few new mutations, indicating adaptation largely via SGV. Compared to the ancestor, evolved lines have many more alleles at extreme frequencies, possibly due to rapid purging of deleterious alleles and fixation of beneficial alleles during adaptation. Evolved lines also have reduced nucleotide diversity than the ancestor. The magnitude of these two effects is broadly correlated with the initial selection imposed in each resource (i.e., strongest in corn, which is most suboptimal). Interestingly, allele frequencies changed parallelly both within (i.e., across replicate populations) and between resources, suggesting similar underlying mechanisms of adaptation to different habitats. I also found evidence suggesting large selective sweeps, some involving entire chromosomes. We are now analyzing candidate genes under selection to predict the functional basis of an increase in fitness in novel resources. We are also performing reciprocal transplant experiments with ancestral stocks and evolved lines in all resources to ask if there are any fitness-related trade-offs associated with adaptation to novel environments. In conclusion, rapid adaptation to various resources can occur in this pest beetle using standing genetic variation and the same large effect alleles across populations.

Poster by Varat Sivayyapram:

(116) Molecular phylogeny, biogeography, and species delimitation of segmented spider genus *Liphistius* (Araneae: Liphistiidae) in Thailand

Paleo- and macro- ecology in tropical Asia

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The segmented spider family Liphistiidae is the most basal family among living spiders. These spiders can be differentiated from other spiders by the retention of several spider plesiomorphic characteristics, such as the presence of abdominal tergite plates and the presence of spinnerets on the median area of the abdomen. *Liphistius* Schiödt, 1849 is endemic in southeast Asia. *Liphistius* includes 69 described species placed in seven species groups based primarily on genitalic characters. In Thailand, there are 39 *Liphistius* species in four species groups including the birmanicus-group, the bristowei-group, the linang-group, and the trang-group. In addition, the large trang-group has been subdivided into six species complexes. However, there is lack of consensus concerning phylogenetic relationships at the species and species-group levels. This study sampled 162 *Liphistius* specimens from 52 collecting sites in Thailand and Myanmar. We used five nucleotide loci (mitochondrial COI and 16S, and nuclear H3, 28S, and ITS2) to reconstruct phylogenetic relationships, infer historical biogeography, and delimit *Liphistius* species. The concatenated alignments include 2,011 bps (COI: 168 sequences, 550 bps, 16S: 168 sequences, 316 bps, H3: 146 sequences, 241 bps, 28S: 159 sequences, 630 bps, and ITS2: 161 sequences, 245 bps). Phylogenetic results are primarily congruent with morphology-based classifications, in supporting the monophyly of the genus, the bristowei-group, and the trang-group. However, our results do not support the monophyly of the six species complexes within the trang-group. Ancestral area reconstruction suggested *Liphistius* originated in Sibumasu and diversified into several species-groups via dispersal and vicariance processes during the early Eocene (50–53 MA). Most taxa found in Thailand belong to the bristowei- and the trang-groups. The bristowei-group originated in the area that corresponds to their current distribution in the northwestern mountain range of Thailand during the late Eocene (33 MA). The large trang-group originated in the Thai-Malaysian peninsula during the mid-Eocene (47 MA) and diversified into five monophyletic clades in the late Eocene and the mid-Miocene (17–41 MA). Three of which diversified inhabited the same area. The two remaining clades crossed the isthmus of Kra, one clade distributed northward and inhabited mainland Sibumasu while the other distributed eastward and colonized Indochina during the early Oligocene (31–32 MA). The species delimitation results (ASAP, GMYC, PTP, STACEY, and BFD) delimited specimens from discrete locations as separate species; variation in number of species proposed (53 to 72) stemmed from variation in delimitation of sympatric cryptic species.

Talk by Alexander Skeels:

(117) Phylogenomics of a hyper-diverse plant clade (Grevilleoidea; Proteaceae) reveals the paleoenvironmental origins of a fractured distribution

Open category

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The Grevilleoideae (Proteaceae) are distributed widely throughout former Gondwanan landmasses (South America, Australia, New Zealand, New Caledonia, Africa, and Madagascar) and have even crossed Wallace's Line into tropical Asia. Fossil evidence suggests the group originated in mesic biomes but present-day hotspots of mega-diversity are found in dry temperate and Mediterranean ecosystems. This group is a thus prime candidate for understanding the role of historical environmental change on regional biodiversity patterns, but to date no species-level phylogeny has been available to analyze diversification patterns. We generated a species-level phylogenomic dataset for nearly all members of the subfamily Grevilleoidea (>800 species), and produced a set of alternative phylogenetic hypotheses, accounting for discordant gene-tree histories. We compiled a large fossil dataset and applied alternative calibration strategies for divergence dating, capturing uncertainty in fossil placements. This pipeline allows us to test the role of historical climate change and plate tectonics on the biogeography and diversity of Grevilleoideae, accounting for many sources of uncertainty in phylogenetic inference. We used paleoenvironmental reconstruction of biomes around the globe to constrain biogeographic estimation models and inferred the biogeographic origin of the clade, and vicariance and dispersal events between major biomes throughout the southern hemisphere and Asia. Our results highlight the role of paleoenvironmental dynamics on the evolution of a megadiverse plant group.

Talk by Jui-Hung, Tai:

(118) Antagonist pleiotropy caused by the dual demand of the viral life cycle shapes genetic diversity and adaptive changes in SARS-CoV-2

Virus evolution: from basic research to public health applications

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The impact of a virus's dual obligations - to maintain high inter-host transmissibility while also effectively adapting within hosts - on viral genetic diversity remains largely unexplored. We posit that these demands could induce uncorrelated selection pressure even antagonistic pleiotropy, a scenario where mutations enhance certain fitness aspects at others' expense, and contribute to the maintenance of genetic variation and promote adaptation. The vast wealth of SARS-CoV-2 genetic data gathered from within and across hosts offers an unparalleled opportunity to test above hypothesis. By analyzing a large set of SARS-CoV-2 sequences (~ 2 million) collected from early 2020 to mid-2021, we found that high frequency mutations within hosts are usually detrimental during inter-host transmission. This highlights potential inverse selection pressures within versus between hosts. We also identified a group of nonsynonymous changes, which are probably maintained by antagonistic pleiotropy, as their frequencies are significantly higher than four-fold degenerate sites but never experienced clonal expansion. Analyzing one such mutation, spike M1237I, reveals that spike I1237 boosts viral assembly but reduces in vitro transmission, highlighting its antagonistic effect. Though they make up about 2% of total changes, they represent 37% of genetic diversity. These mutations are notably prevalent in the Omicron variant from late 2021, hinting that antagonistic pleiotropy may promote positive epistasis and new adaptive variants. As many viral dynamics assumptions rest on mutations being selectively neutral, these fitness-effect mutations might skew estimates like transmission bottleneck and effective population sizes.

Talk by **Nobuto Takeuchi**:

(119) Low relatedness can drive the evolution of reproductive division of labour

Open category

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Reproductive division of labour (RDL), where sterile 'helpers' assist specialised 'reproducers' in transmitting genetic information, has evolved repeatedly and at vastly different biological scales. Examples include eusocial insects with queens and workers, multicellular organisms with germline and soma cells, and cells with genomes and enzymes (enzymes provide catalysis, 'helping' genomes transmit genetic information). This recurrent evolution of RDL poses an apparent paradox to the theory of natural selection: helpers sacrifice their own reproduction to perform functions beneficial to a group, but such altruists are susceptible to invasion by 'cheaters'—selfish individuals that avoid cooperation and maximise their own fitness to the detriment of the group. The classical approach to resolve this paradox is through kin selection: altruism can be selected if individuals within groups are genetically related. Under this theory, high relatedness is an essential driver for the evolution of RDL. Here, we demonstrate the converse scenario that low relatedness drives the evolution of RDL. We hypothesise that RDL can function to protect a group against the evolution of cheaters by limiting the transmission of genetic information to a small number of reproducers per group (e.g., genomes, germline cells, and queens), thereby increasing relatedness within groups. Under this hypothesis, RDL is more likely to evolve for lower relatedness because the protective benefit of RDL amplifies as the risk of cheater evolution heightens. To test this prediction, we investigate an agent-based model in which individuals are partitioned into groups that reproduce. Each individual invests a fraction of its resources in self-reproduction and the remainder in the provision of a public good required for the reproduction of individuals in its group. An individual's reproduction is tied to the group's reproduction because a group splits if the number of individuals in the group exceeds a constant threshold. This creates a conflict: greater investment in public-good provision is advantageous for a group but disadvantageous for an individual, as it diminishes that individual's reproduction rate relative to other individuals within the same group. Our results show that individuals within a group differentiate through evolution into two types: reproducers, which invest all their resources in reproduction, and helpers, which invest a large fraction of their resources in public-good provision and do not transmit genetic information across generations—hence, the evolution of RDL. Critically, this evolution occurs only if the average number of individuals per group is sufficiently large, a condition that implies large genetic variation within groups, i.e., low relatedness, as predicted by our hypothesis. Finally, we find that RDL elevates relatedness within a group, stabilising a group against fitness decay caused by cheater evolution. Therefore, the evolution of RDL is a cause, rather than a consequence, of high relatedness in our model. Taken together, our findings provide a novel perspective in evolutionary theory by revealing that the evolution of RDL can be driven by protection against cheaters, with this benefit occurring only if relatedness is sufficiently low.

Poster by **Kouki Tamai**:

(120) The diversity of caudal fin ray branching in the three-spined sticklebacks.

Open category

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Fish fins are essential for postural control and movement in the water. In particular, the caudal fin is known to generate a driving force during swimming and to have evolved a highly diverse morphological structure across a wide range of lineages. However, the molecular genetic mechanisms underlying this diversification are not well understood. To elucidate these mechanisms, we use the three-spined stickleback, *Gasterosteus aculeatus*, as a model. The three-spined stickleback is originally a marine fish species but has repeatedly colonized different freshwater habitats such as lakes, streams, and ponds, resulting in adaptive phenotypic

diversification. Because these habitats vary in flow velocity and depth, we expected to see diversification in caudal fins between populations. Morphological analysis revealed the interspecific variation in the branching pattern of caudal fin rays in sticklebacks. In particular, a freshwater population inhabiting mainland of Japan had a significantly higher rate of second branching of the caudal fin rays than other marine and freshwater populations. The second branching may provide more support for the fin membrane, allowing water to be pushed out more efficiently. Furthermore, this freshwater population has reduced defensive structures against predators such as armor plates and spines. Thus, the increased rate of second branching might be involved in the escape strategy by burst swimming rather than using weakened defensive traits. In addition, to investigate when the second branching occurs in this freshwater population, we analyzed the branching pattern of caudal fin rays from juvenile to adult stages in the natural habitat. Second branching was found in individuals approximately larger than 35 mm in size, which is expected to be around one year old. Further molecular analysis at this stage may reveal the genes and mutations responsible for the diversification of caudal fins and escape behavior in response to predators.

Talk by **Eunice J. Tan**:

(121) Colourful stick insects reduce daytime mating activity to lower predation risk

The evolution of invertebrate sensory ecology and behaviours

Eunice J. Tan¹

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Stick insects are conventionally thought to adopt camouflage to avoid predation and consequently constrain foraging and mating activities to the night. For example, during copulation, winged male stick insects may additionally exhibit behaviours such as flapping of wings and vigorous abdomen shaking, which could reduce their camouflage and thereby increase predation risk. Thus, more brightly coloured species represent an opportunity to understand how stick insects avoid detection and predation when mating. We examined the mating behaviour of the stick insect *Marmessoidea rosea*, which are largely green with pink wings. While this species mates both in the day and night, the latency to mate was shorter and mating was more likely to occur in night. In addition, male stick insects shift their mating behaviours according to the time of day, with more conspicuous behaviours constrained to night copulation events. We therefore suggest that brightly coloured stick insects may modulate mating behaviours to optimise mating opportunities, while selectively displaying conspicuous behaviours at night to reduce exposure and detection by potential predators.

Talk by **Min Tan**:

(122) The Flicker Fusion Camouflage Effect in Jumping Spiders

The evolution of invertebrate sensory ecology and behaviours

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Animals with high-contrast patterns are often thought to become more conspicuous when they move. More recently, studies have shown otherwise: high-contrast patterns can blur when an animal moves quickly enough through a strategy known as flicker fusion camouflage. However, there is limited empirical evidence for this notion. Here, we tested for the effectiveness of this strategy using the jumping spider (*Menemerus bivittatus*) and computer-generated stimuli of different patterns (i.e. black, grey, thin and vertically striped, thick and vertically striped, horizontally striped, and background matching) moving at three speeds. To understand how patterns can be used to exploit the visual constraints of the viewer, jumping spiders were also subjected to three different eye-masking treatments (i.e. unmasked, antero-median eyes (AME)-masked, and antero-lateral eyes (ALE)-masked), and their responses to stimuli were recorded. Our results showed that stimulus speed, pattern, and eye-masking significantly affected jumping spider responses. Jumping spiders generally showed lower responses when stimulus speed was fast. Compared to the grey stimuli, thin and vertically striped

stimuli elicited higher responses for unmasked spiders. ALE-masked spiders responded less than unmasked and AME-masked spiders. However, ALE-masked and AME-masked spiders had low responses to the striped stimuli at high speeds. Taken together, our findings suggest that faster stimulus speeds may effectively exceed the flicker fusion frequency threshold of jumping spiders so that salticids may be unable to resolve the moving thin striped patterns, thus supporting for the flicker fusion camouflage hypothesis.

Talk by **Yonas I. Tekle**:

(123) Unveiling Cryptic Sexual Cycles: Genomic and Cytological Insights into Microbial Eukaryotes from the Supergroup Amoebozoa

Why sex? insights from asexual genomes

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The origin and evolution of sex in microbial eukaryotes is a significant challenge to understand. This is compounded by the historical exclusion of microbial eukaryotes from discussions, based on the assumption of their primitiveness and asexuality. Recent research has revealed that microbial eukaryotes, including amoeboid lineages, display evidence of sexual like behaviors. While genomic data has begun to shed light on sexual reproduction in some eukaryotic microbes, the precise mechanisms underlying these processes remain elusive. For example, the well-studied microbes such as the slime mold model organism, *Dictyostelium discoideum*, and the human pathogen, *Entamoeba histolytica*, their sexual life cycle still remains poorly understood. A significant obstacle in the study of sexual mechanisms in microbial organisms is the limited knowledge of the diverse and often cryptic nature of their life cycles. In this study, we present compelling genomic and cytological evidence of sexual reproduction characterized by distinct life cycles in various microbial eukaryotes belonging to the supergroup Amoebozoa. Our findings not only provide robust genetic support for the presence of sexual processes in seemingly asexual microbes but also hint at the existence of cryptic sexual cycles that are yet to be fully elucidated.

Talk by **Chawatat Thanoosing**:

(124) Biogeography of bumblebees (Hymenoptera: Apidae: Bombus) in Southeast Asia: a case of *Bombus flavescens*

An evolutionary perspective on pollinator biodiversity, systematics, and conservation

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Bumblebees are vital pollinators, especially in temperate areas, due to their buzz-pollinated ability. Bumblebees can be found in the tropical of Southeast Asia, mainly in the highlands. There are 23 species in 7 subgenera, recorded in Southeast Asia. Only three subgenera *Megabombus*, *Melanobombus*, and *Pyrobombus*, have been reported both in the mainland and archipelago. Studying the biogeography of Southeast Asian bumblebees might reveal the tropical adaptation process and distribution pattern which are vital for the conservation plan. However, the genetic relationship between mainland and island species for performing biogeographic analysis is still incomplete. In this study, we chose *B. (Pyrobombus) flavescens* Smith as a model for biogeographic reconstruction because this species is the most widespread bumblebee species in Southeast Asia. The biogeographic scenarios were estimated from a Bayesian phylogenetic analysis of *B. flavescens* populations across the current range, combining COI, 16S, and PEPCK data, using S-DIVA analysis in RASP and BioGeoBEARS with DIVALIKE+J analysis. The result suggested that *B. flavescens* diverged from its sister lineage in the Himalayas and dispersed into Southeast Asia in the

Pleistocene. Then, the oscillation of sea level and rising of global temperature in the late Pleistocene facilitated the allopatric divergence process of *B. flavescens*, including population isolation and higher latitude immigration, for example, the Cameron Highlands in Malaysia. For the next step, a species distribution model with paleoclimatic data, including temperature and humidity, would be a promising tool to illustrate the biogeographic scenarios of *B. flavescens* comprehensively. Keywords DNA barcoding, Museum specimens, Polymorphism, Philippines, Taxonomic impediment

Poster by **Regine Tiong**:

(125) Inbred hawksbill turtle nesting population in Singapore

Genomic diversity in nonequilibrium populations

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Critically endangered hawksbill turtles nest in Singapore, and they preserve coral reef ecosystems with its dietary niche on sponges that compete with corals for space. However, rising sea levels and global warming are threatening turtle populations by reducing nesting habitats and hatchling success rates. Population genetic studies contribute to conservation strategies and reveal their population history in response to environmental changes. Previous genetic studies of hawksbill populations used limited data including maternal lineages using mitochondrial DNA (mtDNA), which cannot fully represent the genetic diversity in populations. We produced the first de novo genome assembly of the hawksbill turtle and population genome sequencing datasets to examine the genetic diversity of the population nesting in Singapore. We collected dead hatchlings and eggs from hawksbill nests on Singapore beaches from 2018 to 2022. DNA was extracted from whole eggs and liver tissues of hatchlings. We sequenced 69 samples by Sanger sequencing for the mitochondrial (mt) DNA control region and 40 samples using Illumina HiSeq X for whole genomes. Our results revealed five mtDNA haplotypes, and three are endemic to Singapore while, most haplotypes are identical. Using whole genome sequencing datasets, we estimated the degree of genetic diversity and homogeneity within the population. The analysis shows a small genetic diversity with close relationships between individuals, indicating inbreeding within the population. Furthermore, the inferred effective population size using multiple sequentially Markovian coalescence (MSMC) shows a sharp decline of population, coinciding with the last deglaciation period, suggesting the impact of past climate change on sea turtles. This study highlights the vulnerability of endangered populations and emphasizes the importance of population genomics studies for the conservation of endangered wildlife.

Talk by **Nobuhiko Tokuriki**:

(126) Protein evolution and molecular determinants of protein evolvability

Fitness landscapes bridge evolution and molecular biology

Nobuhiko Tokuriki¹

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Over the last decades of research on protein evolution and engineering, we have recognized that the success of protein engineering campaigns is overly different depending on the systems. What are molecular determinants to dictate the evolution of new protein functions? In this talk, I will discuss several key molecular properties that can be associated with evolvability of proteins, the ability of proteins to promptly evolve a new function. Especially, I will discuss the causes and consequences of mutational epistasis, interactions between mutational effects, that affect the pathways and outcomes of evolution. Under the prevalence of epistasis, the effects of a mutation can vary from positive to negative, and vice versa, depending on genetic backgrounds, which causes the prediction of mutational effects difficult. In-depth understanding and predicting epistasis are essential for developing better-directed evolution and protein engineering strategies. I will present statistical pictures of mutational epistasis that are observed in diverse experimental and natural evolutionary trajectories. Then, I will show several major molecular mechanisms which cause large

epistatic effects, e.g., molecular conflict; two mutations perform similar molecular consequences and thus antagonize each other, reinforcing; the effect of the initial mutations is enhanced by subsequent mutations by fine-tuning the position of the initial mutation to generate synergistic effects. Finally, I will discuss potential strategies to overcome those epistatic consequences in directed evolution.

Talk by **Masahito Tsuboi**:

(127) Ecology as the link between evolvability, development, and macroevolution: a case study using wing and body morphology of Odonata

Evolvability: a common currency of evolution, ecology and development

Masahito Tsuboi¹

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Understanding causal and explanatory mechanism of phenotypic diversity across the tree of life is a common goal of ecology, evolutionary biology, and developmental biology. Although recent advancements in the concept of evolvability clarified how this goal may be achieved through strategic and interdisciplinary collaborations among related but distinct subfields of biological sciences, the role of ecology—research of the relationships among living organisms and their physical environments—remains unclear. In my talk, I will begin with a proposal of the place of ecology in evolvability research program from the vantage point of evolvability in quantitative genetics. Through a literature survey and schematic illustration of the geometry of moving adaptive landscape, I will argue that the task of ecologists is to identify causes of variation in natural and sexual selection, preferably in natural habitats of living organisms. Subsequently, using wing morphology and body size in two species of damselflies (*Ischnura elegans* and *Enallagma cyathigerum*) as the model case, I will illustrate how we can empirically go about with this research program through a combination of field work and experiment anchored by quantitative genetic theories. To conclude, evolvability framework offers opportunities to weave ecology into evolutionary and developmental biology. Yet, there are empirical and conceptual challenges when translating ecological insights into causal and explanatory mechanisms of biodiversity. I would like to discuss these issues both as part of my talk and as a general theme of the symposium with contributors and the audience.

Talk by **Saburo Tsuru**:

(128) Genetic properties influencing transcriptional plasticity and evolvability

Evolvability: a common currency of evolution, ecology and development

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The rate and direction of phenotypic evolution depends on availability of phenotypic variants induced either genetically or environmentally for selection act upon. It is widely accepted that organisms don't display uniform phenotypic variation, where certain variants arise more frequently than others in response to genetic or environmental perturbations. Previous studies using numerical simulations suggest that genetic interactions governing phenotypes could explain how the bias in phenotypic variation arises. However, it remains unknown whether the phenotypic variation is explained by a real known genetic interaction as expected. To address this question, we characterized variability in transcriptional phenotype in *Escherichia coli* in response to environmental and genetic perturbations. Using the rich knowledge of the genetic interactions of *E. coli*, we identified the common genetic properties that affect transcriptional variability in both environmental and genetic causes. Our findings support the relevance of the genetic interactions to shape phenotypic variability that is shared by different perturbations. This study provides an insight into a molecular mechanism underlying generalized response to new environments.

Talk by **Sudipta Tung**:

(129) Impact of Isocaloric Dietary Manipulation on Life-History Traits and Gene Expression in Outbred *Drosophila melanogaster* Population

Open category

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Organisms' survival hinges on their food intake, which influences growth, maintenance, and reproduction by providing essential macronutrients. However, an optimal macronutrient mix that maximizes an organism's evolutionary fitness isn't always accessible, leading to dietary discrepancies that can affect performance. To delve deeper into these dietary consequences, we studied how macronutrient composition impacts specific organismal traits and gene expression. We employed *Drosophila melanogaster*—a suitable model for such dietary evaluations—to assess the effects of isocaloric diets differing in protein-to-carbohydrate ratios on eight critical life-history attributes in a substantial outbred population ($n \approx 2,500$). Results showed that reducing carbohydrates in an isocaloric diet sped up pre-adult development and enhanced reproduction, without altering pre-adult viability or body size. However, higher carbohydrate levels curtailed lifespan, as indicated by faster aging, evidenced by reduced locomotion and deteriorating gut health. Additionally, gene expression showed noticeable plasticity based on diet: high-carbohydrate diets primarily increased gene activation, while protein-rich diets leaned towards suppression. Our study illuminates how macronutrient mix shapes life history characteristics and their connections, providing valuable perspectives on the possible adaptive mechanisms organisms might employ in response to consistent dietary challenges in our rapidly changing environment.

Talk by **Masahiro Uesaka**:

(130) The developmental hourglass model and the vertebrate body plan conservation: insights from single-cell level transcriptome analysis

Open category

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Throughout 500 million years of evolution, vertebrates have diversified their morphologies while somehow conserving their basic anatomical features, or the body plan. The developmental hourglass model posits an intriguing hypothesis to explain why the body plan is conserved. This model suggests that the body plan conservation can be attributed to the conserved developmental period, known as the phylotypic period, during which the body plan elements commence their development. Consistent with this notion, previous comparative transcriptome studies have revealed evolutionary conservation during the mid-embryonic organogenesis period across vertebrates at a whole embryo level, with earlier and later stages displaying more divergence. While this mid-embryonic conservation lends support to the developmental hourglass model, whether developmental processes underlying the body plan are truly conserved remains unknown, and it remains plausible that the whole embryo-level conservation observed during the middle embryonic period might be unrelated to the evolutionary conservation of the body plan. In this study, we examined the cell type-level conservation of the phylotypic period by conducting single-cell transcriptome comparisons across five vertebrate species: *Mus musculus*, *Gallus gallus*, *Pelodiscus sinensis*, *Danio rerio*, and *Oryzias latipes*. By profiling tens of thousands of single-cell transcriptomes, we identified about 25 distinct cell clusters for each species. We subsequently linked these identified cell clusters across species using orthologous gene

information, leading to the identification of homologous cell clusters characterized by shared gene expression profiles. Leveraging publicly available cell atlases, we annotated these identified homologous cell types and quantified the transcriptome similarities among the examined species, serving as a proxy for assessing the evolutionary conservation of cell types. Our results show that cell types exhibiting higher transcriptome similarities are predominantly associated with various body plan elements, including the heart, neural tube, and notochord. This finding suggests that cell types integral to the body plan exhibit a high degree of conservation across vertebrates, prompting speculation that the conservation of developmental processes at the cell type level contributes to the phenotypic constraints governing vertebrate body plans. Additionally, we will present preliminary results and discuss potential molecular mechanisms underpinning the evolution of vertebrate body plans.

Talk by **Valeria Vaskaninova**:

(131) Unexpected hypophyseal morphology of early vertebrate fossils challenges the utility of developmental biology for unravelling vertebrate evolution

Early evolution of vertebrates from evo-devo and paleontological perspectives

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The vertebrate ‘new head’ is an evolutionary novelty dominantly generated by the neural crest and the cranial sensory placodes – embryonic tissues originating within the ectodermal borders of the neural plate. The anterior most placode is the adeno-hypophyseal placode, which later in development forms the anterior lobe of the pituitary – the major hormonal control organ of the vertebrate body. In all extant jawed vertebrates, the pituitary is of dual developmental origin, composed of the anterior adeno-hypophyseal lobe and a posterior neurohypophysis. The neurohypophysis is derived from the ventral evagination of the hypothalamus. The adeno-hypophyseal placode is initially incorporated into the ectoderm of the roof of the oral cavity. Later in embryogenesis, it invaginates to form an epithelial fold – the Rathke’s pouch – and connects with the neurohypophysis. It is widely accepted that the adeno-hypophyseal placode is unpaired in both jawless (where it is fused with the nasal placode to form a naso-hypophyseal placode) and jawed forms. The division of the originally single nasal placode is considered a synapomorphy of jawed vertebrates. The current phylogenetic consensus divides the extant jawed vertebrates (gnathostomes) into two major clades – Chondrichthyes and Osteichthyes. The greatest uncertainty arises in placing the fossil early gnathostomes relative to the osteichthyan–chondrichthyan node. The present majority view is that all ‘placoderms’ are stem gnathostomes arranged in a paraphyletic series with ‘acanthothoracids’ near the bottom and ‘maxillate placoderms’ at the top. All ‘acanthothoracids’ share an extended precerebral trabecular region – so-called ‘upper lip’ – a feature in some respects intermediate between the jawless and jawed conditions, which anchors their basal position on the tree. However, our research on the dentition of ‘acanthothoracids’ demonstrates that they differ fundamentally from the ‘placoderm’ dentitions, which had been thought to characterise stem gnathostomes, and instead resemble the dentitions of crown gnathostomes. The character similarity suggests that osteichthyans could be rooted close to the ‘acanthothoracids’, but in the consensus phylogeny they are widely separated. Recently, we made an important anatomical discovery concerning the hypophyseal area of the ‘acanthothoracid’ genus *Radotina*. Its palate displays paired adeno-hypophyseal cavities separated from the neurohypophysis and opening directly into the mouth cavity. Our subsequent comparative study of hypophyseal cavities from tomographic data of selected early vertebrate fossils belonging to both gnathostome stem and crown groups shows a completely unexpected pattern. The character distribution provides evidence for an ancestral superficial and paired adeno-hypophysis and, by extension, paired adeno-hypophyseal placodes. Interestingly, the hypophyseal cavities of the stem chondrichthyan *Gydoselache* are almost indistinguishable from the morphology observed in most studied ‘acanthothoracids’. On the contrary, the ‘acanthothoracid’ *Kosoraspis* (which has the most osteichthyan-like dentition and upper jaw morphology among ‘acanthothoracids’) resembles the condition in the stem osteichthyan *Ligulalepis* – implying a major convergence between crown osteichthyans and chondrichthyans. This observation may have radical implications on the construction of the gnathostome tree with the chondrichthyan lineage branching off very early after the emergence of jaws. This configuration is supported by the fossil record and is in accordance with the proposed evolution of macromery.

Talk by **Todd Vision**:

(132) Endemic species, introduced species, and two faces of secondary contact on oceanic islands

Impact of introgressive hybridization on tropical diversification

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Hybridization is thought to have played an important role in shaping the evolutionary history of diverse island taxa. Yet secondary contact doesn't always result in introgressive hybridization, and it is important to consider the wide range of ecological and evolutionary outcomes of secondary contact, particularly in the face of widespread secondary contact between island endemics and recently introduced species. While there are biological reasons to predict secondary contact and heterospecific mating to be common on islands for many taxa, there are also reasons to expect that the consequences of secondary contact will differ depending on the nature of the species involved. We present the results from a quantitative analysis of published empirical research on secondary contact on remote oceanic islands for 705 vertebrate, invertebrate, and plant species spanning 167 genera and 99 families, with a focus on the Canary Islands, the Galápagos Islands, New Zealand, the Caribbean, and Hawaii. We weigh evidence for the drivers of secondary contact and heterospecific mating in these systems. In particular, we compare cases of secondary contact between endemic species versus secondary contact between endemic and introduced species. We find that the three main drivers of secondary contact and heterospecific mating on islands most frequently reported in the literature are disturbance, long-distance (e.g. inter-island) dispersal, and compromised assortative mating. We find support for the hypothesis that introgression is a more common outcome between endemic species while reproductive interference is a more common outcome between endemic and introduced species. Contact between recently-diverged endemic species is likely responsible for the apparent frequency of hybridization on islands, whereas reproductive interference between endemic and introduced species presents a cryptic and underappreciated conservation threat to endemic island taxa.

Talk by **Mrinalini Walter**:

(133) Asymmetric reproductive isolation and differential gene flow drive incipient speciation in allopatric populations of dung flies

The genomics of adaptation and speciation

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Speciation and the processes that establish barriers to gene flow among diverging populations are central to evolutionary biology. Speciation research has largely focused on post hoc testing of evolutionary hypotheses in species with established divergence or on investigating genetic and phenotypic divergence on a microevolutionary scale. Moreover, few empirical studies (e.g. in bacteria, fruit flies) have used integrative and/or systematic approaches to demonstrate isolating mechanisms that can lead to speciation, and even less so in non-model species. Here we use a widespread dung fly species, *Sepsis punctum*, to investigate how rapid evolution of divergences among allopatric populations in North America and Europe result in reproductive isolation and barriers to gene flow that drive incipient speciation. We take an integrative approach that combines diverse datasets from *S. punctum*, including population genomics, DNA barcoding, reproductive transcriptomics, novel gene evolution, and genetic variant analysis. In conjunction, we perform evolutionary hypotheses testing in an experimental framework using population crosses to evaluate the role of reproductive traits. We find that *S. punctum* is in the process of rapidly accumulating reproductive and molecular divergences at the population level, likely driven by a range of behavioural, reproductive, and seminal fluid incompatibilities. These pre-mating and post-mating pre-zygotic (PMPZ) reproductive barriers

occur asymmetrically and at varying degrees among population crosses, thereby producing differentials in gene flow and reproductive isolation that underpin incipient speciation in *S. punctum*.

Talk by **Jing Wang**:

(134) Novel insights from Mollusca into ancient sex chromosome evolution and sexual regulation

Marine evo-devo: new frontiers from emerging marine model organisms

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Sexual reproduction is widespread in the animal kingdom and sexual evolution has been honored as “the queen of problems in evolutionary biology”. To date, our understanding of sexual evolution is largely biased to animals with heteromorphic sex chromosomes, which formed the classic theory of sex chromosome evolution. Molluscs constitute the second largest, Precambrian-originated animal phylum with a diversity of sexual systems, including simultaneous hermaphroditism, sequential hermaphroditism, strict gonochorism and even parthenogenesis. However, this ideal animal group for studying sexual evolution has long been neglected partly for its uncharacterized homomorphic sex chromosomes and sex-determining genes (SDGs). Our group has been focusing on the ancient bivalve mollusc family of Pectinidae and carried out systematic studies using histology, genomics and regulatome methods. We have traced the gonadal sex differentiation of scallop and accurately determined the molecular sex differentiation prior to morphological sex differentiation. We identified the first characterized 350-Myr homomorphic sex chromosomes (representing the oldest known sex-chromosome in the animal kingdom) and SDGs (e.g., FOXL2) in Mollusca through the large-scale sexual genome sequencing. We report the novel mechanism for “inheritance” turnover of SDGs by regulatory element translocation. The long-term undifferentiation of scallop sex chromosomes were surprisingly found to be potentially sustained by intertwined regulation of reversible sex-biased genes (SBGs). Recently, we have introduced the dwarf surfclam *Mulinia lateralis* as the mollusc model to further study the bisexual regulatory flexibility by focusing on the molecular regulation between SDGs and SBGs. Our findings provide not only novel insights into the evolution and regulation of ancient homomorphic sex chromosomes, but also guidance for establishing the sex control breeding of scallop.

Talk by **Min Wang**:

(135) Insight into the evolutionary assemblage of cranial kinesis from a Cretaceous bird

Open category

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The independent movements and flexibility of various parts of the skull, called cranial kinesis, is an evolutionary innovation that is found in living vertebrates only in some squamates and crown birds, and considered to be a major factor underpinning much of the enormous phenotypic and ecological diversity of living birds, the most diverse group of extant amniotes. Compared to the postcranium, our understanding of the evolutionary assemblage of the characteristic modern bird skull has been hampered by sparse fossil records of early cranial materials, with competing hypotheses regarding the evolutionary development of cranial kinesis among early members of the avialans. Here, a detailed three-dimensional reconstruction of the

skull of the Early Cretaceous enantiornithine *Yuanchuavis kompsosoura* allows for its in depth description, including elements that are poorly known among early diverging avialans but are central to deciphering the mosaic assembly of features required for modern avian cranial kinesis. Our reconstruction of the skull shows evolutionary and functional conservation of the temporal and palatal regions by retaining the ancestral theropod dinosaurian configuration within the skull of this otherwise derived and volant bird. Geometric morphometric analysis of the palatine suggests that loss of the jugal process represents the first step in the structural modifications of this element leading to the kinetic crown bird condition. The mixture of plesiomorphic temporal and palatal structures together with a derived avialan rostrum and postcranial skeleton encapsulated in *Yuanchuavis* manifests the key role of evolutionary mosaicism and experimentation in early bird diversification.

Talk by **Shi Wang**:

(136) Widespread presence of bone marrow-like hematopoietic stem cell niche in invertebrate skeletons

Marine evo-devo: new frontiers from emerging marine model organisms

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The skeletal harboring of hematopoietic stem cells (HSCs) is generally considered as vertebrate-specific innovation during water-to-land transition. However, this long-standing view has not been rigorously evaluated as hematopoietic sites remain poorly understood in most invertebrate groups. Herein, we report the first discovery of abundant HSCs in adult mollusk shells, an invertebrate hematopoietic niche that resembles vertebrate bone marrow (BM). Bulk and single-cell transcriptome profiling showed that mollusk shells are composed of abundant HSC-like cells, which distinguish shells from adult soft tissues or organs and functionally resemble vertebrate BM-HSCs. Cell lineage analysis and functional assays revealed the developmental origin of HSCs during larval shell formation and their participation in hemocyte-mediated shell regeneration and soft body blood supply. Widespread skeleton-related HSC-like cells are found in diverse invertebrate groups. Contrary to the common view of vertebrate-specific innovation, our study reveals the widespread and potentially deep evolutionary origins of invertebrate skeletal HSC niches, thereby boosting new paradigms for hematopoiesis and stem cell research in invertebrates.

Poster by **Xiaopei Wang**:

(137) The Haldane model of genetic drift as an alternative to the conventions - II. Drift in multi-copy genetic systems

Open category

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Genetic drift should encompass all random forces that change gene frequency stochastically. However, the conventional model such as the WF (Wright-Fisher) or Moran model is limited to sampling errors between generations. The Haldane model based on the branching process is more intuitive, versatile and powerful and has been proposed as an alternative to the conventions. Indeed, genetic systems that have multiple copies within individuals such as mitochondrial DNAs, transposons, viruses and multi-copy genes cannot be analyzed by the WF model. For example, rRNA genes, with a median of $C \sim 150$ copies per haploid in humans, appear to evolve rapidly. Without the means to determine genetic drift, positive selection has been invoked even in DNA segments of no apparent functions. By using the Haldane model, we determine the strength of genetic drift in rRNA genes to be ~ 20 times higher than single-copy genes in human and mouse polymorphisms. The large

increases in drift, likely due to the homogenizing forces (such as unbiased gene conversion) within individuals, reduce N_e^* to $< 10N_e$, despite $C \sim 150$ (N_e^* and N_e being the effective population sizes of rRNA genes and single-copy genes respectively). Significantly, when the divergence between species is analyzed, some variants appear to experience extremely strong drift such that N_e^* becomes smaller than N_e , as if $C < 1$. By these analyses, positive selection is detected in the great apes but not evident in mice. To account for random evolutionary forces, the results provide further support for the Haldane model as a powerful alternative to the conventional models.

Poster by **Xinyi Wang**:

(138) Purifying selection leads to low protein diversity of the mitochondrial cyt b gene in avian malaria parasites

Open category

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Background: Mitochondrial respiration plays a central role in the survival of many eukaryotes, including apicomplexan parasites. A 479-bp fragment from the mitochondrial cytochrome b gene is widely used as a barcode to identify genetic lineages of avian malaria parasites *Plasmodium* and related haemosporidians. Here we looked for evidence of selection in the avian *Plasmodium* cyt b gene, using tests of selection and protein structure modeling. We also tested for the association between cyt b polymorphism and the host specificity of these parasites. **Results:** Based on 1,089 lineages retrieved from the Malawi database, we found that the frequency of the most conserved amino acids in most sites was more than 90%, indicating that the protein diversity of the avian *Plasmodium* cyt b barcode was low. The exceptions were four amino acid sites that were highly polymorphic, though the substitutions had only slight functional impacts on the encoded proteins. The selection analyses revealed that avian *Plasmodium* cyt b was under strong purifying selection, and no positively selected sites were detected. Besides, lineages with a wide host range tend to share cyt b protein haplotypes. **Conclusions:** Our research indicates that purifying selection is the dominant force in the evolution of the avian *Plasmodium* cyt b lineages and leads to its low diversity at the protein level. Host specificity may also play a role in shaping the low mitochondrial diversity in the evolution of avian malaria parasites. Our results highlight the importance of considering selection pressure on the cyt b barcode region and lay a foundation for further understanding the evolutionary pattern of mitochondrial genes in avian malaria. **Keywords:** Purifying selection, Cytochrome B, Host specificity, Avian malaria

Talk by **Yangzi Wang**:

(139) Population genomics provide insights into the evolution of facultative asexuality in plants

Why sex? insights from asexual genomes

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For the facultative species, clonal reproduction is beneficial for short-term competition in a relatively stable environment, while sexual reproduction promotes genomic diversity for adaptation in a changing environment. Thus, the alteration between the two reproductive modes might affect fitness. However, what causes the alteration from sexual reproduction to asexual mode remains largely unknown. Here, we investigate 228 genomes of the giant duckweed (*Spirodela polyrrhiza*) that were collected worldwide. Four populations were observed and named according to their geographic distribution: America, Southeast Asia (SE-Asia), India, and Europe populations. Substantial differences were observed among those four populations,

including genomic diversity, recombination rate, decay of linkage disequilibrium, and selection efficiency. However, different sexual reproduction rates might be the initiator. Further investigation suggests that the changes in sexual reproduction rate are associated with two structure variations that involved MADS-box genes. In addition, genome-wide scans revealed that multiple genes involved in flowering and embryogenesis were under positive selection, consistent with the hypothesis that natural selection drove the evolution of asexuality during the recent habitat expansions in this plant. Together, these results provide new insights into the evolution of plant reproductive systems and suggest that natural selection can drive the evolutionary changes of asexuality, which in turn alters the levels of genomic diversity.

Poster by **Yu-Ren Wang**:

(140) Evolution of natal down patterns across avian phylogeny and the functional correlations with nest characteristics

Genetics of adaptation and evolution of novel traits

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Natal down is a layer of down feathers that cover the body of nestlings in varying areas and densities. However, the evolutionary pattern and function of these differences are still unclear. Here, we performed ancestral state reconstruction of natal down and examined the correlated evolution with several traits that may affect it. Pictures of nestling from 187 avian families were collected and the natal down characters from seven body parts were classified into three categories according to their feather density. Ancestral state reconstruction showed that there is a similar evolutionary pattern of all body parts. Nest and parental care are key factors affecting the protection of nestling. Functional interactions between these factors and natal down may affect the evolutionary pattern of natal down. We examined the correlated evolution between natal down and parental care, nest structure, attachment, and site. The results revealed that species with higher parental care and nest protection tend to lose their natal down. This study can provide important insights into the evolutionary history, behavioral ecology, and conservation needs of different bird species.

Talk by **Yue Wang**:

(141) Plants maintain climate fidelity in the face of dynamic climate change

Paleo- and macro- ecology in tropical Asia

Yue Wang¹

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Plants will experience considerable changes in climate within their geographic ranges over the next several decades. They may respond by exhibiting niche flexibility and adapting to changing climates. Alternatively, plant taxa may exhibit climate fidelity, shifting their geographic distributions to track their preferred climates. Here, we examine the responses of plant taxa to changing climates over the past 18,000 y to evaluate the extent to which the 16 dominant plant taxa of North America have exhibited climate fidelity. We find that 75% of plant taxa consistently exhibit climate fidelity over the past 18,000 y, even during the times of most extreme climate change. Of the four taxa that do not consistently exhibit climate fidelity, three — elm (*Ulmus*), beech (*Fagus*), and ash (*Fraxinus*) — experience a long-term shift in their realized climatic niche between the early Holocene and present day. Plant taxa that migrate longer distances better maintain consistent climatic niches across transition periods during times of the most extreme climate change. Today, plant communities with the highest climate fidelity are found in regions with high topographic and microclimate heterogeneity that are expected to exhibit high climate resilience, allowing plants to shift distributions locally and adjust to some amount of climate change. However, once the climate change buffering of the region is exceeded, these plant

communities will need to track climates across broader landscapes but be challenged to do so because of the low habitat connectivity of the regions.

Talk by **Natapot Warrit**:

(142) Building a barcode reference library and occurrence database for Asian bees

An evolutionary perspective on pollinator biodiversity, systematics, and conservation

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Bees (Apoidea; Anthophila) are widely acknowledged as the most important terrestrial pollinators. Their conservation depends on our knowledge of all facets of their life history and distribution. Asia holds 15% of total bee diversity, with many unique lineages, but these many species comprise only 1% of public global bee specimen data, in part because identification of the fauna is extremely difficult and requires referencing type specimens often stored on the other side of the world. Many groups also require taxonomic revision due to cryptic species complexes. A primary solution for this taxonomic impediment is to integrate molecular resources with morphology to build foundational knowledge on Asian bee diversity. Here, we present preliminary results on the assembly of a DNA library based on more than 1000+ DNA barcode sequences (COI) from verified bee specimens collected across Asia, mainly from China, India, Singapore, and Thailand. Topics inferred from the generic-level phylogenies of various bee groups are discussed: taxonomic status, species identification and diagnostic characters, cryptic species, and gender matching. This standardized method will provide a reliable backbone data for future research and bee conservation programs in Asia.

Talk by **Hiroshi Watanabe**:

(143) Evolutionary Origin of the Central Nervous System: Insights from the Development and Function of the Cnidarian Pharyngeal Nervous System.

Marine evo-devo: new frontiers from emerging marine model organisms

Hiroshi Watanabe¹

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The evolutionary origin of the central nervous system (CNS) is one of the major unresolved questions in evolutionary biology. It is assumed that the nervous system began to function as a net-like structure similar to that seen in modern cnidarians, and that subsequent neural centralization led to the development of an information processing system that connects various input and output systems. However, the early evolutionary process of how and why integrated systems developed in simple neural networks still largely remains to be explored. In recent years, comparisons of the expression patterns of genes involved in bilaterian CNS development during embryonic and larval stages have revealed widely conserved genetic features. To understand the role of these genes in the early neural centralization, it is necessary to clarify their functions in the neural development of the lineage that diverged before the emergence of Bilateria. Using Cnidaria, the closest sister to all Bilateria, and we have been analyzing the developmental and cell physiological characteristics of their nervous systems. In this symposium, I present our latest findings on the developmental control mechanisms and functions of the Pharyngeal Nervous System (PhNS), which constitutes a subgroup of the neural network of the cnidarian *Nematostella vectensis*. By using RNASeq data during regeneration of the

oral region, and single-cell RNASeq data, we identified 7 types of PhNS neuronal clusters and 356 PhNS genes including the orthopedia homeobox (Otp) and neuropeptide RFamide. Inhibition of Otp function in *Nematostella* developing embryos resulted in reduced expression of 193 PhNS genes, including RFamide. Furthermore, we found that the uptake of food (rotifers) was reduced in Otp-deficient *Nematostella* polyps, which was recovered by the addition of synthetic RFamide peptide, indicating that PhNS is necessary for controlling feeding behavior. Otp is required for the development of hypothalamus in the vertebrate CNS. Furthermore, hypothalamic neurons expressing RFamide-type neuropeptides are known to play a role in controlling feeding behavior. The above findings obtained in the *Nematostella* indicate that the cnidarian PhNS may have evolutionarily conserved characteristics at the molecular level as a feeding control center.

Talk by **Junya Watanabe**:

(144) New look at statistics of evolvability measures in quantitative genetics

Evolvability: a common currency of evolution, ecology and development

Junya Watanabe¹

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In quantitative genetics, evolvability of a trait is measured as the amount of genetic variance available to directional selection in a population. This concept has been generalized into multivariate phenotypes using the (additive) genetic covariance matrix (G matrix), so that various aspects of evolvability and genetic constraints are expressed as functions of a G matrix and selection gradient vector—the Hansen–Houle evolvability measures. Growing evidence for descriptive and predictive values of these evolvability measures foregrounds their relevance in investigations into the evolution of complex phenotypes. However, mathematical and statistical properties of the evolvability measures have not yet been fully appreciated, even in the specialized quantitative genetics literature. In this talk, I will introduce some distribution theories on evolvability measures, in particular focusing on their probability distributions when the selection gradient vectors vary across directions in the trait space. Key in looking at statistical properties of evolvability measures is that they are mathematically expressed as ratios of quadratic forms in selection gradients. This form of statistics is frequently encountered in the statistical and econometric literature, from which we can borrow useful distribution theories. One of these is a mathematical toolkit called the zonal and invariant polynomials of matrix arguments, which enable evaluation of some relevant integrals over a (hyper)sphere. On one hand, the distribution theories provide explicit expressions for average evolvability measures, for which only approximate evaluation methods were known in the literature. This enables us to quantify and compare evolvability and constraints accurately in biologically meaningful manners. On the other hand, theories also allows for drawing exact probability distributions for certain evolvability measures. These are useful in conducting a retrospective hypothesis test on the role of genetic constraints in empirical evolutionary trajectories. Importantly, these theories are not restricted to the simple case with spherically distributed selection gradients but can accommodate arbitrary mean and covariance for the selection gradients, thereby extending the scope of evolvability measures to various scenarios like directional and/or correlated selections. Main results have been implemented in my R package *qfratio* available from the CRAN and GitHub repositories. Hopefully, the enhanced accessibility and expandability of evolvability measures stimulate future quantitative investigations into multivariate trait evolution.

Talk by **Alison K.S. Wee:**

(145) Adaptive chilling stress response in Asian mangroves at latitudinal range limits

Open category

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Mangroves are one of the most threatened ecosystems in the world. Climate change is projected to result in not only a poleward range shift in mangroves, but also mortality from higher intensity and frequency of extreme weather events (e.g. cold spell). Thus, the physiological and molecular adaptation of mangrove species to chilling stress is crucial to understanding their response to climate change, form effective management strategies, and conserve their long-term evolutionary potential. Here, we present a series of cold treatments that assessed the chilling stress response in key Asian mangrove species, including *Bruguiera gymnorhiza*, *Avicennia marina*, *Rhizophora apiculata*, *Kandelia obovata* and *Kandelia candel*. We compared the photochemical efficiency, enzyme activity, foliar phosphorus fractions and gene expression profiles throughout the cold treatment to determine the intra- and inter-specific latitudinal differentiation in chilling tolerance and to identify adaptive strategies that may lead to chilling tolerance. Our findings indicated that (1) the distributional range limits of tropical versus subtropical species were associated with adaptive differences in the regulation of photosynthesis under chilling stress; (2) adaptation to different temperature brackets contributed to geographic divergence and potentially speciation in mangroves, and (3) several strategies were involved in chilling tolerance, including efficient foliar phosphorus allocation and photoprotection. Collectively, these findings point toward the interactive effects among macroclimate, regulation of photosynthesis, nutrient enrichment, and stress adaptation in marginal populations of coastal plants.

Talk by **Bernetta Kwek Zi Wei:**

(146) Female preference for males with lower pattern contrast follows Weber's law of proportional processing in jumping spiders

The evolution of invertebrate sensory ecology and behaviours

Bernetta Kwek Zi Wei¹, Wei Zhou², Long Yu³, Guohua Ding⁴, and Daiqin Li⁵

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According to Weber's law of proportional processing, perceptual discrimination between stimuli of different magnitudes is based on their proportional differences in magnitude (not absolute differences). Proportional processing operates in various sensory modalities and behavioural contexts. However, whether female mate preference for colour patterns in animals follows Weber's law of proportional processing remains untested. We addressed this research gap using the jade jumping spider, *Siler semiglaucus*, whose males exhibit remarkable sexually selected colour patterns and whose females show preferences for males with low abdomen pattern contrast (pattern contrast is defined as the spatial feature of the relative abundance of two adjacent colour patches). By manipulating the dorsal abdomen colour patterns of *S. semiglaucus* males, we created males with varying abdomen pattern contrasts. We then assessed female preference for males that varied in both absolute and proportional differences in pattern contrast. We found that females preferred males with lower abdomen pattern contrasts and discriminated between males based on both absolute and proportional differences in pattern contrast. While proportional difference alone was not a significant predictor of female mate choice, discrimination based on proportional difference, coupled with absolute difference had a greater influence on female mate preference than absolute difference alone. Hence, our findings suggest that *S. semiglaucus* female preference for males with lower pattern contrast follows Weber's

law, and female discrimination may have the potential to limit the exaggeration of sexually selected colour patterns.

Poster by **Dongya Wu**:

(147) Horizontal transfer and the birth of biosynthetic gene cluster in grass

Genetics of adaptation and evolution of novel traits

Dongya Wu¹

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Benzoxazinoids are a class of protective and allelopathic plant secondary metabolites that have been identified in multiple grass species and are encoded by the Bx biosynthetic gene cluster (BGC) in maize. Data mining of 41 high-quality grass genomes identified complete Bx clusters (containing genes Bx1–Bx5 and Bx8) in three genera (*Zea*, *Echinochloa*, and *Dichanthelium*) of Panicoideae and partial clusters in Triticeae. The Bx cluster probably originated from gene duplication and chromosomal translocation of native homologs of Bx genes. An ancient Bx cluster that included additional Bx genes (e.g., Bx6) is presumed to have been present in ancestral Panicoideae. The ancient Bx cluster was putatively gained by the Triticeae ancestor via horizontal transfer (HT) from the ancestral Panicoideae and later separated into multiple segments on different chromosomes. Bx6 appears to have been under less constrained selection compared with the Bx cluster during the evolution of Panicoideae, as evidenced by the fact that it was translocated away from the Bx cluster in *Zea mays*, moved to other chromosomes in *Echinochloa*, and even lost in *Dichanthelium*. Further investigations indicate that purifying selection and polyploidization have shaped the evolutionary trajectory of Bx clusters in the grass family. This study provides the first candidate case of HT of a BGC between plants and sheds new light on the evolution of BGCs.

Talk by **Martin Wu**:

(148) Microbial genomic trait evolution is dominated by frequent and rare pulsed evolution

Open category

Martin Wu¹

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On the macroevolutionary time scale, does trait evolution proceed gradually or by rapid bursts (pulses) separated by prolonged periods of stasis or slow evolution? Although studies have shown that pulsed evolution is prevalent in animals, our knowledge about the tempo and mode of evolution across the tree of life is very limited. This long-standing debate calls for a test in bacteria and archaea, the most ancient and diverse forms of life with unique population genetic properties. Using a likelihood-based framework, we show that pulsed evolution is not only present but also prevalent and predominant in microbial genomic trait evolution. We detected two distinct types of pulsed evolution (small frequent and large rare jumps) that are predicted by the punctuated equilibrium and quantum evolution theories. Our findings suggest that major bacterial lineages could have originated in quick bursts and that pulsed evolution is a common theme across the tree of life.

Talk by **Ningning Wu**:

(149) Widespread Gene Expression Divergence in Butterfly Sensory Tissues Facilitates Speciation

The genomics of adaptation and speciation

Ningning Wu¹

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Neotropical *Heliconius* butterflies are well known for their intricate behaviors and multiple instances of incipient speciation. Chemosensing plays a fundamental role in the life history of these groups of butterflies and in the establishment of reproductive isolation. However, chemical communication involves synergistic sensory and accessory functions, and it remains challenging to investigate the molecular mechanisms underlying behavioral differences. Here, we examine the gene expression profiles and genomic divergence of three sensory tissues (antennae, legs, and mouth parts) across sexes (females and males) and life stages (different adult stages) in two hybridizing butterflies, *Heliconius melpomene* and *Heliconius cydno*. By integrating comparative transcriptomic and population genomic approaches, we found evidence of widespread gene expression divergence supporting a crucial role of sensory tissues in the establishment of species barriers. We also show that sensory diversification increases in a manner consistent with evolutionary divergence based on comparison with the more distantly related species *Heliconius charithonia*. Our study strongly supports the unique chemosensory function of antennae in all three species, the importance of the Z chromosome in interspecific divergence, and the nonnegligible role of nonchemosensory genes in the divergence of chemosensory tissues. Collectively, our study provides a genome-wide illustration of diversification in the chemosensory system under incomplete reproductive isolation, revealing strong molecular separation in the early stage of speciation. Here, we provide a unique perspective and relevant view of the genetic architecture (sensory and accessory functions) of chemosensing beyond the classic chemosensory gene families, leading to a better understanding of the magnitude and complexity of molecular changes in sensory tissues that contribute to the establishment of reproductive isolation and speciation.

Poster by **Shijie Wu**:

(150) From multicellular to single-celled organism: cell domestication and rapid evolution

Open category

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The evolution from single-celled to multicellular organisms took millions of years, but the details are poorly understood. Although people have explored whether single-celled organisms are multicellular in previous studies, this does not provide a good understanding of the whole process of evolution. Recently, we have tried to domesticate mammalian cells through the process of reverse evolution, inducing the cells of multicellular organisms to evolve rapidly in the direction of single-celled organisms, and obtaining mammalian cells that only need to provide some basic nutrients and vitamins and have certain independent survival ability. For these autonomous cells with independent survivability, we analyzed the newly generated mutations during domestication. These findings may help us understand the details of how a single-celled organism evolved into a multicellular organism.

Poster by **Chen Xiangnyu**:

(151) Evaluation of ActD therapeutic effect by longitudinal ctDNA monitoring and a comparison between ddPCR-based and deep UMI-based amplicon panel sequencing for multi-site detection

Open category

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The level of ctDNA in the blood cannot only reflect the occurrence of tumors and the stage of cancer, but also translate the effectiveness of treatment and predict the relapse of tumors. In order to further validate the translation of treatment effectiveness by ctDNA, we used multiplex ddPCR technology to dynamically monitor the levels of ctDNA in mice treated with ActD-based hydrogel targeting five SVs and four SNPs, as well as untreated mice. The results showed that after 14 days of treatment, the levels of ctDNA in the relapse group and the remission group exhibited completely opposite trends. The ctDNA levels in the relapse group continued to increase, while gradually decreasing to undetectable levels in the cured group. And the untreated group showed a gradual increase in ctDNA level with the growth of the tumor. Furthermore, we employed deep UMI-based amplicon sequencing (UMI-AS) to identify ctDNA in a cohort of seven cancer patients, achieving an overall patient detection rate of 100% (7/7) and an overall mutation detection rate of 57.44% (27/47), and LOD can reach 0.01%. This underscores the capability of UMI-AS to effectively pinpoint low-frequency mutation sites, rendering it more adept at the concurrent detection of multiple mutation sites compared to ddPCR with an LOD of 0.1%. As a result, UMI-AS is a highly promising option for clinical cancer diagnosis.

Talk by **Rachel Seah Wan Xin**:

(152) Effects of UV Light Exposure on Relative UV Opsin Genes rh3 Expression and Sexual Behaviour in *Cosmophasis umbratica*

The evolution of invertebrate sensory ecology and behaviours

Rachel Seah Wan Xin¹

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Surrounded by a world of light and colours, the visual systems of animals help them to detect and discern different wavelengths of light. While the visible wavelength of light falls within the 400-700nm range, the ultraviolet range of light (280nm - 400nm) is a field of vision that only some animals are privy to. Visual pigments found in retinas called opsins are responsible for light sensitivity in organisms. Among invertebrates, the opsin gene rh3 is responsible for the detection of UV light. Studies have revealed that the visual systems is highly plastic; exposure to different lighting conditions can induce significant changes in opsins gene expressions among vertebrates. Due to a dearth of studies on the plasticity of the visual systems in invertebrates, our study makes use of *Cosmophasis umbratica*, a tropical ornate spider that is well known for using UV light for communication and sexual behaviour. We aim to determine the effects of UV light exposure on both the behavioural and molecular levels in the different life stages of *C. umbratica*. On the molecular front, the results of our study indicate that the interaction between the life stage of *C. umbratica* and the lighting conditions that they are exposed to, influences the relative expression of rh3. Between the dark and light (UV-) treatment, our study found no significance difference in rh3 gene expression for all life stages (juveniles, adult females, adult males). However, UV light treatment (UV+) induced a decrease in rh3 expression in juveniles, an increase in rh3 expression for females but there was no significant difference in rh3 expression in males. These preliminary findings suggest the high plasticity of the UV visual systems in relation to the life stages and environmental lighting conditions of *C. umbratica*. In conclusion, this study offers insights into the role of UV in influencing visually guided sexual behaviour and opsin gene expression. It is our hopes that this study sets the wheels in motion for further investigations into the genetic basis of sexual behaviour mechanisms that underlie the plasticity of visual systems in invertebrates.

Talk by **Ryo Yamaguchi**:

(153) The phoenix hypothesis of speciation: development of reproductive isolation among populations experiencing extinction risk

The genomics of adaptation and speciation

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Genetic divergence among allopatric populations builds reproductive isolation over time. This process is accelerated when populations face a changing environment, but abrupt change also places populations at risk of extinction. Here we use simulations of Fisher's geometric model with explicit population dynamics to explore the genetic changes that occur in the face of environmental changes. We show that evolutionary rescue leads to the fixation of mutations whose effects are larger on average and that these mutations are more likely to lead to reproductive isolation, compared with populations not at risk of extinction. We refer to the formation of new species from the ashes of populations in decline as the phoenix hypothesis of speciation. The phoenix hypothesis predicts more substantial hybrid fitness breakdown among populations surviving a higher extinction risk. The hypothesis was supported when many loci underlie adaptation. When, however, there was only a small number of potential rescue mutations, we found that mutations fixed in different populations were more likely to be identical, with parallel changes reducing isolation. With a limited genomic potential for adaptation, we find support for a modified version of the phoenix hypothesis where reproductive isolation builds fastest in populations subject to an intermediate extinction risk.

Poster by **Chun-Hsin Yang**:

(154) Buffering the Path to Evolution: Hsp90 as a Genetic Capacitor in Facilitating Adaptive Mutations in Yeast

Fitness landscapes bridge evolution and molecular biology

Chun-Hsin Yang¹, Fu-Hsuan Ko², and Jun-Yi Leu³

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Maintaining protein homeostasis is vital for cellular survival. Heat shock protein 90 (Hsp90), a highly conserved molecular chaperone, facilitates the maturation of a wide variety of protein clients, and therefore engages in numerous cellular process. By maintaining protein stability and/or folding, Hsp90 can buffer the detrimental effects of genetic mutations. Cryptic genetic variations were released under stress conditions of Hsp90 activity insufficiency. Yet, our knowledge in the molecular mechanism underlying Hsp90 buffering is limited. In this study, we aimed to seek mutations which can be buffered by Hsp90. Through EMS-mutagenesis, we collected clones with growth defects under Hsp90 inhibition condition. To further investigate the causal mutations, we conducted bulk-segregant analysis coupling with whole-genome sequencing. We identified a mutation on ACS2, which is an essential gene encoding acetyl-coA synthetase, as one of the Hsp90 buffering targets. Via error-prone PCR library screening, we found another two putative single mutations on ACS2 buffered by Hsp90. We hypothesized that the Hsp90 buffering system allows cells to accumulate additional mutations to compensate the deleterious effect of the initial one during evolution. In the future, we would like to further dissect the molecular mechanism of Hsp90 buffering effect and its impact on evolution.

Talk by **Yi-Jun Yang**:

(155) Heterogeneous bonds and relationships: uncovering the convergent evolutionary history between Golden snub-nosed monkeys with *Homo sapiens*.

Behavioral evolution in vertebrates: diversity, genomics and mechanisms

Yi-Jun Yang¹

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Group living confers both benefits and challenges. Members in a group compete with one another in a variety of contexts from foraging, mating, and especially reproducing. As the key to group living, at least in primates, where individuals are truly connected (though in a variety of forms and degrees), cognitive abilities evolved for building and maintaining social networks. What are those cognitive abilities, and how do they help balance the costs and benefits of group living? Answering those questions helps unravel the myth of human evolution, as the evolution of shared intentionality, empathy, and sympathy provides the foundation of human uniqueness (e.g., complex societies, language, and culture). We use a population of wild golden snub-nosed monkeys (*Rhinopithecus roxellana*) as the model of our comparative study. Our monkeys live in multi-level societies, where one-male units are nested in higher-level social organizations, including band, herd, and troop. Different social organizations serve different foraging or reproductive functions, and the highest level of organization is observable only when two herds temporarily fuse. As a result, social roles and relationships are heterogeneous and intricate, and both matrilineal and patrilineal kin are present, resembling human hunter-gatherer societies (e.g., the Hadza). My past research aimed specifically at unraveling the nature of these relationships, using both behavioral and sociobiological approaches, and at uncovering the competition and cooperative functions embedded in these relationships. In this presentation, I will present the two latest research of the team, one uncovering the intrasexual competition among same-unit females and the other revealing the role of contact calls in maintaining band cohesion (i.e., between one-male units). By presenting the two cases, I will confirm the existence of intense competition over reproductive and nutrient needs between and within units, as well as the evolved solutions that resolve conflicts and maintain a friendly atmosphere. In addition, I will present the two ongoing research on our study population with the aim of specifying how individual differences are related to the differences in social and reproductive strategies, how individual differences predict fitness, and how vocalization and its combinations are used in different social contexts targeting different audiences. Through the above topics, I want to give a comprehensive picture of the aims and scope of the golden snub-nosed monkey research group, as well as the ambition to uncover the convergent evolutionary history of social brain/cognition between Asian colobines with the *Homo* lineage.

Poster by **Yong Yang**:

(156) Population structure and dynamic characteristic of the endangered plant *Dolichandrone spathacea* in Hainan island

Fitness landscapes bridge evolution and molecular biology

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Dolichandrone spathacea is a species of critically endangered mangrove plants in China, which is naturally distributed in Hainan Island and Leizhou Peninsula. In order to reveal the survival potential and endangered mechanism of *D. spathacea*, we investigated the survival potential and spatial distribution of *D. spathacea* in Hainan Island. The population structure and dynamic characteristics of *D. spathacea* were analyzed to explore its development tendency. The results showed that only 275 *D. spathacea* were found in Hainan Island, only 4 populations distributed in Wenchang, Wanning and Sanya. The population of *D. spathacea* showed a state of overall dispersion, local concentration and piecemeal distributed. The age class structure is incomplete. Young, middle and old plants accounted for 17.45%, 65.46% and 17.09%, respectively, which belonged to the decay type. They were sensitive to external interference, and the population showed a sharp decline in the early period, but stable in the middle and late period. The high mortality rate of young individuals caused by human

disturbance resulted in the low regeneration potential of the *D. spathacea* population, which was an important reason for its endangerment. In order to protect the germplasm resources of *D. spathacea*, it is necessary to strengthen the publicity and education, carry out the artificial cultivation and care of seedlings and artificial population restoration, so as to realize the scientific protection of *D. spathacea*.

Poster by **Akifumi Yao**:

(157) Gonadal transition during sex change and ovotestis formation in the harlequin sandsmelt *Parapercis pulchella*

Open category

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Sex is an essential feature for sexual reproduction. Teleost fishes are acquired remarkably diverse sexual patterns (e.g., sex change, hermaphroditism) compared to other vertebrate lineages. However, little is known about how sex changes and intersex traits emerge. This study focused on a marine teleost fish, harlequin sandsmelt *Parapercis pulchella*. This fish changes sex from female to male after sexual maturation. Also, females possess intersex gonads, called ovotestes, that consist of both ovarian and testicular tissues. Because *P. pulchella* possesses two interesting features (i.e., sex change and intersex trait), this fish could become an excellent model for studying sexuality in teleost fishes. Nevertheless, the detailed gonadal features and dynamics remain unclear. Therefore, this study aims to uncover the sex change process and ovotestis structure through histological observations and single-cell RNA sequencing. Histological observations demonstrated that female ovotestes comprised many oocytes and a few cysts of spermatogenic cells. Although early stages of spermatogenic cells (i.e., spermatogonia and spermatocytes) were present, spermatids and sperms were not observed in female ovotestes. In addition, immunohistochemistry using an antibody against Proliferating cell nuclear antigen (Pcna) as a cell proliferation marker revealed that spermatocytes were Pcna negative, suggesting that spermatogenesis is arrested at the spermatocyte stage in female ovotestes. At the initial phase of sex change, male germ cells increased, and spermatogenesis proceeded. Farther on, oocytes decreased and finally disappeared. The gonads became functional male testes after the sex change. During the sex change, oocytes degenerated through apoptotic cell death (active cleaved-Caspase3a positive by immunohistochemistry). In comparison, some female follicle cells proliferated (Pcna positive), suggesting that such cells were reused in the testes after the sex change. However, the histological observations alone did not fully identify cell types and functions in female ovotestes. Therefore, single-cell RNA sequencing of female and male gonads was conducted. Because genomic data of this fish is not available, reference transcriptome sequences were assembled and curated. Then, single-cell analyses were performed by mapping to the reference. Based on these analyses, we successfully identified various cell populations, e.g., germ, supporting, and hormone-producing cells, which were essential for spermatogenesis and oogenesis. Such cell atlas and expression data could become valuable resources for understanding ovotestis formation in the focal species and fishes.

Talk by **Moriaki Yasuhara**:

(158) Hotspots of Cenozoic tropical marine biodiversity

Paleo- and macro- ecology in tropical Asia

Moriaki Yasuhara¹

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Hotspots of tropical marine biodiversity are places that harbour disproportionately large numbers of species or species richness compared to the rest of the tropics. Richness and location of these hotspots have changed throughout the Cenozoic era. Here we review the global dynamics of Cenozoic tropical marine biodiversity

hotspots, including the four major hotspots of the Indo-Australian Archipelago (IAA), western Tethys (present Mediterranean), Arabian Sea and Caribbean Sea. Our review supports the 'Hopping Hotspots' model, which proposes that locations of peak biodiversity are related to Tethyan faunal elements and track broad-scale shallow-marine habitats and high coastal complexity created by the collision of tectonic plates. A null hypothesis is the 'Whack-A-Mole' model, which proposes that hotspots occur in habitats suitable for high diversity regardless of taxonomic identity or faunal elements. Earlier 'Centre-of' theories (e.g. centres of origin with diversity decreasing with distance from supposed areas of exceptionally high rates of speciation, for which easy connection to adjacent regions to the east and west is important) were based on the analysis of recent biotas with no palaeontological foundation and may better explain diversity dynamics within a hotspot rather than those between hotspots. More recently, however, human disturbance is massively disrupting these natural patterns.

Talk by **Xiao Yi**:

(159) Synthetic Evolution: Unleashing the power of evolution using synbio technologies

Fitness landscapes bridge evolution and molecular biology

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Theory and empirical observations elude to a plausible world of life of which the observed lives in nature is only a part. Here, we propose the approach of Synthetic Evolution in which synthetic biology technologies are specifically developed to explore the regions in the adaptive landscape that are hidden in nature. In terms of synthetic mutation rate, we designed a protein complex of targeted artificial DNA replisome (TADR) that operates in live cells to processively replicate one strand of a plasmid with errors. It enhanced mutation rates of target plasmid up to 2.3×10^5 -fold with only a 78-fold increase in off-target mutagenesis. Applying TADR, we evolved an E. coli specific phage to lyse Salmonella within two months, expanding host range of the phage beyond the boundary between species. In terms of synthetic selective pressure, we designed a bacterial treadmill, an automated machine in which a large population of bacteria was constantly selected for growth and chemotaxis without any population bottle-necking. This extreme selective pressure found mutant bacteria with surprising behaviors. Synthetic Evolution is promising in deepening our understanding of life and generating useful biological products.

Talk by **Xueling Yi**:

(160) Sex chromosome turnover in hybridizing stickleback lineages

Open category

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Recent discoveries of sex chromosome diversity across the tree of life have challenged the canonical model of conserved sex chromosome evolution and evoked new theories on labile sex chromosomes that maintain less differentiation and frequent turnover. However, theories of labile sex chromosome evolution lack direct empirical support due to the paucity of case studies demonstrating ongoing sex chromosome turnover in nature. Two divergent lineages (viz. WL & EL) of nine-spined sticklebacks (*Pungitius pungitius*) with different sex chromosomes (linkage group [LG] 12 in the EL, unknown in the WL) hybridize in a natural secondary contact zone in the Baltic Sea, providing an opportunity to study ongoing turnover between coexisting sex chromosomes. We first identified an 80 kbp genomic region on LG3 as the sex-determining region (SDR) in the WL using whole-genome resequencing data of family crosses. We then verified this region as the SDR in most

other WL populations, and demonstrated a turnover in admixed marine populations where the evolutionarily younger and homomorphic LG3 sex chromosomes replace the older and heteromorphic LG12 sex chromosomes. Our results provide a rare evolutionary snapshot on the process of a turnover, supporting the hypothesis of sex chromosome turnover driven by selection against deleterious mutation load.

Talk by **Hongwei Yu**:

(161) Pan-evolutionary and regulatory genome architecture delineated by integrated macro- and microsynteny approach

Open category

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The forthcoming genome data generated by the Earth BioGenome Project opens up a new era of comparative genomics, whereby genome synteny analysis provides a necessary framework. Profiling of genome synteny between extant species or between ancestor and extant species represents an essential step for elucidating genome architecture, regulatory blocks/elements and their evolutionary history. Based on the published algorithms or tools developed by our and other groups, we introduce a detailed protocol for the most comprehensive and up-to-date genome synteny pipeline (called PanSyn) and provides step-by-step instructions as well as application examples for demonstrating how to use it. The PanSyn pipeline includes three major modules (microsynteny analysis, macrosynteny analysis, and integrated micro & macro analysis). PanSyn inherits both basic and advanced functions from existing popular tools and also gains several additional advantages over many existing tools, including: (i) advanced microsynteny analysis by functional profiling of microsynteny genes and associated regulatory elements; (ii) comprehensive macrosynteny analysis with many features about inference of karyotype evolution from ancestors to extant species; and (iii) functional integration of microsynteny and macrosynteny that allows for pan-evolutionary profiling of genome architecture, regulatory blocks as well as integration with external functional genomics datasets from 3D/4D genome and ENCODE projects. The PanSyn pipeline not only fills a gap in available software packages for a user-friendly, highly-customized tool for genome macrosynteny analysis but also allows for integrated pan-evolutionary and regulatory analysis of genome microsynteny and macrosynteny which are not yet available in public synteny software or tools.

Poster by **Long Yu**:

(162) Factors influencing the efficacy of bird dropping masquerade in a crab spider

The evolution of invertebrate sensory ecology and behaviours

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Masquerading prey gain protection from predators by being misidentified as inedible objects such as twigs or bird droppings. Although recent studies have demonstrated that Phrynarachne crab spiders benefit from bird dropping masquerade, the factors influencing the efficacy of their masquerade remain largely unexplored. Phrynarachne spiders possess mosaic white and dark colour patterns, which vary considerably in the proportion and location across and within species. These spiders also vary in body size. Here, we explored whether the white/dark patch proportion and their location on the spider's body, as well as the size of the

spider influence the efficacy of *Phrynarachne*'s bird dropping masquerade using 3D-printed artificial spider models as prey and naïve spider-eating jumping spiders as predators. Our results confirm the protective function of the bird dropping masquerade. Predators took longer to detect and attack models, and they attacked them less frequently than non-bird dropping-like crab spider models that featured green and white patches. However, prey spider size and their white/dark patch proportion and location had no significant effects on detection time, attack latency, or likelihood of attacks so long as prey spider models possessed a combination of both white and dark patches. Our results therefore suggest that *Phrynarachne* species may have evolved visual appearance and body size with different white/dark patch proportions and patch locations that confer similar protection through bird dropping masquerade against predators.

Talk by **Jia-Xing Yue**:

(163) The pathogenicity evolution of papillomavirus revealed by a compendium of 3,562 human and animal papillomavirus genomes

Virus evolution: from basic research to public health applications

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Papillomaviruses (PVs) are a ubiquitous group of DNA viruses that infect a wide range of vertebrate hosts, including human. It is well established that the infection of some PV types (e.g., HPV16 and HPV18) are strongly associated with the occurrence and progression of cancers in human, but it remains elusive how such pathogenicity got evolved at the genomic level. In this study, we curated and annotated a compendium of 3,562 PV genomes (including 3,329 human PVs and 233 animal PVs) and performed the largest ever comparative genomics analyses on PVs with regard to their global and taxonomical distribution, host and niche specificity, population and phylogenetic stratification, as well as gene repertoire and genetic variants, especially those contribute to PVs' pathogenicity. Substantial variation in PV's genome size and GC% was noticed, with the latter being positive correlated with those of their hosts, suggesting a co-evolution between PVs and their hosts. With time-resolved phylogenetic analysis, a high-resolution view was obtained regarding the early divergence, niche adaptation, and horizontal host switch events that collectively shaped PVs' evolution. Key evolutionary events and genomic variants that defined their early divergence and carcinogenicity were identified, with those high-risk-associated PV variants showing higher potential for host immune evasion. Based on 90 independently acquired clinical samples of cervical squamous cell carcinoma (CSCC) and oropharyngeal squamous cell carcinoma (OPSCC) patients, we further discovered a set of HPV16 variants that predict patients' survival. Such illumination on the relationship among PV's genome evolution, pathogenicity, and clinical prognosis paves the road for better prevention, control, and treatment of PV-related cancers.

Talk by **Weiwei ZHAI**:

(164) Harnessing epistatic interactions in the fitness landscape for predicting adaptive evolution in the Influenza H3N2 virus

Virus evolution: from basic research to public health applications

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Seasonal H3N2 influenza evolves rapidly, leading to extremely poor vaccine efficacy. Substitutions occurred in embryonated eggs during vaccine production (i.e., egg passage adaptation) can contribute to the poor vaccine efficacy (VE), but the evolutionary mechanism remains elusive. Using a probabilistic approach known as the

mutational mapping and an unprecedented number of hemagglutinin sequences ($n > 100,000$), we found that the egg passage adaptation is driven by temporally-fluctuating convergent changes across different codons. Strikingly, the fitness landscape of passage adaptation is dominated by pervasive epistasis between two leading residues (186 and 194) and multiple other positions. Convergent evolutionary paths driven by strong epistasis explain most of the variation in VE, which has resulted in extremely poor vaccines for the past decade. Leveraging the unique fitness landscape, we developed a novel machine learning model that can predict egg passage substitutions for any candidate vaccine strain before the passage experiment, providing a unique opportunity for selecting optimal vaccine viruses. Our study demonstrated that that evolutionary trajectories can be harnessed for predicting Influenza adaptation and subsequently improving influenza vaccines.

Talk by **Chao Zhang**:

(165) CASTER: Direct species tree inference from whole-genome alignments

Open category

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Genomes contain mosaics of discordant evolutionary histories. While genome-wide data are routinely used for discordance-aware phylogenomic analyses, due to modeling and scalability limitations, the current practice leaves out large chunks of the genomes. Analyzing whole genome alignments using existing methods is impractical. Furthermore, the most scalable discordance-aware methods require recombination-free unlinked locus trees as input, making them unsuitable for analyzing the entire genome. As more high-quality genomes become available across the tree of life, we urgently need methods that can infer the tree from multiple genome alignments using all the reliably aligned sites and accounting for discordance across the genome. Here, we introduce CASTER, a site-based method that is statistically consistent under ILS and achieves levels of scalability that make it possible to analyze hundreds of mammalian genomes. We show both in simulations and in applications to real data that CASTER is scalable and accurate and that its per-site scores can reveal interesting patterns of evolution across the genome.

Talk by **Chaowei Zhang**:

(166) Pedigree-based germline mutation rate in sticklebacks

The genomics of adaptation and speciation

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Germline mutations, transmitted from parents to offspring, constitute the ultimate source of genetic variability. The rates at which these de novo mutations (DNM) occur are important for demographic, phylogenetic and population genetic inference, yet accurate estimates of DNM rates are still scarce, even for popular model systems in evolutionary biology. We estimated DNM rates for two populations of marine nine-spined sticklebacks (*Pungitius pungitius*) from deep coverage whole genome resequencing data for 128 individuals, representing 106 parent-offspring trios. After mapping the data to the species' latest reference genome version and applying stringent filtering, 308 DNMs were discovered. These DNMs translated to DNM rate of 4.56×10^{-9} per base pair per generation, which is 3.1 times lower than the commonly used substitution rate in phylogenetic dating of sticklebacks. Replacement of the latter with our DNM rate resulted in substantial increases in estimated divergence times among different stickleback lineages and better aligned with the

known fossil record. Moreover, we also observed a relatively high parental mosaicism at around 20% in comparison to humans, apes and mice. The accurate estimate of DNM rate should provide a useful resource for teleost fish research, and that of sticklebacks in particular.

Talk by **Chi Zhang**:

(167) Bayesian phylogenetic analyses on the evolution of Jurassic lampreys

Early evolution of vertebrates from evo-devo and paleontological perspectives

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Lampreys, one of two living lineages of jawless vertebrates, are always intriguing for their feeding behavior via the toothed suctorial disc and life cycle comprising the ammocoete, metamorphic, and adult stages. Here we present a recent study on two superbly preserved lampreys from the Middle-Late Jurassic Yanliao Biota of North China and update the interpretations of the evolution of the feeding apparatus, life cycle, and the historic biogeography of the group. I will focus on the methodological details of the Bayesian phylogenetic methods used for this study. The results reveal that modern lampreys' three-staged life cycle might not be established until the Jurassic, when they evolved enhanced feeding structures, increased body size and encountered more penetrable host groups.

Talk by **Dezhi Zhang**:

(168) Reconstructing the species tree in the face of incomplete lineage sorting and gene flow in three clades within the avian family Paridae

Impact of introgressive hybridization on tropical diversification

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Phylogenetic conflict is often caused by incomplete lineage sorting (ILS) and interspecific gene flow. The most frequent gene tree may not necessarily represent the species tree due to the influence of gene flow. Gene trees that are consistent with species tree are suggested to be enriched in genomic regions less affected by ILS and gene flow, such as regions with low recombination and nucleotide diversity. Here, we investigated the phylogenetic relationships within three clades comprising a total of 13 species in the songbird family Paridae (tits) using one de novo genome assembly and 82 re-sequenced genomes. Based on multiple phylogenetic inference approaches and divergence time estimates of genomic regions reflecting different phylogenetic topologies, we found that the true species tree was not represented by the most frequent gene tree in one of the three clades (Poecile tits), mainly due to the effect of gene flow. For the two other clades, gene trees concordant with the species trees were significantly enriched in autosomal genomic regions with low recombination and low nucleotide diversity, but no such enrichment was observed in the Poecile clade. Interestingly, gene trees consistent with the species tree were over-represented on the Z chromosome in all three clades, possibly due to faster lineage sorting and lower gene flow on the Z chromosome than on autosomes. Our study highlights the confounding effects of recombination and nucleotide diversity on species tree estimation and the potential role of the Z chromosome in phylogenetic reconstruction in the face of ILS and gene flow.

Talk by **Guojie Zhang**:

(169) Evolutionary and developmental mechanisms of ant social caste system

Plenary talk

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An ant colony is a higher-level organism consisting of specialized germline (queens & males) and soma (workers) individuals that differentiate early in development. A full understanding of the molecular mechanisms on the queen-worker division requests investigation on both organismal and superorganismal levels. At organismal level, the brain cell repertoire variations among the colony individuals provide cellular basis for the division of social functions. We develop *Monomorium pharaonis* ant species as a model to investigate the evolution and development of caste differentiation process. Comparison of brain single-cell transcriptome data of queens, gynes (uninseminated queens), workers and males from same colony detected a high degree of specialization in the brain cellular composition of all four adult phenotypes, particularly in males and workers. At superorganismal level, we investigate the gene regulatory networks that mediate individual caste developmental fates by integrating Wheeler's concept and Waddington's epigenetic landscape. By constructing transcriptional trajectories for > 1400 individuals covering most developmental stages of two ant species, we found that caste differentiation is increasingly canalized from early development onwards, particularly in germline individuals (gynes/queens). The canalized genes with gyne/queen-biased expression were enriched for ovary and wing functions while canalized genes with worker-biased expression were enriched in brain and behavioural functions. This canalization process differentiated caste development can be disturbed by manipulating canalized genes inducing non-adaptive intermediate phenotypes between gynes and workers. Our series of studies suggest a strong selection in maintaining the canalization process that regulating the caste differentiation in social insects.

Talk by **Shichang Zhang**:

(170) The strategies of male fighting against female's sexual cannibalism in spiders

Behavioral evolution in vertebrates: diversity, genomics and mechanisms

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Female sexual cannibalism refers to the phenomenon that females attack, kill or even consume males during mating process. It is an extreme manifestation of sexual conflict, which is common in spiders, such as black widow spider. To circumvent the attack of female spiders, males have evolved a variety of behavioural adaptations. Here I summarized related discoveries of my lab recently. For example, I found in *Nephila pilipes* that male would perform a mating binding behaviour to calm down the female when she is trying to capture the male. Both tactile and chemical are crucial for mate binding to succeed in rendering females less aggressive, but that tactile cues are more important. In many spider species, male mate with a female when she is disturbed or when she is feeding or undertaking moulting, called opportunistic mating. I found that the occurrence of male opportunistic mating was positively, though not statistically significantly, correlated with the intensity of female sexual cannibalism after investigating three species of web-building spiders with different intensities of female sexual cannibalism: *Nephila pilipes*, *Nephilengys malabarensis*, and *Parasteatoda tepidariorum*. In addition, After testing five typical species of web-building spiders, I found that males would choose the palp that contains more sperm to perform his first insertion, supporting the "better charged palp" hypothesis and "fast sperm transfer" hypothesis. Besides, I found in wolf spider *Pardosa pseudoannulata* that male conducted traumatic mating, in which male damages the inner walls of the female genital tracts with the sharp part of its intromittent organ. The traumatic mating caused hemolymph hemorrhage, which mixed with seminal fluid and gradually formed an impermeable amorphous mating plug after about 15 days, completely blocking the female copulatory opening, leading to a strict monandry of the female. Finally, I found in a communal orb weaving spider *Philoponella prominens* that males undertake a split-second catapult action immediately after mating, thereby fleeing their partner. I demonstrate that males achieve their superfast

action (up to 88.2 cm/s) by extending the tibia–metatarsus joint of their first leg pair via hydraulic pressure in a joint that is known to lack extensor muscles in spiders. This rapid expansion greatly reduces the likelihood of the male being sexually cannibalized. These findings strengthened our current understanding of sexual selection and sexual conflict theory. We assumed that sexual selection has driven the evolution of these strategies in spiders as the degree of sexual cannibalism is more likely to occur in species which sexual dimorphism is obvious and female is choosy.

Talk by **Wei Zhang**:

(171) Leaf Masquerade Mimicry in Oakleaf Butterflies

Plenary talk

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Oakleaf butterflies in the genus *Kallima* have a polymorphic wing phenotype enabling these insects to masquerade as dead leaves. This iconic example of protective resemblance provides an interesting evolutionary paradigm that can be employed to study biodiversity. We integrated multi-omic data analyses and functional validation to infer the evolutionary history of *Kallima* species and investigate the genetic basis of their variable leaf wing patterns. We find that *Kallima* butterflies diversified in the eastern Himalayas and dispersed to East and Southeast Asia. Moreover, we find that leaf wing polymorphism is controlled by the wing patterning gene cortex, which has been maintained in *Kallima* by long-term balancing selection. Our results provide macroevolutionary and microevolutionary insights into a model species originating from a mountain ecosystem.

Talk by **Wenyu Zhang**:

(172) Tracing the origin and evolutionary fate of recent gene retrocopies in natural populations of the house mouse

Genetics of adaptation and evolution of novel traits

Wenyu Zhang¹

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Gene retroposition is known to contribute to patterns of new gene evolution and evolution of novel traits. However, most of the previous studies were conducted in comparisons between species, and less attention has been paid to the evolutionary dynamics and patterns of very recently derived retrocopies that are still polymorphic within natural populations. Herein, we used house mouse as the study system to trace the origin of evolutionary fate of newly arrived retrocopies. We found the primary rate of retroposition is orders of magnitude higher than the long-term rate. Comparisons with single-nucleotide polymorphism distribution patterns in the same populations show that most retroposition events are deleterious. Transcriptomic profiling analysis shows that new retroposed copies become easily subject to transcription and have an influence on the expression levels of their parental genes, especially when transcribed in the antisense direction. These results imply that the impact of retroposition on the mutational load has been highly underestimated in natural populations. Despite of their largely deleterious effects, we also found a small subset of new retrocopies with rapid increasing frequency in populations. They were likely involved in a recent adaptation process, evidenced by the strong signature of positive selection. Overall, our study shows the dual roles of gene retrocopies at population scale.

Talk by **Yixiang Zhang**:

(173) Mutation rates and genome evolution in asexual and sexual reproduction organisms

Why sex? insights from asexual genomes

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The origin of genetic variation in biology is a fundamental driving force of evolution. Evaluating the mutation rate and mutation types within species is crucial for a comprehensive understanding of evolution. In recent years, with the widespread use of whole-genome sequencing, it has become possible to directly estimate mutation rates in both sexually and asexually reproducing species within the tree of life. Understanding the variations in mutation rates between sexual and asexual reproduction in different species sheds light on the choices made during the species' evolutionary processes. Here, we estimated the spontaneous mutation rate for blue alfalfa aphid (*Acyrtosiphon kondoi*), which is $9.33\text{E-}10$ (95% CI: $6.23\text{E-}10$, $1.32\text{E-}09$) per haploid genome per parthenogenic generation. We accomplished this by conducting a mutation accumulation experiment. Additionally, we estimated the rates of insertion and deletion mutations to be $9.98\text{E-}11$ (95% CI: $1.47\text{E-}11$ to $1.85\text{E-}10$). We also compared per-generation mutation rates in 152 species, including 18 bacteria, 118 eukaryotes, 8 plant species, and 8 avian species. Among these, 43 species reproduce asexually, while 109 reproduce sexually. The results revealed that, in most branches of the tree of life, species reproducing sexually exhibit significantly higher mutation rates compared to asexual species. However, within the arthropod group Branchiopoda, some asexual species display relatively high mutation rates. Furthermore, our analysis indicated that asexual species typically possess smaller genomes and lower mutation rates due to their longer generation times when considering phylogenetic relationships. Notably, although nucleotide diversity is inversely correlated with effective population size, species with larger long-term effective population sizes tend to have lower per-generation mutation rates, supporting the drift barrier hypothesis. However, asexual species do not conform to this trend. In summary, our comparative analysis provides ecological insights into the evolution of mutation rates in animals, by examining mutation rate variations in sexual and asexual reproduction based on species' evolutionary trees.

Talk by **Yu Zhang**:

(174) Comparative Phylogenomics and Phylotranscriptomics Provide Insights into the Genetic Complexity of Nitrogen Fixing Root Nodule Symbiosis

Open category

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Plant root nodule symbiosis (RNS) with mutualistic nitrogen-fixing bacteria is restricted to a single clade of angiosperms, the Nitrogen-Fixing Nodulation Clade (NFNC), and is best understood in the legume family. Nodulating species share many commonalities, explained either by divergence from a common ancestor over 100 million years ago or by convergence following independent origins over that same time period. Regardless, comparative analyses of diverse nodulation syndromes can provide insights into constraints on nodulation—what must be acquired or cannot be lost for a functional symbiosis—and what the latitude is for variation in the symbiosis. However, much remains to be learned about nodulation, especially outside of legumes. Here, we employed a large-scale phylogenomic analysis across 88 species, complemented by 151 RNA-seq libraries, to elucidate the evolution of RNS. Our phylogenomic analyses further emphasize the uniqueness of the transcription factor, NIN, as a master regulator of nodulation, and identify key mutations affecting its function across the NFNC. Comparative transcriptomic assessment reveals nodule-specific upregulated genes across diverse nodulating plants, while also identifying nodule-specific and nitrogen-response genes. Approximately 70% of symbiosis-related genes are highly conserved in the four representative species, whereas defense-related and host range restriction genes tend to be lineage-specific. Our study also

identifies over 900,000 conserved non-coding elements (CNEs), of which over 300,000 are unique to sampled NFNC species. NFNC-specific CNEs are enriched with the active H3K9ac mark and are correlated with accessible chromatin regions, and thus represent a pool of candidate regulatory elements for genes involved in root nodule symbiosis. Collectively, our results provide novel insights into the evolution of nodulation and lays a foundation for engineering of RNS traits in agriculturally important crops.

Talk by **Ying Zhen**:

(175) Evolution of firefly toxins

Genetics of adaptation and evolution of novel traits

Chengqi Zhu¹ and Ying Zhen²

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Fireflies were believed to originally evolve their novel bioluminescence as warning signals, which was later adopted in adult mating. Although evolution of bioluminescence has been investigated extensively, the evolution of firefly toxins has not been systematically examined. In this study, we systematically surveyed the presence or absence of firefly toxin lucibufagins (LBGs) in Lampyridae and outgroup species using LC-MS. We collected transcriptomes to reconstruct firefly phylogeny and ancestral states of LBGs. The presence of LBGs in the common ancestor of Lampyrinae is highly supported, but not supported in more ancient nodes. We further examined effects of amino acid substitutions in firefly ATP α on its interactions with LBGs and found that ATP α in LBGs-containing fireflies are moderately insensitive to LBGs, suggesting that target site insensitivity may contribute to LBGs-containing fireflies to deal with their own toxins. Our results suggest that firefly LBGs probably evolved much later than the evolution of bioluminescence in fireflies, implying that firefly bioluminescence probably did not originally evolve as direct warning signals to LBGs.

Talk by **Wei Zhou**:

(176) Proportional assessment of weapons

The evolution of invertebrate sensory ecology and behaviours

Wei Zhou¹ and Daiqin Li²

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Sexual selection through male contests leads to the evolution of exaggerated weapons enhancing the access of males to potential mates. Perceptual processing may mediate contest behaviors. Weber's law of proportional perception states that perceptual discrimination between stimuli is based on proportional (not absolute) differences in stimulus magnitude. Proportional perception operates in female mate-choice in some animal taxa, but its role in animal contests remains empirically untested. Studying the ant-mimicking jumping spider, *Toxeus maxillosus*, where only males have exaggerated chelicerae, which serve as weapons, we staged two males matched for body size with varying chelicera sizes to test whether males assess and compare their chelicera size with that of their opponents and make contest decisions based on proportional differences in chelicera size following Weber's law. While males armed with longer chelicerae had greater chances of winning contests, contest outcomes were better explained by proportional (not absolute) differences in chelicera size. Furthermore, contest duration was negatively correlated with proportional difference in chelicera width in the assessment stage but this correlation was absent in the combat stage. This suggests that the loser may persist for a shorter time and retreat earlier when proportional difference in chelicera width between two males is larger. Our simulated contest data further provided the diagnosis plots which support the discrimination between mutual assessment with proportional perception and other assessment strategies. Together, our results indicate that proportional perception plays a role in male contests, therefore having the potential to influence the important selective pressure of intrasexual competition and shape the evolution of exaggerated animal weapons.

Talk by **Xin Zhou**:

(177) What forces shape you? The genomics toward the dark side

An evolutionary perspective on pollinator biodiversity, systematics, and conservation

Xin Zhou¹

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The Asian honeybee, *Apis cerana*, is one of the only two extant honeybee species that have successfully expanded their range from Asian tropical to the temperate region. Its widespread range has largely overlapped with Asia's major agricultural region, therefore making significant pollination contribution to the humans. Our recent study on the mainland *A. cerana* indicated that the current population structure and distribution pattern is a result of repeated range expansions and retractions, in response to climatic oscillation of the ice age. In particular, the common ancestral population has independently invaded distant valleys of the eastern and southern Himalayans, establishing local populations adaptive to mountain habitats. A shared morphological change among mountain honeybees is the convergent elevation of body pigmentation. Although generally assumed as an adaptation to low temperature, it remains unclear how does the darkened coloration improve the fitness of individual foragers and the entire colony, and what the underlying molecular mechanism is. Here we employed 3 pairs of mountain-plain *A. cerana* populations and ask: 1) how does darkened body coloration benefit the species at low temperature? 2) whether the same genes are responsible for the convergent morphological change and how could natural selection repeatedly work on the same trait/gene? We showed that the darkened foragers increased body temperature more rapidly under rising ambient temperature, and eventually reached a higher balanced temperature. In addition, common garden experiments demonstrated that heat lost during foraging was significantly decreased in darkened foragers, which in-turn improved thermal regulation of the colony. Comparative genomics analyses suggested that the *mycC* gene, an ortholog of *ebony*, was repeatedly selected among the 3 independent mountain populations. The expression pattern of *mycC* was in concordance with the pigmentation process during pupal development. And *mycC* RNAi led to apparent increase in body darkness, confirming its role in shaping body coloration. Further fine screening of the *mycC* sequences revealed that selection signals were condensed either in its upstream regulation region or the coding region, in varied populations. These results indicated that the mountain honeybees had evolved improved capability in maintaining colony temperature via darkened body coloration of individual foragers. This parallel adaptive trait was enabled by natural selection independently operating on varied region of the same pigmentation gene.

Talk by **Chao-Dong Zhu**:

(178) New Research from China on the Ecology and Evolution of Plant-Pollinator-Parasitoid Systems

An evolutionary perspective on pollinator biodiversity, systematics, and conservation

Chao-Dong Zhu¹

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Pollinators are central ecosystem service providers, but research on them in Asia remains incipient on many fronts. With one of the highest human populations in the world, China's populace is heavily reliant on pollination for food security. Conversely, there are many undescribed species in China, requiring a much stronger taxonomic and systematic foundation in the country and region. Focusing on pollinator bees, we are studying plant-pollinator bees-parasitoid (PPP) systems sampled from three different forest ecosystems to explore population dynamics, species diversity, and species interaction networks. Standard protocols will be also recommended to citizen scientists to gather more data. These efforts will be key to better exploring the ecology and evolution of the Chinese bee fauna.

Poster by **Chengqi Zhu**:

(179) Spatial metabolomics reveal the potential organ involved in lucibufagin toxins production in *Pyrocoelia* firefly

Genetics of adaptation and evolution of novel traits

Chengqi Zhu¹

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Lucibufagins (LBGs) are defensive cardiotonic steroid toxins produced by fireflies. These toxins specifically target the ubiquitous cell-membrane protein Na⁺,K⁺-ATPase and inhibit the ability for ion transport. However, little is known about how and where LBGs are biosynthesized in vivo. Our previous research has shown that LBGs are only found in the Lampyrinae subfamily. In this study, we firstly employed UPLC to detect the temporal content of LBGs across different life stage in the LBGs-containing firefly *Pyrocoelia analis*. Additionally, matrix-assisted laser desorption/ionization mass spectrometry imaging (MALDI-MSI) was used to visualize the spatial distribution of LBGs in firefly tissue sections. Our preliminary experiments found enrichment of LBG toxins in the adult metathorax. Our study highlights the potential of mass spectrometry imaging for understanding toxin biosynthesis pathway in LBGs-containing fireflies.

Talk by **You-an Zhu**:

(180) Complete bony fish from the early Silurian of China reveals mosaic character combination of stem-group osteichthyan

Early evolution of vertebrates from evo-devo and paleontological perspectives

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The osteichthyans, or bony fishes and their terrestrial descendants, have been highly successful both on land (tetrapods), and in water (actinopterygians) from at least mid-Devonian until today. However, the origin and the earliest diversification of osteichthyans remain obscure due to a lack of well-understood stem-group, before the split of the two major groups. Previously, the earliest osteichthyan fossils in the Silurian were primarily composed of micro-remains, and articulated osteichthyan fossils were only discovered in the late Silurian (Ludfordian, Ludlow, ~425 Ma) of Yunnan, South China. The early Silurian Chongqing Lagerstätte (late Telychian, Llandovery, ~436 Ma) and the slightly older micro-remain findings from Guizhou offer a unique opportunity to examine the morphology and diversity of early Silurian gnathostomes. A previous report on the Lagerstätte revealed a large number of placoderm fossils and a bizarre, armoured chondrichthyan. Here, we report a completely-preserved osteichthyan from the Chongqing Lagerstätte. The fish is tiny, with a total body length of approximately 3 cm, and is represented by two articulated specimens, including a completely one that reveals the morphology from head to tail. The skull roof is longitudinally divided into two parts, similar to that of the sarcopterygians and the late Silurian *Guiyu oneiros*. The roofing median dorsal plates or scutes are much more extensively developed than those in *Guiyu*. The cheek complex and the single, posteriorly placed dorsal fin are actinopterygian-like. Strikingly, the new fish exhibits an anal fin spine, previously thought to be exclusive to “acanthodians”. Phylogenetic analyses resolved the new osteichthyan into the stem-group, suggesting that the character combination displayed by the new taxa may be ancestral in osteichthyan lineage, before the split of two major groups.

Talk by **Yuxiang Zhu**:

(181) When and how did introgression happen? A pan-genomic multiomics study of Genus *Quercus* L.

The genomics of adaptation and speciation

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Introgression can be an important source of new alleles for adaption under rapidly changing environments, perhaps even more important than standing variation. Though introgression has been extensively studied in many plants and animals, key questions on the underlying mechanisms of introgression still remain unanswered. In previous study by studying introgression between populations of two widespread sympatric Asian oak species, we found introgression between two species is determined not only by the genetic distance but also by the similarity of the environments in which they live—populations occupying similar ecological sites tended to exchange same genomic regions. And we found introgressed genes often have more conservative expression levels between two species. To further investigate the mechanisms of introgression in entire genus *Quercus* L., we constructed a graph pangenome of oaks. This pangenome included 9 reference-level genome assemblies, which served as an unbiased reference for constructing a phylogeny tree based on 69 oak species. We meticulously computed the introgression regions within the genomes of these species, revealing a multitude of introgression events within the *Quercus* L. genus. We also generated high-quality multiomics genomic resources, including resequencing, ATAC-seq, WGBS and transcriptome sequencing, for 18 oak species and 2 other Fagaceae species sampled in multiple forests of China. Furthermore, we correlated the introgression patterns with the whole-genome methylation map and chromatin accessibility map, suggesting a potential link between epigenetic modifications and introgression. Our results provide new avenues of research for revealing the mechanisms by which introgression occurs among closely related species. **Keywords :** introgression, *Quercus*, pangenome.

Poster by **Zhengting Zou:**

(182) Species clades with different lifestyles exhibit different relative amino acid exchangeability in protein evolution

Open category

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Relative exchangeabilities (REs) between amino acid pairs are major components in protein sequence substitution models, which is core to molecular evolution analyses such as inference of phylogeny and positive selection. Contradicting conventional assumption of its consistency across a phylogenetic tree, recent studies have discovered that REs show considerable variation among different clades of species on the Tree of Life. However, the underlying mechanism of this RE heterogeneity is largely unknown. Investigating 79 closely related pairs of genomes widely sampled across all prokaryotes, we found that their REs can be clustered into three groups. Remarkably, these groups exhibit notable differences in features like genome size and gene number, despite their statistically indistinguishable divergence levels and overall selection strengths (dN/dS). Functional annotation suggests that different groups enrich prokaryotes with different lifestyles, e.g., generalists versus specialists. Comparing between these groups, we found that different lifestyles may favor radical amino acid substitutions of different physicochemical properties, thus leading to between-clade RE difference. We further investigated a group of 20 eukaryotic clades to find unique RE and conservativeness patterns. Hence, RE patterns among species clades correspond to their distinct lifestyles, providing a mechanistic explanation of this proteome evolution heterogeneity.

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