

## Abstract Book

# 2<sup>nd</sup> Meeting of the Israeli Society for Evolutionary Biology

ISEB 2020

9-10 December 2020

[www.iseb.org.il](http://www.iseb.org.il)



**Steering committee:** Tal Pupko, Lilach Hadany, Ariel Chipman

**Organizing committee:** Einat Hazkani-Covo, Dan Mishmar, Tzachi Pilpel, Eran Tauber, Eyal Privman

**Program committee:** Yoav Ram, Dorothee Huchon, Oren Kolodny, Einat Hazkani-Covo

**Hosted by:** The Open University of Israel

## Plenary Talk #1

### Kevin N. Laland

School of Biology, University of St Andrews

## Evolutionary Origins of the Human Niche

Demographically, ecologically and cognitively, humans are an odd species. How did our species' distinctive niche evolve, and what role did our ancestors play in its origin? In this seminar I will suggest that understanding the origins of the human niche requires recognition of the manner in which organisms in general construct aspects of their world. Empirical and theoretical studies show how the activities of organisms modify selection and influence evolution, and how this was a particularly important process in human evolution. That is largely because our species' capacity for niche construction is scaled up by a potent capacity for culture. While other animals exhibit some cultural capabilities, humans and their immediate ancestors have constructed a dominant cultural realm, and then adapted to it. I will describe some theoretical and experimental projects suggesting feedback mechanisms that may have been instrumental to the evolution of human cognition. These include the findings of an international competition (the 'social learning strategies tournament') which sheds light on why copying is widespread in nature, and why humans happen to be so good at it; comparative statistical analyses across primates that revealed that innovation and social learning frequencies co-vary positively with relative brain size, tool use, longevity and cognitive performance measures; experimental archaeological investigations of the transmission of lithic technology; and a comparative experimental study of the cognitive underpinnings of cumulative culture, in children, chimpanzees and capuchin monkeys. Collectively, these studies imply that the truly unique characteristics of our species are not adaptive responses to external conditions such as climate, predators or disease. Rather, the learned and socially transmitted activities of our ancestors shaped our intellects through accelerating cycles of evolutionary feedback.

### Reference

Laland, K.N. 2017. Darwin's Unfinished Symphony: How Culture Made the Human Mind. Princeton, NJ: Princeton University Press.

## Plenary Talk #2

**Katia Koelle**

**Department of Biology, Emory University**

### **SARS-CoV-2 phylodynamics: with and without phylogenies?**

Virus sequence data have been increasingly used to infer geographic patterns of disease spread between regions and to estimate rates of viral spread within regions. Here, I will first briefly review common approaches used for viral phylogeographic and phylodynamic inference. I will then present our group's recent work on SARS-CoV-2 that uses these methods to gain insight into SARS-CoV-2 circulation patterns and some ongoing methodological developments that can further shed light on identifying patterns of SARS-CoV-2 spread and recombination.

## Plenary Talk #3

### Maitreya Dunham

Department of Genome Sciences, University of Washington

### High throughput studies of the consequences of natural variants in yeast

With genome sequencing no longer a bottleneck, the field now has the growing challenge of interpreting how large numbers of genetic variants impact phenotype. Classical methods such as quantitative trait mapping are difficult to scale, while computational predictions still require improvements in accuracy, particularly for combinations of variants. We have developed a high throughput experimental method to test the phenotypic consequences of thousands of natural alleles simultaneously, and used a sulfate transporter locus, *SUL1*, as a testbed. Our results measure the distribution of fitness effects across a collection of >1000 yeast strains, demonstrating a large number of loss of function alleles in *SUL1*. By comparing our results to our previous saturation mutagenesis study, we were able to conclude that some of the causative variants are in the promoter, while others are in coding regions. We next plan to extend this approach to other genes and other genetic backgrounds.

## Plenary Talk #4

Nicolas Galtier

Institut des Sciences de l'Evolution de Montpellier, CNRS - University Montpellier - IRD - EPHE

### (Mal)adaptive protein evolution in animals and the effective population size.

The effective population size,  $N_e$ , is a key parameter of the population genetic theory. Its role and impact on patterns of molecular evolution have been a subject of intense debate ever since the introduction by Kimura of the Neutral theory in 1969.  $N_e$  determines the intensity of drift, so if drift is not negligible, then  $N_e$  is expected to control the amount of neutral polymorphism and the load of slightly deleterious mutations carried by species.  $N_e$  also determines the number of new mutants produced per generation, so if mutation limits adaptation, then  $N_e$  should be positively correlated to the adaptive rate. With the advent of high-throughput genomics it is now possible to test these hypotheses by taking a comparative approach across species with contrasted population sizes. I will present a series of studies that we have recently conducted along these lines, with the goal of clarifying and quantifying the impact of  $N_e$  on coding sequence evolution in animals.

#### References

- Romiguier et al 2014. Comparative population genomics in animals uncovers the determinants of genetic diversity. *Nature* 515:261-263.
- Galtier N. 2016. Adaptive protein evolution in animals and the effective population size hypothesis. *PLoS Genetics* 12:e1005774.
- Rousselle M et al. 2020. Is adaptation limited by mutation? A timescale-dependent effect of genetic diversity on the adaptive substitution rate in animals. *PLoS Genetics* 16:e1008668.
- Galtier N., Rousselle M. 2020. How much does  $N_e$  vary among species? *Genetics* 216:559-572.

## Plenary Talk #5

Patricia J. Wittkopp

Dept. of Ecology and Evolutionary Biology & Dept. of Molecular, Cellular, and Developmental Biology,  
University of Michigan

### Molecular and evolutionary processes generating variation in gene expression

Genetic variation affecting gene expression is wide-spread within and among species. This variation reflects the combined actions of mutation introducing new genetic variants and selection eliminating deleterious ones. Comparative studies of gene expression in fruit flies, yeast, plants, and mice have shown that the relative contributions of cis- and trans-acting variants to expression differences change over evolutionary time, indicating that selection has different effects on cis- and trans-regulatory variants. To better understand the reasons for this now widely observed pattern, we have been systematically studying the effects of mutation and selection on expression of the TDH3 gene of the baker's yeast *Saccharomyces cerevisiae*. This work has revealed differences between cis- and trans-regulatory mutations in their frequency, effects, and dominance. Differences in pleiotropy are also generally assumed to exist between cis- and trans-regulatory that affect their evolutionary fate, but have been difficult to measure. In this talk, I will discuss how newly arising cis- and trans-regulatory mutations affecting expression of this focal gene are structured within the regulatory network, their pleiotropic effects on expression of all other genes in the genome, and how these pleiotropic effects influence fitness.

## Plenary Talk #6

Sarah P. Otto

Department of Zoology, University of British Columbia

### Selective interference and the evolution of sex

Selection acts upon genes tied together on chromosomes. This physical association reduces the efficiency by which selection can act because, in the absence of sex, alleles must rise and fall together in frequency with the genome in which they are found. This selective interference underlies such phenomena as clonal interference and Muller's Ratchet and is broadly termed Hill-Robertson interference. In this talk, I discuss the potential for selective interference to account for the evolution and maintenance of sex, discussing the positive and negative evidence from both theoretical and empirical studies and highlighting the gaps that remain.

## **Invited and Contributed Talks**

By alphabetic order

### **Noa Aharon-Hefetz**

**Weizmann Institute of Science**

### **A systematic analysis of codon usage adaption of viral genomes to proliferation- differentiation codon usage signatures**

*Noa Aharon Hefetz: Weizmann Institute, Yitzhak Pilpel: Weizmann Institute*

Viruses and their host cells present an ancient co-evolution in which each entity aims to improve its fitness. As human viruses are fully dependent on the mRNA translation machinery of the host cell, an adaption of the viral genome to the host genome, in terms of codon demand, may improve translation efficiency and hence increase viral protein yield. However, the human codon usage is dynamic and changes between tissues and cellular stages. We previously deciphered two distinct codon usage signatures for proliferation and differentiation cellular states. What are the selecting forces that shape viral codon usage? Here, we investigated more than 1000 whole genomes of human-infecting viruses and explored codon usage similarities between viral and human genes, based on the correlation to the proliferation-differentiation codon usage signatures. We found that as most human genes show a high correlation to the differentiation signature, viral genes tend to be characterized by the proliferation signature. Codon usage analysis of the viral genes based on the Baltimore classification reveals that dsDNA viruses are more adapted to human genes in terms of similarity to the proliferation- differentiation signature, while RNA viruses have less constricted correlation to the typical codon usage signature of human genes. Further examination of the dsDNA viruses according to the viral family reveals that viral tropism and the proliferation state of the host cells dictate the codon usage selection of the dsDNA viruses, such as Papillomaviridae and Adenoviridae viral families. These promising results highlight the complexity of codon usage complementarity between the different virus types to human codon usage. A deeper understanding of the viral genome evolution may set the ground for better therapeutic strategies against viral infections and pandemics.



## Polpass Arul Jose

The Hebrew University of Jerusalem

### Microbiome plasticity promotes polyphagy in the Mediterranean fruit fly (*Ceratitis capitata* Wiedemann)

*Polpass Arul Jose, Department of Entomology/Plant Pathology and Microbiology, Faculty of Agriculture Food and Environment, The Hebrew University of Jerusalem, Rehovot 7612001, Israel; Boaz Yuval, Department of Entomology, Faculty of Agriculture Food and Environment, The Hebrew University of Jerusalem, Rehovot 7612001, Israel; Edouard Jurkevitch, Department of Plant Pathology and Microbiology, Faculty of Agriculture Food and Environment, The Hebrew University of Jerusalem, Rehovot 7612001, Israel.*

Many microbiome studies suggest a role for microorganisms in the evolution and adaptation of insects to different habitats. This study tested the hypothesis that microbiome plasticity enables the Medfly to develop in numerous fruit hosts. In our field-like experiment, an initial Medfly colony was reared out of infested-fruits collected from the field. Matured females of the initial colony and their progenies were individually allowed to infest different fruits in the laboratory. At each of three generations, the fruits were shifted. The microbiomes of larvae and adults of every generation, and of their respective mother were analyzed by 16S rDNA-targeted community sequencing. Bacteria belonging to the Enterobacteriaceae commonly dominated the Medfly microbiome, followed by Acetobacteraceae, Gammaproteobacteria-unclassified, and Burkholderiaceae. Yet, significant shifts in microbiome composition were detected between fruits, supporting our hypothesis, pointing at microbiome-driven local adaptations as a mechanism that enables polyphagy.

## Darar Bega

Tel Aviv University

### Mortality Risk Sources and the Evolution of Senescence

*Darar Bega, School of Plant Sciences and Food security, Tel-Aviv University; Lilach Hadany, School of Plant Sciences and Food security, Tel-Aviv University*

Senescence is a process of damage accumulation that results in increased mortality risk with age. Damage is accumulated and repaired with great variability throughout the tree of life leading to a vast variation of life-histories. Understanding the different selection pressures that underlie that variation can help focus research efforts to extend human health-span, an underfunded scientific goal relatively to its potential benefit. Increasing reproduction rate and sustaining it are both beneficial to some extent. Thus, given the possibility, selection would drive them up until one can only improve at the expense of the other. For example, damage-repair mechanisms cost energy and time that can be used for reproduction. The trade-off between senescence and reproduction is highly influential in determining species life-history. In classic models for the evolution of senescence, mortality risks can be age dependent (independent of the environment) or environment dependent (independent of age), but the interaction between age and environmental risk is neglected. Yet, the most common death causes in nature, like predation and starvation, clearly demonstrate interaction between age and environment in many organisms. We constructed a new model, based on damage accumulation, that takes interaction into account with biologically interpretable variables. I will present the effects of environmental risk, its interaction with age, and the trade-off between aging and reproduction on the evolution of senescence.

## Smadar Ben-Tabou de-Leon

University of Haifa

### The tolerance to hypoxia is defined by a time-sensitive response of the gene regulatory network in sea urchin embryos

*Majed Layous, Lama Khalaily, Tsvia Gildor and Smadar Ben-Tabou de-Leon, Department of Marine Biology, Leon H. Charney School of Marine Sciences, University of Haifa, Haifa 31905, Israel.*

Deoxygenation, the reduction of oxygen level in the oceans induced by global warming and anthropogenic disturbances, is a major threat to marine life. Acute diurnal changes in oxygen levels could be especially harmful to vertebrate and sea urchin embryos that utilize endogenous hypoxia gradients to drive morphogenetic events during normal development. Here we show that the tolerance to hypoxic conditions changes between different developmental stages of the sea urchin embryo, due to the structure of the gene regulatory networks (GRNs). We demonstrate that during normal development, the bone morphogenetic protein (BMP) pathway restricts the activity of the vascular endothelial growth factor (VEGF) pathway to two lateral domains and by that controls proper skeletal patterning. Hypoxia applied during early development strongly perturbs the activity of Nodal and BMP pathways that affect the VEGF pathway, dorsal-ventral (DV), and skeletogenic patterning. These pathways are largely unaffected by hypoxia applied after DV axis formation. We propose that the structure of the DV GRN, which includes feedback and feedforward loops, increases its resilience to changes of the initial oxygen gradients and helps the embryos tolerate transient hypoxia.

## Talia Borofsky

Stanford University

### Static environments with limited resources select for multiple foraging strategies rather than conformity

*Talia Borofsky, Department of Biology, Stanford University; Marcus Feldman, Department of Biology, Stanford University*

Social learning and conformity are essential for the evolution of culture and group identities in animals and humans. Previous theoretical work studied the evolution of social learning and conformity when environmental states change and found that conformity evolves for a large range of environmental conditions. However, the foraging environment can affect the adaptive benefits of social learning and conformity. Conformity can cause a population to focus mainly on one out of multiple available resources, which can incite competition if the first resource is limited. We study the evolution of social learning and conformity in a limited-resource environment using a replicator model of a forager population feeding on two resources. In sharp contrast to previous models, anti-conformity, rather than conformity, evolves from a population of non-conformists under most environmental conditions. Numerical simulations suggest that both social learning and conformity cause the foragers to favor one resource over the other even though the resources provide the same benefit to foragers. Resource limitation favors anti-conformity because anti-conformity tends to force both resources to be exploited equally. Similarly, depletion of resources selects against social learning. However, increasing social learning is adaptive when independent discovery of foraging cues is difficult because it increases the frequency of individuals learning to find food. Consequently, in an environment with difficult-to-learn food cues, increased social learning is more likely to evolve. However, for social learning to emerge in a population of individual learners, at least half of the population must have learned how to find food, which requires that individual learning be sufficiently reliable. Our results show that competition and consumer-resource interactions can alter the evolutionary course of social learning and transmission bias. Since there are many examples of conformity in the animal kingdom and among humans, future models should explore what conditions would allow conformity to first evolve.

## Robin Burns

**Gregor Mendel Institute of Plant Molecular Biology**

### Gradual evolution of allopolyploidy in *Arabidopsis suecica*

*Robin Burns, Polina Yu. Novikova, Magnus Nordborg*

Polyploidy has played a major role in the evolution of most eukaryote genomes, including our own. However, because polyploidization in the ancestry of most genomes is ancient the process is not well understood. Recent polyploids allow us to study the process of polyploidization and are common in flowering plants. Speculation of large genomic changes or “genome shock” have been linked to polyploidy but these studies are largely based in crops and artificial polyploids that may not be representative of natural ones. We focused on *Arabidopsis suecica*, a ~16kya allotetraploid generated by the hybridization of two species, *A. thaliana* and *A. arenosa*, that differ in almost everything from genome size to ecology. Here, we present a chromosome level assembly of *A. suecica* along with polymorphism and transcriptome data for multiple individuals of it and the parent species, as well as synthetic *A. suecica* made in de novo in the lab. The main conclusion of our study is that polyploidization is gradual process rather than an event. We confirm previous results that *A. suecica* shares most genetic polymorphisms with the parent species demonstrating it had multiple rather than a unique origin. We find no evidence for genome shock – the genome is colinear, transposons are not out of control and there is no subgenome dominance in expression. Instead, we find evidence that *A. suecica* is adapting to polyploidy, with changes in gene expression related to the meiotic machinery and plastid interactions. This finding, along with the observation that synthetic *A. suecica* is often aneuploid and shows genome rearrangements suggest that the main hurdle to overcome in polyploidy is selective, and that crops may not be representative of natural polyploids as domestication can dramatically alter selection patterns, though clearly many more examples are needed.

## David Burstein

Tel Aviv University

### Discovery of CRISPR-Cas systems in metagenomic data

*Lucas Harrington, Department of Molecular and Cell Biology, University of California, Berkeley; Dov Gertz, Shmunis School of Biomedicine and Cancer Research, Tel Aviv University; Jillian F. Banfield, Department of Earth and Planetary Sciences, University of California, Berkeley; Jennifer Doudna, Department of Molecular and Cell Biology, University of California, Berkeley; David Burstein, Shmunis School of Biomedicine and Cancer Research, Tel Aviv University*

Current understanding of microorganisms, which shape the evolution and functioning of Earth's ecosystems, is based primarily on cultivated organisms. However, only a tiny fraction of the microbial diversity can be cultured and the overwhelming majority of microbes were never successfully grown in a lab. We apply cultivation-independent approaches, namely genome-resolve shotgun metagenomics, to study the functions encoded by uncultured organisms. Recently, we used this methodology to seek new CRISPR-Cas systems that will give rise to new biotechnological tools and contribute to our understanding of the arms race between viruses and their microbial hosts. We discovered a number of novel CRISPR-Cas systems, including streamlined systems found exclusively in uncultivated microbes, tiny Cas effector proteins targeting single-strand DNA, and the first reported Cas9 in the archaeal domain of life. Notably, all the required functional components were identified by environmental metagenomics and metatranscriptomics, enabling to functionally test the activities of the newly discovered systems. Our discoveries provide hints regarding the evolution of CRISPR-Cas and demonstrate the potential of metagenomics to reveal novel microbial systems.

## Victor China

**Ben-Gurion University of the Negev**

### Hydrodynamic constraints shape the performance landscape of the feeding mechanism of fish larvae during the critical period

*Victor China, Ben-Gurion University of the Negev, The Jacob Blaustein Institutes for Desert Research & The Interuniversity Institute for Marine Sciences in Eilat; Roi Holzman, Tel-Aviv University, Department of Zoology & The Interuniversity Institute for Marine Sciences in Eilat.*

Larval fishes experience extreme mortality rates, with up to 90% of a cohort perishing within days after starting to actively feed. Over a century ago, Hjort (1914) famously attributed this “critical period” of low survival to the larvae’s inability to obtain sufficient food. However, no consensus has emerged regarding the role of different mechanisms in determining larval mortality, and specifically in explaining the larvae’s inability to obtain food. In my study, I explored the role of hydrodynamics in structuring predator-prey interactions. Using feeding experiments and modeling, as well as high-speed video observations of larval feeding strikes, I found that successful feeding strikes were characterized by Reynolds numbers that were an order of magnitude higher than those of failed feeding strikes. I also found that the pattern of increasing strike success with increasing age was driven by the ontogeny of traits that facilitate the transition to higher Reynolds numbers. Modeling the performance landscape for larval feeding revealed that larvae climb towards a peak of higher performance as they mature, and that the landscape is not age-specific. Concomitantly, constraints on the kinematics that are associated with successful feeding strikes relax throughout ontogeny, resulting in older larvae displaying a wider kinematic repertoire. My study demonstrates how understanding an organism’s hydrodynamic environment promotes our understanding of ecological processes; and how large-scale ecological patterns can be governed by small-scale physics.

## Pnina Cohen

Steinhardt Museum of Natural History

### Genome Wide Association Study of nestmate recognition in *Cataglyphis niger* ants

*Pnina Cohen, University of Haifa, Shani Inbar, University of Haifa, Eyal Privman, University of Haifa*

Nestmate recognition underlies social behaviour in social insects as it forms the basis for kin identification and kin selection. The chemical profile of an ant colony, which is used for nestmate recognition, is composed of varying amounts of cuticle hydrocarbons (CHCs). We carried out a Genome Wide Association Study (GWAS) of CHCs in *Cataglyphis niger* by sampling 47 colonies, fully sequencing six workers from each colony and measuring the relative amounts of their 34 CHCs. Under the Gestalt colony odour hypothesis, social interactions between nestmates, in which CHCs are being transferred, are essential in creating a uniform colony CHCs profile. We carried out a second GWAS between the colonies and their uniform Gestalt odour by averaging nestmate genotypes and comparing them to their averaged CHCs amounts. Together, these two analyses identified 99 QTLs associated with 18 of the CHCs. 13 clusters of two to four QTLs located within 10cM from each other were identified, seven of which contained QTLs from both analyses. We conclude that nestmate recognition, a quantitative and complex colony-level trait, has a genetic component to its phenotypic variation. More research is needed to determine whether social interactions between nestmates also contribute to colony chemical identity.



## Tal Dahan-Meir

**Weizmann Institute of Science**

### Genetic diversity of a wild wheat population under climate change

*Tal Dahan-Meir, Department of Plant and Environmental Sciences, Weizmann Institute of Science, Rehovot, Israel; Thomas James Ellis, Gregor Mendel Institute, Austrian Academy of Sciences, Vienna BioCenter, Vienna, Austria; Hanan Sela, Department of Evolutionary and Environmental Biology, Haifa University, Israel. The Institute for Cereal Crops Improvement, Tel-Aviv University, Tel Aviv, Israel. , Amir Raz, Migal, Galilee Technology Center, Kiryat Shmona, Israel. Department of Plant and Environmental Sciences, Weizmann Institute of Science, Rehovot, Israel. , Moshe Feldman, Department of Plant and Environmental Sciences, Weizmann Institute of Science, Rehovot, Israel. , Yehoshua Anikster, The Institute for Cereal Crops Improvement, Tel-Aviv University, Tel Aviv, Israel. , Magnus Nordborg, Gregor Mendel Institute, Austrian Academy of Sciences, Vienna BioCenter, Vienna, Austria; Avraham A. Levy, Department of Plant and Environmental Sciences, Weizmann Institute of Science, Rehovot, Israel.*

Long-term studies of natural populations, especially those involving genetic data, are an invaluable tool for capturing the full dynamics of populations as they respond to a changing environment. However, there is currently an acute shortage of studies that have examined populations for more than a few years. Here we take advantage of a population of wild emmer wheat, a wild progenitor of modern wheat, located at the species' center of distribution near kibbutz Ammiad in northern Israel, for which seeds have been intensively sampled since 1984. During this 36-year period, local temperature and atmospheric CO<sub>2</sub> concentration have risen steadily, providing a unique opportunity to assess the temporal evolution of a wild population under climate change. We genotyped 879 plants from four transects using a reduced-representation genotype-by-sequencing approach. Although the population is highly polymorphic, we find clear clusters of identical genotypes in space that are remarkably stable through time. Simulations indicate that this structuring cannot be accounted for by limited dispersal and genetic drift alone. Moreover, observed clustering corresponds to micro-habitats, suggestive of adaptation to ecological niches on a very fine scale. Despite this, there is some evidence of a few genotypes increasing in frequency through time, which may reflect adaptation to new climatic conditions. Together, our results indicate that genetic diversity in this population is primarily shaped by environmental heterogeneity, rather than by the temporal climatic changes observed in the last four decades.

## Tzion Fahima

University of Haifa

### Polyphyletic origin of the tandem kinase-pseudokinase (TKP) protein family and a proposed decoy model for their involvement in plant immunity

*Tzion Fahima, Andrii Fatiukha, and Valentyna Klymiuk, Institute of Evolution and the Department of Evolutionary and Environmental Biology University of Haifa, Haifa, Israel; Gitta Coaker, Department of Plant Pathology, University of California, Davis, CA, USA*

Yellow rust, caused by *Puccinia striiformis* f. sp. *tritici* (Pst), is a devastating fungal disease threatening much of global wheat production. Yr15 is a broad-spectrum resistance (R)-gene, derived from wild emmer wheat (WEW). Yr15 encodes a protein with kinase-pseudokinase domain architecture, designated as Wheat Tandem Kinase 1 (WTK1) that comprises an unusual R-gene structure in wheat. WTK1 orthologs and paralogs are found in all group 1 and 6 wheat chromosomes. Proteins with similarity to WTK1's domain architecture were also identified in 92 putative proteins across the plant kingdom, suggesting that they are members of a distinct family of plant proteins, termed here tandem kinase-pseudokinases (TKPs). We found that 175 out of 184 kinase/pseudokinase domains of these TKPs are associated with receptor-like kinases, suggesting that TKPs are involved in plant defense mechanisms. Phylogenetic analysis indicated that TKP family members originated from either gene duplication or gene fusion events, implying a polyphyletic origin of the TKPs by convergent evolutionary processes. Here, we propose a decoy model to describe the potential function of the pseudokinase domain in the TKP family. In this model, the pathogen secretes effector proteins to suppress the activity of host kinases involved in the resistance response, while pseudokinase domains serve as decoys for these effectors. After interacting with the pathogen effector, the pseudokinase protein may act as a "molecular switch" to activate the kinase domain, which then phosphorylates downstream substrates resulting in disease resistance. This model can explain the molecular function of the TKP protein family and provide support for their polyphyletic origin and evolution. This "molecular switch" has a crucial role in controlling the activation of local programmed cell death only in the presence of pathogen. Further studies are underway to elucidate the mechanism of resistance conferred by this extraordinary protein family.

## Tamar Friedlander

The Hebrew University of Jerusalem

### Evolution of new regulatory functions on biophysically realistic fitness landscapes

*Tamar Friedlander, Roshan Prizak, Nicholas H. Barton and Gasper Tkacik*

Gene expression is controlled by networks of regulatory proteins that interact specifically with external signals and DNA regulatory sequences. These interactions force the network components to co-evolve so as to continually maintain function. Yet, existing models of evolution mostly focus on isolated genetic elements. In contrast, we study the essential process by which regulatory networks grow: the duplication and subsequent specialization of network components. We synthesize a biophysical model of molecular interactions with the evolutionary framework to find the conditions and pathways by which new regulatory functions emerge. We show that specialization of new network components is usually slow, but can be drastically accelerated in the presence of regulatory cross-talk and mutations that promote promiscuous interactions between network components.

## Jonathan Friedman

The Hebrew University of Jerusalem

### Positive interactions within and between populations decrease the likelihood of evolutionary rescue

*Yaron Goldberg, Department of Plant Pathology and Microbiology, The Hebrew University ; Jonathan Friedman, Department of Plant Pathology and Microbiology, The Hebrew University.*

Positive interactions play crucial roles in shaping the structure and function of many ecosystems. Despite the importance of positive interactions, their influence on the ability of species to adapt to new environments is still poorly understood. Here, we use simulations and theoretical analyses to study how positive interactions impact the likelihood that populations survive after an environment deteriorates - a scenario known as evolutionary rescue. We find that the probability of evolutionary rescue in cooperating populations is reduced significantly. This effect is exacerbated in mutualistic populations, and reduced even further in populations invaded by cheaters, making evolutionary rescue extremely unlikely in these systems. Our results indicate that positive interactions can hinder adaptation to changing environments, elevating the risk of population collapse. Furthermore, our results suggest that selective pressure for adaptation to changing environments could have contributed to driving co-dependent unicellular species to form more adaptable organisms, potentially including multicellular life.

## Uri Gat

The Hebrew University of Jerusalem

### The Collagen-like Gene Family in the Development and Regeneration of the sea anemone *Nematostella* and General Evolution Trends in Metazoan Animals

*Uri Gat, Dept. Cell and Developmental Biology, Hebrew University in Jerusalem, Tal Nir, Dept. Cell and Developmental Biology, Hebrew University in Jerusalem, Lucas Leclere, Laboratoire de Biologie du Developpement de Villefranche-sur-Mer (LBDV), Sorbonne Universite, CNRS, Villefranche-sur-Mer, France*

The collagen triple helix repeat containing protein (Cthrc1) gene was identified at first as being induced upon injury to arteries in rats. The human gene CTHRC1 was later reported to be aberrantly expressed in multiple human cancers and to be functionally associated with cancer cell migration, tumor invasiveness and metastasis. The data about the functions and molecular modes of operation of this gene are still preliminary and knowledge about its phylogeny was very limited. We discovered a family of these genes in a transcriptional screen in order to explore whole-body regeneration in the sea anemone *Nematostella vectensis* (Nv), a cnidarian model animal. Eight members of this gene family were defined in Nv in terms of sequences, structure and genomics and we explored the general phylogeny of Cthrc's in metazoans which was hitherto unknown. The expression patterns of the different family members along the developmental stages, in adult polyps and during the time course of regeneration were also analyzed. Upon regeneration, these genes show a highly dynamic and unique mode of temporal and spatial expression, suggesting a putative role in the re-construction of the missing body parts. Our evolutionary studies showed that Cthrc1 animal groups-specific diversifications occurred multiple times in cnidarians as well as in most metazoan clades where we detected these genes. Most vertebrates display a single highly conserved gene. Interestingly, this high conservation in sequence coincided with the origin of its conserved upstream neighboring gene found only in vertebrates, Frizzled 6 (FZD6), which in mice has been shown to functionally interact with Cthrc1. Thus, we suggest that Cthrc1 is playing a role together with FZD6 in regulation of the Wnt-PCP developmental pathway in vertebrates in a new mode specific to this group.

## Gili Greenbaum

The Hebrew University of Jerusalem

### Designing gene drives to limit spillover to non-target populations

*Gili Greenbaum, Department of Ecology, Evolution & Behavior, The Hebrew University of Jerusalem, Jaehee Kim, Department of Biology, Stanford University, Marcus W. Feldman, Department of Biology, Stanford University, Noah A. Rosenberg, Department of Biology, Stanford University*

Gene drive are engineered genetic constructs that can spread deleterious phenotypes in wild populations. The potential application of CRISPR-based gene drives to control disease vectors such as mosquitoes, invasive species, and agricultural pests has generated much excitement, in the scientific community and in the general society. However, this revolutionary technology has also raised serious concerns of the potential unintentional spillover of gene drives from the target population to other, non-target, populations, and even to other species. We developed a population-genetic modeling framework for studying gene drive spillovers by integrating gene flow into dynamical equations describing the evolutionary dynamics of gene drives. Using this framework, we show that it is possible to exploit unstable equilibria in the system to achieve ‘differential-targeting’ – having the gene drive spread in the target population, but in the non-target population, thus avoiding spillovers. We outline how differential targeting can be achieved by careful design of the gene drive parameter. However, we also find that, in our model, if gene flow is not very low than differential targeting is sensitive to the configuration of the gene drive, and therefore it is unlikely to be feasible with the current state of CRISPR-based gene drive technology. To understand the applicability of our approach, we studied two potential gene drive applications – suppression of *Anopheles* mosquitoes in Africa and eradication of invasive rodents on islands – and we find that the considerations of gene drive design vary from system to system. Our models suggest that differential targeting could potentially be used as one of several safeguards against spillovers, and we outlines guidelines for designing gene drives with lower spillover risks.

## Yael Gurevich

Tel Aviv University

### Floral complexity can help maintain plant diversity by inducing pollinator fidelity

*Yael Gurevich, Lilach Hadany*

The global decline in plant biodiversity throughout recent human history has attracted broad scientific attention, as biodiversity plays a key role in promoting a productive ecosystem. Pollination is a major factor in plant survival but carries an additional cost for locally rare plant species: they are likely to receive high levels of incompatible pollen that does not contribute to reproduction and can even impair seed production. Therefore, floral traits that diminish the risk of incompatible pollen may be favored by natural selection. We developed a theoretical framework to explore the influence of floral traits that may contribute to plant reproductive success through their effect on pollination quality. We show that when a rare plant species is morphologically complex, there may be an incentive for pollinators to specialize, increasing pollination quality significantly for the less common plants. Our results show that, through its influence on pollinator foraging behavior, complex floral morphology can contribute to the maintenance of plant diversity.

## Ricardo Gutierrez

The Hebrew University of Jerusalem

### Adaptive antibiotic resistance at supra-inhibitory concentrations in *Bartonella*

*Ricardo Gutiérrez, Yoav Ram, Judith Berman, Keyla Carstens Marques de Sousa, Yaarit Nachum-Biala, Malka Britzi, Daniel Elad, Gad Glaser, Shay Covo & Shimon Harrus*

Antibiotic resistance is one of the most critical and universal health threats. *Bartonella* bacteria are zoonotic and slow-growing pathogens that exhibit a remarkable emergence of antibiotic resistance in vitro. Interestingly, *Bartonella* spp. harbor reduced genomes lacking typical stress-induced mutagenesis systems, such as error-prone polymerases, RpoS, or RecBCD. In this study we show that sensitive *Bartonella* can survive and acquire resistance-associated mutations at supra-inhibitory antibiotic concentrations, presenting adaptive evolution during antibiotic therapy. A mathematical model showed that both mutation and phenotype switching rates (from “sensitive” to “hetero-resistance”) must be increased over 10 and 100-fold, respectively, to explain our in vitro results. Furthermore, we demonstrated that the studied phenomenon occurs only with certain antibiotics, is significantly associated with high oxygen levels, and depends on antibiotic concentration accumulation. Finally, we delineated the *Bartonella* RNA expression response during antibiotic treatment and significantly identified stress and mutator responses. Hence, this study presents an alternative bacterial capacity to evolve adaptive drug resistance at supra-inhibitory conditions.



## Noam Harel

Tel Aviv University

### The analysis of intra-host variation of SARS-CoV-2 resolves epidemiological investigations

*Noam Harel, Yael Paran, Ronen Ben-Ami, Adi Stern*

Genome sequencing coupled with phylogenetic analysis have become key in tracking the spread and dynamics of the recent COVID-19 pandemic and informing public health policy. In fact, genomic data is increasingly being used to complement traditional epidemiological investigations, supplying objective information on relationships between genomes of infected individuals. Here, we describe an outbreak in the Tel-Aviv Sourasky medical center that involved 17 patients and staff members. Interestingly, our results showed that using a single viral sequence per patient for phylogenetic analysis can lead to deficient results, and that it is critical to take into account intra-host diversity in order to fully resolve transmission patterns. Furthermore, we found that there may be key differences in the intra-host diversity of nasopharyngeal and plasma samples. Our research illustrates the importance of treating viral samples from patients as a population and not as a single variant.

## Keith Harris

The Hebrew University of Jerusalem

### Are only certain traits selected as reliable signals? Zahavi's interpretation of Fisherian runaway revisited

*Keith D. Harris, Department of Ecology, Evolution, and Behavior, The Hebrew University of Jerusalem, Yair Daon, Courant Institute of Mathematical Sciences, New York University, Vidyand Nanjundiah, Centre for Human Genetics, Bangalore*

The evolution of sexually dimorphic traits whose elaboration require extensive investment have been the focus of many verbal and mathematical explanations. Identifying the counter-intuitive “wastefulness” of such traits, Darwin ascribed their evolution to a selection mechanism that he termed sexual selection. This mechanism could explain how, for instance, a male peacock could benefit from developing a trait that was detrimental to its survival, if it increased its reproductive success through attractiveness to females. Fisher later formalised this model, showing how female preference of a trait could overcome natural selection, leading to the elaboration of otherwise inefficient traits. In 1975, Zahavi returned to Fisher's model, and suggested that the elaboration of certain traits serves the functional role of transmitting reliable information regarding the signalling. Since then, there have been numerous attempts to determine whether waste is a necessary aspect for some or all reliable signals. However, these models have not tested Zahavi's main hypothesis – that only certain traits can become signals. Here we return to Zahavi's verbal model, identifying assumptions that are crucial to Zahavi's hypothesis regarding the selection of signals. Introducing these assumptions into an individual-based mate choice model with multiple potential signals crucially affects signal selection according to the cost of production (marginal cost). Signals inflate as in Fisher's runaway model at low marginal costs, but provide limited distinction between signallers at higher marginal costs. Our results suggest that marginal cost optima can arise from the trade-off between signalling constraints, through their effect on informative ranges of signalling levels.

## Amiyaal Ilany

Bar-Ilan University

### The implications of social inheritance on genetic structure of populations

*Irith Aloni, Faculty of Life Sciences, Bar-Ilan University, Amiyaal Ilany, Faculty of Life Sciences, Bar-Ilan University*

Social structure is an important selective factor, affecting both reproductive success and survival, which consequently affect the genetic structure of populations. Multiple factors can influence the structure of social networks and their dynamics. A social inheritance model, in which offspring inherit their mother's social bonds, has been recently suggested as a process shaping animal social networks. Here, we aim at assessing the implications of social inheritance on the genetic structure of animal populations. Social inheritance, in which newborns bond mostly with individuals socially connected to their parents, leads to the formation of social groups with distinct genetic structure. Our results suggest that genetic distances, as measured by Wright's and by Wier & Cokerham's F statistics, reflect values obtained from genetic studies of wild populations. Our models pave the way to explain genetic structure of populations through fine-scale animal social networks. Assuming that social network structure plays a major role in inheritance, shaping the genetic population structure of future generations, such models may provide an important tool for understanding evolution as well as for applying conservation measures.

## Dikla Kolan

University of Haifa

### Examining the trade-off between resistance to phages and nitrogen fixation in cyanobacteria

*Dikla Kolan, Sarit Avrani*

While atmospheric nitrogen (N<sub>2</sub>) is over 78% of the air we breathe, it is not available to most of the organisms on earth. Cyanobacteria are one of the few organisms that can fix atmospheric nitrogen, generating biologically available nitrogen compounds. Nitrogen fixation is highly sensitive to oxygen, which is in excess during photosynthesis. Cyanobacteria developed a few strategies to overcome this, one of which, evolved in filamentous cyanobacteria, is a spatial separation between photosynthesis and nitrogen fixation, which is performed in specialized cells called heterocysts. This ability to fix nitrogen gives cyanobacteria a competitive advantage over other phytoplankton species and enables them to form blooms under nitrogen starvation. While nitrogen can potentially exert bottom up control on cyanobacteria populations, cyanophages (viruses that infect cyanobacteria) can serve as top down selecting agents. Becoming resistant to cyanophages has a great benefit under cyanophage selection, however such resistance often comes with various adaptive costs. In this study we characterize the trade-off between resistance to cyanophages and the ability to induce heterocyst cells and to fix nitrogen in the filamentous bloom-forming cyanobacteria *Cylindrospermopsis raciborskii*. We isolated 92 *C. raciborskii* strains resistant to three cyanophages and sequenced their whole genome in order to identify the mutations that conferred this resistance. Preliminary results show a significant decrease in heterocysts differentiation in the resistant strains and in their survival under nitrogen starvation, compared to their susceptible paired controls. Such mutant strains with a significant reduced ability to grow under nitrogen starvation will not be able to form a bloom in the following season. These central, however contrasting, selective pressures can thus highly influence the composition and diversity of cyanobacterial populations worldwide.

## Talia Kustin

Tel Aviv University

### The rate of genomic insertions and deletions in SARS-coronavirus-2 and additional zoonotic viruses.

*Talia Kustin, Noam Harel, Gil Loewenthal and Adi Stern*

The study of genomic sequences has played an important role in furthering our understanding of SARS-Coronavirus-2 (SARS-CoV-2), the virus responsible for the COVID-19 pandemic. We and others have detected multiple deletions and insertions (termed indels) of varying lengths and across varying genomic locations in SARS-CoV-2 genomes. This phenomenon was also detected in previous outbreaks of coronaviruses, caused by SARS-CoV-1 and MERS-CoV, all of which are zoonotic viruses, i.e., viruses that jumped from an animal reservoir to humans. These observations have raised several questions regarding the rates and dynamics of indels in the evolution of viruses and specifically in zoonotic viruses. Two non-mutually exclusive hypotheses can be raised: these indels are neutral, or only slightly deleterious, and are tolerated by the virus, or these indels may be adaptive to the virus. Furthermore, it is possible that the adaptive value of indels may be related to zoonosis events, allowing adaptation to the new host. To investigate this, we set out to characterize rates of indels across different viruses from the coronaviridae family as well as additional zoonotic and non-zoonotic viruses. Our results reveal that in zoonotic coronaviruses, indel rates vary dramatically among different proteins, with accessory proteins generally displaying higher indel rates. This is intriguing since accessory proteins often modulate the host innate antiviral response. Moreover, in all zoonotic viruses we detected higher indel rates in the new hosts as opposed to the reservoir hosts. Overall, our results suggest that insertions and deletions may be a driving force in virus evolution that should not be overlooked.

## Aparna Lajmi

University of Haifa

### Understanding the genomic basis of social polymorphism in the desert ant

*Aparna Lajmi, Pnina Cohen, Chih-Chi Lee, Eyal Privman*

Social insects such as ants show a huge variation in social organization, sometimes even within the same species. The desert ant, *Cataglyphis niger*, shows polymorphism in colony structure that has a profound effect on their behavior and colony size. While most social insect colonies have a single queen, this polymorphism results in colonies that have multiple unrelated queens. As a consequence, colonies comprise of multiple unrelated workers that co-operate with each other. Similar polymorphism has been reported in two other distantly related species of ants, which is known to be caused by a supergene— a group of genes located in close proximity on a chromosome. We aim to understand the genomic basis of this polymorphism in the desert ant and their evolution with respect to the two known supergenes in ants. Genome-Wide Association analyses on preliminary data show multiple SNPs located on the same chromosome to be correlated with the social form indicating the presence of a supergene. To generate a more robust dataset, 30 nests of this species were sampled from a single population in Tel Baruch where both the social forms are prevalent. Currently, we are applying reduced-representation genomic sequencing to 20 workers from each sampled nest. Behavioral assays were carried out on these nests, which combined with kinship analyses using the genomic data will help us identify their social structure. Genome-Wide Association analyses on the larger dataset will help us detect more SNPs with greater confidence and identify the social chromosome. I will present our work so far and plans for future directions to better understand the genomic basis of this social polymorphism.

## Ehud Lamm

Tel Aviv University

### Conformational adaptations: the species-environment complex and its implications for stability and long-term evolution

*Ehud Lamm, Cohn Institute for History and Philosophy of Science, Tel Aviv University; Oren Kolodny, Department of Ecology, Evolution, and Behavior, The Hebrew University of Jerusalem*

Species' adaptation to their environments occurs both via genetic adaptation and via non-genetic mechanisms of adaptation. We propose a third category of eco-evolutionary dynamics: cases in which adaptation to the environment occurs via "conformational adaptation", in which the adaptation is conferred via structural or compositional structure of the population or its environment. For example, consider a case of habitat choice in which each individual searches for other individuals of the species, and joins them. In this case, the information for survival is encapsulated in the species' demography as a whole, i.e. in the spatial distribution of the species' individuals. The information needed to produce the adaptive trait of an individual cannot be reduced to information found in a single genome or a fixed small set of genomes or behaviors, but instead consists of interactions between multiple individuals in the population and their ecological interactions.

In the talk we will define the concept of conformational adaptation, and explain the challenges in identifying them. We explain their implications for understanding evolutionary dynamics, in particular the effects of changes in population size on evolutionary dynamics. Finally, we will discuss Allee effects, i.e. correlation between population size or density and the mean individual fitness. We suggest that our perspective may explain Allee effects for which the causality is often unclear. Accordingly, conformational adaptations may be significant for species conservation and re-introduction.

## Chih-Chi Lee

**Kyoto University**

### Population genomics reveals a potential adaptive evolution in the yellow crazy ant

*Chih-Chi Lee, Division of Applied Biosciences, Kyoto University; Chin-Cheng Scotty Yang, Department of Entomology, National Chung Hsing University, Department of Entomology, Virginia Polytechnic Institute and State University;*

Invasive species provides opportunities for exploring evolution over contemporary timescale in novel environments. The yellow crazy ants, *Anoplolepis gracilipes*, is a worldwide distributed invasive species that majorly dwell in the tropical area but extend their range to a humid subtropical climate region. Such broad geographic isolation limited the gene flow in this ant, which normally dispersal through the dependent founding, unless human-mediated jump dispersal breakthrough the geographic boundaries. To investigate whether the adaptive evolution occurs as a consequence of the biological invasion, we surveyed the population structure using nuclear marker and mitochondrial COI of *A. gracilipes* plus the phylogenomic analysis of an endosymbiont in *A. gracilipes*. We collected *A. gracilipes* colonies across 12 geographical regions from Southeast Asia, East Asia, Australia, and Hawaii islands. The concordance of nuclear, mitochondria, and an endosymbiont phylogeny providing evidence of a genetic barrier between two distinct genetic clades. The population structure and geographic analysis suggested the two divergent genetic clades, one limited in the tropical region and another extending to subtropical habitat. We further pinpointed 17 genome regions potential under positive selection used outlier approaches. Our study provides new evidence for a potential adaptive evolution in an invasive ant.



## Magda Lewandowska

The Hebrew University of Jerusalem

### Conserved role of cnidarian RLRs in mediating the antiviral immune response

*Magda Lewandowska, Department of Ecology, Evolution and Behavior, Hebrew University of Jerusalem; Ton Sharoni, Department of Ecology, Evolution and Behavior, Hebrew University of Jerusalem; Yael Admoni, Department of Ecology, Evolution and Behavior, Hebrew University of Jerusalem; Reuven Aharoni, Department of Ecology, Evolution and Behavior, Hebrew University of Jerusalem; Yehu Moran, Department of Ecology, Evolution and Behavior, Hebrew University of Jerusalem*

Animals developed a broad repertoire of innate immune sensors and downstream effector cascades for defense against RNA viruses. Retinoic acid-inducible gene I (RIG-I) -like receptors (RLRs) is a family of metazoan-specific ATP-dependent DExD/H box RNA helicases that function as the major cytoplasmic receptors binding double-stranded RNA (dsRNA), a hallmark of viral infection. Bilaterian RLRs were suggested to carry distinct, non-redundant functions and activate different antiviral pathways in vertebrates and nematodes. In order to provide insights into the ancestral state of RLR-mediated immune response we study these receptors in *Nematostella vectensis*, a model organism representing Cnidaria (sea anemones, corals, jellyfish and hydroids) separated from its sister group Bilateria (the majority of extant animals, including vertebrates and nematodes) by > 600 million years of evolution. We have previously shown that *Nematostella* does not react to the canonical RIG-I agonist, but it develops a strong immune response to the potent ligand of its paralog, melanoma differentiation-associated protein 5 (MDA5). This finding supports our phylogenetic-based inference of the two *Nematostella* RLRs (NveRLRs) being derived from the MDA5 lineage. Here, we aimed to further characterize the ligand specificity of both NveRLRs by the in vitro binding assays of transgenic FLAG-tagged NveRLR to a vertebrate MDA5-specific ligand. Our results show that only NveRLRb binds long dsRNA raising an intriguing question whether NveRLRa might display affinity to other yet uncharacterized ligands. Furthermore, the results of shRNA-mediated knockdown experiments reveal that lack of dsRNA-binding NveRLRb impairs downstream effector pathways including the downregulation of RNA interference-related genes. Our results suggest the conserved role of NveRLRs in initiating immune response to dsRNA that originated before the cnidarian-bilaterian split and lay a strong foundation for future research on the evolution of the immune responses to RNA viruses.



## Ohad Lewin-Epstein

Tel Aviv University

### Microbiome-induced resource sharing and the case of trees-mycorrhiza interactions

*Ohad Lewin-Epstein, School of Plant Sciences and Food Security, Tel-Aviv University; Ranit, Aharonov, IBM Research; Ido Rog, Department of Plant & Environmental Sciences, Weizmann Institute of Science; Stav Livne-Luzon, Department of Plant & Environmental Sciences, Weizmann Institute of Science; Tamir Klein, Department of Plant & Environmental Sciences, Weizmann Institute of Science; Lilach Hadany, School of Plant Sciences and Food Security, Tel-Aviv University;*

Cooperation is a fundamental behavior observed in all forms of life. The evolution of cooperation has been widely studied, but almost all theories aiming to explain it focused on the cooperating individual and its genes. We suggest a different approach, taking into account the microbes carried by the interacting individuals. Accumulating evidence reveal that microbes can dramatically affect their host wellbeing and behavior. We thus propose that host-microbe coevolution may favor microbes that induce their host to cooperate, and show that microbe-induced cooperation can evolve in a wide range of conditions, including when facing hosts' resistance to the microbial effect. The interactions between trees and their mycorrhizal fungi symbionts can be reconsidered in light of this novel theory of microbiome-induced cooperative behavior. Studies showed that resource sharing among neighboring trees in the form of carbon trade is, at least partially, mediated by mycorrhizal networks connecting the tree roots. Moreover, this cooperative behavior was observed even between trees of different species. We investigate trees-mycorrhiza interactions focusing on examining the conditions that favor generalist mycorrhiza species (that can inhabit various tree species) upon specialists (that can inhabit only one tree species), and show that generalist mycorrhizal species may play a role in maintaining diversity in the forest.

## Gabriela Lobinska

Weizmann Institute of Science

### Should you inherit your parent's mutation rate?

*Gabriela Lobinska, Weizmann Institute of Science, Yoav Ram, Tel Aviv University, Yitzhak Pilpel, Weizmann Institute of Science*

In population genetics, the mutation rate is usually treated as a fixed parameter within the population and across generations. In reality, it is determined by a combination of genetic factors (e.g. alleles of DNA polymerases and mutation repair enzymes) and stochastic factors (e.g. random fluctuations in protein concentrations), which results in variation within the population. Due to its capacity to generate beneficial or deleterious mutations, it is also subject to second-order selection. Hence, the mutation rate can also vary at the population level across time. We wondered which mode of mutation rate inheritance – genetic, epigenetic, or randomly determined – results in highest rates of adaptation upon an environmental change. We constructed a mathematical framework combining a classical Wright-Fisher population model with a Markovian process, which modelled the inheritance of one of two possible phenotypes: non-mutator (low mutation rate) or mutator (high mutation rate). The probability of inheriting a mutation rate phenotype different than one's parent is the switching rate. We found that intermediate levels of switching rate between the non-mutator and mutator phenotypes, corresponding to an epigenetic regulation of the mutation rate, result in highest rates of adaptation on rugged landscapes. Populations with an intermediate level of switching rate are able to maintain a high correlation between a mutator phenotype and preexisting genetic variation (necessary for crossing fitness valleys on a rugged landscape) while avoiding the selective pressure against strongly heritable mutators.

## Gil Loewenthal

Tel Aviv University

### A probabilistic model for indel evolution: differentiating insertions from deletions

*Gil Loewenthal, Shmunis school of biomedicine and cancer research, Tel Aviv University; Dana Rapoport, Shmunis school of biomedicine and cancer research, Tel Aviv University; Oren Avram, Shmunis school of biomedicine and cancer research, Tel Aviv University; Asher Moshe, Shmunis school of biomedicine and cancer research, Tel Aviv University; Alon Itzkovitch, Shmunis school of biomedicine and cancer research, Tel Aviv University; Omer Israeli, Shmunis school of biomedicine and cancer research, Tel Aviv University; Dana Azouri, School of Plant Sciences and Food Security, Tel Aviv University; Reed A. Cartwright, School of Life Sciences, Arizona State University; Itay Mayrose, School of Plant Sciences and Food Security, Tel Aviv University; Tal Pupko, Shmunis school of biomedicine and cancer research, Tel Aviv University;*

Insertions and deletions (indels) are common molecular evolutionary events. However, probabilistic models for indel evolution are under-developed. A previous model for indel evolution assumed that the rates and length distributions are the same for insertions and deletions. Here, we propose a richer model that explicitly distinguishes between insertions and deletions by assuming different rate and length parameters. We next developed an Approximate Bayesian Computation (ABC) algorithm for parameter estimation. Moreover, we developed a neural-network model-selection scheme to test whether the richer model better fits biological data compared to the simpler model. Our analyses suggest that both our inference scheme and the model-selection procedure achieve high accuracy on simulated data. We further demonstrate that our proposed indel model better fits a large number of empirical datasets and for these datasets, the deletion rate is higher than the insertion rate, on average. Finally, we studied the relationship between indel rates and the effective population size across various phylogenomic clades.

## Offir Lupo

Weizmann Institute of Science

### Accumulation of cis-regulatory variations shapes the evolution of complex traits

*Offir Lupo, Weizmann Institute of Science*

Regulatory variation plays a key role in the evolution of complex traits. Often, such traits evolve by the re-use, or co-option, of existing programs in new contexts. While co-option is attributed to cis-variations in single large-effect regulators, the extent to which coordinate changes accumulate throughout the network remains largely unknown. Here, we examine two close yeast species that differentially recruit a differentiation program, filamentous growth, when grown in the same environment. By profiling the cell-cycle transcriptome and transcription factors (TFs) binding of the two species and their hybrid, we find that multiple genes in the filamentous and cell cycle pathways gained cis-expression variation in a coordinated and directional fashion, through upregulation of activators and downregulation of repressors. We further characterize a regulatory circuit in which variation in one TF alters both the expression of target genes and the binding specificity of an interacting TF. Our study reveals the complex architecture of regulatory variation associated with distinct activation of a differentiation program. Based on these results, we suggest that rather than relying on a single regulator, co-option is stabilized in a distributed manner through multiple weak-effect variations accumulating throughout the regulatory network.

## Roi Maor

Tel Aviv University

### Novel Daytime Activity Does Not Explain the Cenozoic Mammal Radiation

*Roi Maor, School of Zoology, Tel Aviv University and Centre for Biodiversity and Environment Research, University College London; Tamar Dayan, The Steinhardt Museum of Natural History and School of Zoology, Tel Aviv University; Kate Jones, Centre for Biodiversity and Environment Research, University College London and Zoological Society of London.*

Mammals are the most ecologically diverse class of vertebrates, but what drove their Cenozoic diversification after the K-Pg mass extinction remains unclear. The ‘nocturnal bottleneck hypothesis’ asserts that release from negative interaction with dinosaurs freed the nocturnal mammals to occupy daytime niches after the K-Pg event (‘ecological release’). However, recent evidence suggests that the expansion into diurnal niches followed novel mammalian morphological and physiological adaptation to daytime activity (‘key innovation’), irrespective of the fate of dinosaurs. Here, we analyse Mammalia-wide and order-specific rates of diversification (speciation minus extinction) to test whether daytime activity is associated with increased diversification. We find that cathemeral lineages (active during day and night) exhibit the highest diversification rates, but remain uncommon due net evolutionary transition from cathemerality (towards nocturnal or diurnal specialisation). Only in primates, diurnal lineages diversify faster than nocturnal ones; other diurnal lineages exhibit elevated extinction rates. Overall, diversification- and transition rates show little inter-ordinal congruence. Diurnality is not supported as a diversifying key innovation throughout mammals, but it exhibits key innovation dynamics in primates. We conclude that mammals expanded into the diurnal niche following release from limiting interaction with dinosaurs, consistent with the nocturnal bottleneck hypothesis. The directional evolution of the mammalian temporal niche towards specialisation merits further investigation.

## Yoav Mathov

The Hebrew University of Jerusalem

### Inferring of DNA methylation changes in non-bone tissues of ancient DNA samples

*Yoav Mathov, Department of Genetics, The Alexander Silberman Institute of Life Science, The Edmond and Lily Safra Center for Brain Science (ELSC), The Hebrew University of Jerusalem; Nir Galun, Department of Genetics, The Alexander Silberman Institute of Life Science, The Hebrew University of Jerusalem; Eran Meshorer, Department of Genetics, The Alexander Silberman Institute of Life Science, The Edmond and Lily Safra Center for Brain Science (ELSC), The Hebrew University of Jerusalem; Liran Carmel, Department of Genetics, The Alexander Silberman Institute of Life Science, The Hebrew University of Jerusalem.*

Damage patterns in ancient DNA allow from the computational reconstruction of genome-wide DNA methylation in ancient DNA samples. As methylation patterns are more conserved across tissues than across species, and as the main source for ancient DNA is bones, the reconstructed ancient methylomes mainly reflect methylation patterns in bones, whereas the ability to infer methylation in other tissues is limited. Nonetheless, most tissue-specific methylation patterns are established during embryonic development, and oftentimes show characteristics that are shared by a group of tissues. Here we show that under certain evolutionary circumstances, it is possible to identify such shared methylation patterns using parsimony. Testing the idea on methylation data from brain and blood of humans, chimpanzees and macaques, we demonstrate ~88% precision in identifying such shared methylation patterns. We also show that even when smoothing the data, a common practice for ancient methylomes, we can still achieve over 72% accuracy. This approach is therefore useful to infer differential methylation in non-bone ancient DNA tissues. For example, it can be used to identify differential methylation in neural tissues, separating modern humans and Neanderthals.



## Nittay Meroz

The Hebrew University of Jerusalem

### Coevolution of species pairs predicts the composition of three-species communities in microbial microcosms

*Nittay Meroz, Department of Plant Pathology and Microbiology, Robert H. Smith Faculty of Agriculture, Food, and Environment; Jonathan Friedman, Department of Plant Pathology and Microbiology, Robert H. Smith Faculty of Agriculture, Food, and Environment*

Microbes form diverse communities that play key roles in human health, agriculture, and biotechnology. Managing and engineering microbial communities relies on the ability to predict their composition. While there has been recent progress in predicting community composition over short, ecological timescales, little is known about its predictability over longer timescales, where evolution might play a significant role. Here, we address this knowledge gap by tracking the composition of 87 unique two- and three-species bacterial communities for ~400 generations. We find that community composition typically changes during evolution, decreasing the accuracy of predictions based on ecological timescales. Nonetheless, these changes tend to be repeatable and predictable in a bottom-up approach - changes in the composition of trios were consistent with those that occurred in pairs throughout the experiment. Our results demonstrate that simple assembly rules can hold even on evolutionary timescales, suggesting it may be possible to rationally design microbial communities that function stably over hundreds of generations.

## Itzhak Mizrahi

**Ben-Gurion University of the Negev**

### **Potential drivers of plasticity and persistence in the animal gut microbiome**

*Itzhak Mizrahi*

Plasmids are major contributors to horizontal gene transfer in microbial genomes; however, the forces that shape their functionality and distribution in natural environments are insufficiently understood. In my lecture, I will discuss some of our recent findings of plasmids assortment and functionality across microbial ecosystems present in different individual gut microbiomes.

## Monica Mowery

**Ben-Gurion University of the Negev**

### Differential parasitism of native and invasive widow spider egg sacs

*Monica Mowery, Valeria Arabesky, Yael Lubin, Michal Segoli, Mitrani Department of Desert Ecology, Ben-Gurion University of the Negev*

During colonization, invasive species establish and spread into new habitats, where they may affect native species, whether through direct competition or through indirect effects through predators, prey, or parasites. We conducted field collections and lab behavioural experiments to investigate the differential impact of an egg parasitoid wasp, *Philolema latroducti* (Eurytomidae) on two widow spider species: *Latrodectus pallidus*, native to the Middle East, and *Latrodectus geometricus*, which is globally invasive, originates from southern Africa, and has silk structures on its egg sacs that may protect against parasitism. In field collections of egg sacs from six sites in the Negev Desert, Israel, we found higher rates of parasitism of native white widow egg sacs. In lab behavioural trials, we found that wasps visited white widow sacs more, parasitized more, and oviposited longer. After developing inside the egg sac, wasps that emerged from white widow sacs were larger than those emerging from brown widow egg sacs, suggesting a fitness benefit for the wasp of parasitizing native white widow egg sacs. Our results suggest that physical defences on brown widow egg sacs may impede wasp parasitism and thus increase establishment of this invasive species.

## Chetan Nag

**JAIN ( Deemed to be University)**

### **Behavioral response of Pariah Kite (*Milvus migrans*) at Lalbagh botanical gardens, Bengaluru during covid-19 lockdown**

*Chetan Nag K.S; Ecology & Environmental Sciences, JAIN ( Deemed to be University), Bengaluru, Karnataka, India*

Lockdowns and cessation of non-essential activities as measures to mitigate the spread of COVID-19 across the globe have surprised urbanites with unexpected sightings of wildlife species across cities around the world. However, little is known about habitat usage patterns of wildlife in the absence of human activities. I opportunistically evaluated the occurrence and detectability trends of Pariah kites at Lalbagh botanical gardens, Bengaluru during the April 23- May 16, 2020 lockdown period (Lockdown 2 phase). I observed in general that the pariah Kites were seen actively using the ground more often during the lockdown phase than the post lockdown phase. Additionally, there were no significant differences observed in Flight initiation distance (FID) of kites during the lockdown and post lockdown period indicating the level of tolerance these kites to human presence and insights on immediate responses of wildlife to human absence. I shall also discuss and highlight how the management authorities of Lalbagh botanical gardens could gain unprecedented mechanistic insights into how human activity affects wildlife and introduce global collaborative research initiatives that are currently forming to facilitate coordination and how scientific knowledge gained during this devastating crisis will allow us to develop innovative strategies for sharing space on this increasingly crowded planet, with benefits for both wildlife and humans. (209 words)

## Martin Pontz

University of Vienna

### The effect of epistasis on local adaptation with gene flow

*Martin Pontz, Reinhard Bürger*

There is little consensus on the importance of epistasis for local adaptation. Here, we investigate the possibility of establishment of weakly locally adaptive de-novo mutations in the face of gene flow, linkage and epistasis.

This process is studied by applying a two-type branching process to the underlying two-locus two-allele model with migration from an continental-island type migration. The new mutation appears on the island and its induced offspring distribution depends on the background allele. We use the theory of two-type branching processes to determine the dependence of the establishment probability on the parameters, i.e., selection coefficients of the alleles, migration and recombination rate and epistasis. In general, this establishment probability can not be expressed in closed form, however, we derive an explicit expression that is a good approximation. We use this approximation to predict the average establishment probability over all possible linked mutations. This, in turn, can be used to calculate the approximate size of a genomic island that evolves via the benefit of selection at a linked background locus.

## Eyal Privman

University of Haifa

### Adaptive evolution of chemical communication in ant societies

*Eyal Privman, Rana Saad, Amir Cohanim, Shani Inbar, Pnina Cohen, Besan Saied; Department of Evolutionary and Environmental Biology, Institute of Evolution, University of Haifa, Haifa 3498838, Israel.*

In the transition from solitary to social life, ants evolved complex chemical communication systems. Their diverse chemical vocabulary requires a correspondingly diverse set of chemosensory receptors. Ant odorant receptors (ORs) are the largest known family in insects, characterized by frequent expansions of subfamilies, in which duplicated ORs may adapt to detect new signals through positive selection. We inferred positive selection along every branch of the OR gene tree, identified amino acid sites under positive selection, and mapped them onto the insect OR structure. Two clusters of sites mapped to the extracellular side of the receptor, on either side of a cleft that was previously implicated in ligand activation. These results provide insights into the specific ORs and individual residues that underwent adaptive evolution, potentially explaining the elaboration of chemical signaling in ant societies. On the complementary side, we used genomic mapping approaches to identify the genes responsible for the synthesis of pheromones. We focus on the cuticular hydrocarbons (CHCs), which are the basis for social recognition and communication. We applied multiple mapping approaches using genomic sequencing from 400 population samples of the desert ant *Cataglyphis niger* to map loci responsible for variation in CHC profiles (QTLs). We identified multiple QTLs for most of the CHCs on most of the 26 chromosomes in this species, including candidate genes coding for enzymes of long-chain fatty acid biosynthetic pathways. Together, these results form the basis for unraveling the evolution of social communication via the elaboration of complex chemical signaling and olfactory perception.

## Sviatoslav Rybnikov

University of Haifa

### Fitness dependence preserves selection for recombination across diverse mixed mating systems

*Sviatoslav Rybnikov, Institute of Evolution and Department of Evolutionary and Environmental Biology, University of Haifa, Haifa, Israel; Daniel B. Weissman, Department of Physics, Emory University, Atlanta GA, USA; Sarel Hübner, Institute of Evolution, University of Haifa, Haifa, Israel, and Galilee Research Institute (MIGAL), Tel-Hai College, Upper Galilee, Israel; Abraham B. Korol, Institute of Evolution and Department of Evolutionary and Environmental Biology, University of Haifa, Haifa, Israel*

Meiotic recombination and the factors affecting its rate and fate in nature have inspired many theoretical studies in evolutionary biology. Classical theoretical models have inferred that non-zero recombination can be favored under a rather restricted parameter range. Thus, the ubiquity of recombination in nature remains an open question. However, these models assumed constant (uniform) recombination with an equal rate across all individuals within the population, whereas in natural populations recombination is likely fitness-dependent, with the rate varying among genotypes according to their fitness. Here we use simulations to show that across a range of mating systems with varying frequencies of selfing and clonality, fitness-dependent recombination is often favored even when any non-zero constant recombination is disfavored. In systems with partial clonality, the evolutionary advantage/disadvantage of fitness-dependent recombination is determined mostly by selection against heterozygotes and additive-by-additive epistasis, while partial selfing potentiates the role of additive-by-dominance epistasis. The revealed recombination-protecting effect of fitness dependence is strongest under intermediate rates of selfing or high rates of clonality.

## Yuval Sapir

Tel Aviv University

### Evolutionary drivers and maintenance of flower colour polymorphism

*Yuval Sapir, M. Kate Gallagher, Esther Senden, The Botanical Garden, School of Plant Sciences, Tel Aviv University*

Flower colour is among the most conspicuous and highly diverse traits in nature. Most flowering plant populations have uniform floral colours, but a minority exhibit within-population flower colour variation, either discrete (polymorphic) or continuous. We discuss the evolutionary drivers that create and maintain within-population flower colour variation. Colour variation is commonly maintained by balancing selection through multiple pollinators, contrasting biotic and abiotic selection regimes, or fluctuating selection. Variation can be also maintained by heterozygote advantage and frequency-dependent selection. Neutral processes, or lack of selection, may maintain variation, although this remains largely untested. We suggest several prospective research directions in the area of flower colour evolution and propose that such work may provide insight into the evolutionary theory regarding drivers of variation and its maintenance in nature.



## Franklin Sargunaraj

Ben-Gurion University of the Negev

### Does bacterial infection lead to nutritional deficiency and altered foraging behavior in Allenby's gerbils?

*Douglas F. Makin, Burt P. Kotler, and Franklin Sargunaraj\*, Mitrani Department of Desert Ecology, Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev, Midreshet Ben-Gurion, 8499000, Israel*

Bacterial infections can have both direct (physiological) and indirect (ecological) costs for their hosts. The direct costs of infection may include nutritional deficiencies resulting in modified foraging behaviour of hosts to compensate for any losses over time. Allenby's gerbils are commonly infected with the *Mycoplasma haemomuris*-like bacteria, which may induce choline (essential vitamin) and arginine (amino acid) deficiencies. Gerbils should therefore alter their behaviour to make up for any shortfalls in nutrient production and retention. We tested two predictions - 1) Infected gerbils would compensate for nutrient losses by spending more time foraging in patches, including, during riskier periods of owl presence, and in riskier open microhabitats. Furthermore, infected gerbils would preferentially forage from patches supplemented with choline and arginine enriched food over control food. 2) Alternatively, if infection did not create a nutrient deficiency, then infected individuals would display a similar pattern of patch use to uninfected individuals, and harvest similar amounts of food from supplemented and control patches. Our findings supported the second prediction. There was no observed difference in foraging behaviour between infected and uninfected individuals. Moreover, infected gerbils did not selectively forage more intensively from food patches enriched with either choline or arginine seed over the control patches. These results suggest that this bacteria-gerbil interaction does not result in a nutrient deficiency as observed for other *Mycoplasma*-rodent systems.

## Dvir Schirman

**Weizmann Institute of Science**

### Co-evolution of the splicing machinery and intron architecture across yeast species

*Dvir Schirman, Department of Molecular Genetics, Weizmann Institute of Science, Rehovot, Israel; Orna Dahan, Department of Molecular Genetics, Weizmann Institute of Science, Rehovot, Israel; , Zohar Yakhini, School of Computer Science, Interdisciplinary Center, Herzeliya, and Department of Computer Science, Technion, Haifa; Yitzhak Pilpel, Department of Molecular Genetics, Weizmann Institute of Science, Rehovot, Israel*

mRNA splicing is one of the key processes in eukaryotic gene expression and regulation of splicing efficiency has a major contribution to gene expression regulation. The budding yeast *Saccharomyces cerevisiae*, like other hemiascomycetous fungi, has a low number of intron-containing genes compared to other eukaryotes, and most of them have single intron which is constitutively spliced. Hence yeast serve as a good model system to study both splicing efficiency regulation and the evolution of intron architecture. In this work we used a large synthetic library to create thousands of different intron architectures, integrated them into *S. cerevisiae* genome, and measured their splicing efficiencies using targeted RNA sequencing. We noticed over the entire set of natural and synthetic intron sequences, that there are many unintended splicing events resulting in cryptic spliced isoforms, due to alternative 3' splice site recognition. We then turned to the *S. cerevisiae* genome to check how yeast might avoid such deleterious unintended splicing events and found that 3' splice site motifs are depleted near introns' 3' end.

In addition, we expressed in our library introns taken from orthologs of intron-containing genes in *S. cerevisiae* from 10 different yeast species. These yeast species represented in this set differ by the presence or absence of a specific splicing factor (U2AF1) which is absent in *S. cerevisiae* and is associated with physical connecting the branch site and the 3' splice site during splicing. We first found that introns which come from a host lacking this factor are more efficiently spliced in our *S. cerevisiae* based system, suggesting that the intron sequence is adapted to its host splicing machinery. Second, we examined the depletion of 3' splice site motif as was seen in *S. cerevisiae*, and we found that only species that lack U2AF1 present this depletion. We conclude that a loss of this splicing factor resulted in higher probability of unintended 3' splice site recognition, which in turn caused a selective pressure to avoid 3' splice site motifs near intron 3' ends, demonstrating how intron architecture was co-evolved with the composition of the splicing machinery.



## Tarryn Schuldiner-Harpaz

University of Cambridge

### Evolution of physical linkage between mating cue and preference QTL: a theoretical study of sympatric speciation in *Heliconius* butterflies

*Tarryn Schuldiner-Harpaz & Chris Jiggins, Department of Zoology, University of Cambridge*

Speciation is facilitated when traits under divergent ecological selection also serve as mating cues. Wing color pattern in *Heliconius* butterflies is an example of such a trait. The bright colour patterns warn potential predators of the butterflies' noxiousness, and at the same time serve as cues in mate choice. Recent genomic studies of reproductive isolation in these butterflies revealed a strong physical linkage between colour pattern genes and genetic elements that contribute to mate choice. Such physical linkage has been recorded in several other organisms and is likely to promote speciation by strengthening the association between behavioural and ecological barriers, which could otherwise be broken down by recombination. We developed an individual-based model to test the influence of selection against intermediate phenotypes on the evolution of assortative mating and physical linkage between mating cue and mating preference loci. Model results predict physical linkage only for weak mating preferences and weak selection force. This combination allows for continued mating among separate phenotypes, and for recombination and selection to favour physical linkage between cue and preference loci. These findings correspond to empirical evidence of physical linkage in several insect and fish species, alongside strong association between mating cue and preference despite no physical linkage between the relevant loci.

## Nimrod Shteindel

University of Haifa

### Mobbing behavior of *Pseudomonas aeruginosa*

*Nimrod Shteindel of the University of Haifa, department of Evolutionary and Environmental Biology; Yoram Gerchman of the University of Haifa Science department at the Oranim College of Education.*

Mobbing behavior, communal attack of prey on predator, is a behavior observed in many animals, including, birds, fish, mammals and insects. In this talk I will present mobbing behavior of the common opportunistic pathogen *Pseudomonas aeruginosa* towards protozoan predators. This behavior consists of chemical sensation of the predator, taxis and adhesion en mass to its cell surface, leading to the death of the predator. Mobbing behavior initiated seconds after predators are introduced to the bacterial culture. Bacteria respond to predator population density and to a species specific quorum sensing signal. Mutants which cannot produce the signal are more susceptible to predation and show a corresponding deficiency in their ability to kill a predator. This bacterial behavior may have encouraged eukaryote multi cellularity, as some of our data suggests that the ability of bacteria to sense a protozoan predator from distance relies on nitric oxide leaking from the predator's phagosome. Multicellular bacterivores utilizing digestive systems may be invisible to bacteria and avoid mobbing, enjoying a selective advantage over protozoan predators.

## Viviane Slon

Tel Aviv University

### Retracing the past using ancient DNA in sediments

*Viviane Slon, Department of Anatomy and Anthropology and Department of Human Molecular Genetics and Biochemistry, The Shmunis Family Anthropology Institute, The Dan David Center for Human Evolution and Biohistory Research, Sackler Faculty of Medicine, Tel Aviv University*

In the past years, DNA retrieved from ancient human remains have been instrumental in furthering our understanding of our own evolutionary past, as well as that of our closest extinct relatives, the Neandertals and the Denisovans. Such studies, however, are inherently limited to sites and regions where such remains have been found and made available for destructive sampling. To circumvent this issue, my colleagues and I have developed a methodology to recover, identify and authenticate human DNA fragments from ancient sediments – a source material ubiquitously and abundantly found at any archaeological excavation. Here, I will present the methodology, including its highlights and pitfalls, and demonstrate the potential of this research avenue using examples from prehistoric sites in Europe and Asia.

## Sagi Snir

University of Haifa

### Horizontal Gene Transfer Phylogenetics: A Random Walk Approach

*Sagi Snir, University of Haifa*

The dramatic decrease in time and cost for generating genetic sequence data has opened up vast opportunities in molecular systematics, one of which is the ability to decipher the evolutionary history of strains of a species. Under this fine systematic resolution, the standard markers are too crude to provide a phylogenetic signal. Nevertheless, among prokaryotes, genome dynamics in the form of horizontal gene transfer (HGT) between organisms and gene loss seem to provide far richer information by affecting both gene order and gene content. The synteny index (SI) between a pair of genomes combines these latter two factors, allowing comparison of genomes with unequal gene content, together with order considerations of their common genes. Although this approach is useful for classifying close relatives, no rigorous statistical modelling for it has been suggested. Such modelling is valuable, as it allows observed measures to be transformed into estimates of time periods during evolution, yielding the additivity of the measure. To the best of our knowledge, there is no other additivity proof for other gene order/content measures under HGT. Here we provide a first statistical model and analysis for the synteny index measure. We model the gene neighbourhood as a birth–death–immigration process affected by the HGT activity over the genome, and analytically relate the HGT rate and time to the expected SI. This model is asymptotic and thus provides accurate results, assuming infinite size genomes. Therefore, we also developed a heuristic model following an exponential decay function, accounting for biologically realistic values, which performed well in simulations. Applying this model to 1133 prokaryotes partitioned to 39 clusters by the rank of genus, yields that the average number of genome dynamics events per gene in the phylogenetic depth of genus, is around half with significant variability between genera. This result extends and confirms similar results obtained for individual genera in different manners.

## Rotem Sorek

Weizmann Institute of Science

### Evolutionary origin of innate immunity in bacterial defense against phage

*Rotem Sorek, Department of Molecular Genetics, Weizmann Institute of Science*

The arms race between bacteria and phages led to the evolutionary development of sophisticated anti-phage defense systems, among which is the CRISPR-Cas system. Through comprehensive genomic efforts, we discovered a large number of new defense systems that are located in “defense islands” in microbial genomes. We find surprising parallels between the human and the bacterial innate immune systems, and our data show that important components of the human innate immune system have originated from bacterial defense systems that protect from phage infection.



## Keyla Sousa

The Hebrew University of Jerusalem

### Zooming into genomic structural plasticity in wild rodent-borne *Bartonella*

*Keyla Sousa, Koret Veterinary School, Robert H. Smith Faculty of Agriculture, The Hebrew University; Ricardo Gutiérrez, Koret Veterinary School, Robert H. Smith Faculty of Agriculture, The Hebrew University; Dayana Yahalomi, The Mantoux Bioinformatics institute of the Nancy and Stephen Grand Israel National Center for Personalized Medicine, Weizmann Institute of Science; Tali Shalit, The Mantoux Bioinformatics institute of the Nancy and Stephen Grand Israel National Center for Personalized Medicine, Weizmann Institute of Science; Barak Markus, The Mantoux Bioinformatics institute of the Nancy and Stephen Grand Israel National Center for Personalized Medicine, Weizmann Institute of Science; Yaarit Nachum-Biala, Koret Veterinary School, Robert H. Smith Faculty of Agriculture, The Hebrew University; Hadas Hawlena, Mitrani Department of Desert Ecology, Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev; Evgeniya Marcos-Hadad, Department of Plant Pathology and Microbiology, Robert H. Smith Faculty of Agriculture, The Hebrew University; Einat Hazkani-Covo, Department of Natural and Life Sciences, Open University of Israel; Shimon Harrus, Koret Veterinary School, Robert H. Smith Faculty of Agriculture, The Hebrew University*

Rodent-associated *Bartonella* species have shown a great genetic diversity and marked pathogenic potential. Recently, we demonstrated experimentally that *Bartonella* genomes undergo vertical structural variation events (SVs) associated with prophages. The aim of this study was to further explore the natural intra-specific genomic variations and their role in *Bartonella* evolution. For this aim, we focused on a single species, recently named *Bartonella krasnovii*, a *Bartonella* species, isolated from gerbil rodents and their fleas. Twenty genomes including 16 different genetic variants were fully characterized through a hybrid sequencing assay, based on short and long reads, and validated through pulse field gel electrophoresis (PFGE). All genomic analyses were performed in comparison to the type strain, isolated two years earlier. Single nucleotide polymorphism (SNP) calling analysis revealed 270-6,689 SNPs per genome (ANI 99.01-99.89%). Remarkably, over 700 SVs, comprising deletions, insertions, inversions and translocations were detected across the genomes. Interestingly, a large proportion of these SVs (>40%) were associated with prophages (ranging from 5-12 prophages per genome). Further analyses, based on the fully assembled and validated circular genomes, revealed that the vast majority of the SVs overlapped at the chromosome replication termination site, suggesting it as a hotspot for SVs. Moreover, the evolutionary trajectory produced by the SVs follow the *Bartonella* tree

topology and correlates with the phylogenetic distance of the genomes at the nucleotide level. Our results support the remarkable genomic structural plasticity of *B. krasnovii* in nature and the role of prophages as promoters of large SVs, further evidencing their contribution to the evolution of *Bartonella*.

## Gavin Stark

Tel Aviv University

### Climate change and ecological interactions: How vegetation cover affect the performance of desert lizards?

*Gavin Stark; Ofir Levy*

Global warming affects how organisms interact with each other and with the environment they inhabit. The ability of organisms to compensate for climate change highly depends on the ability of other species to make similar compensations. Hence, we need to look beyond single-species studies and ask how a species depends on other species for survival, especially where some of the other species are predicted to decline under climate change. To fill this gap, we quantify how lizard's physiology is affected by the availability of vegetation cover and insect abundance in a desert community. In particular, we studied a desert lizard (*Messalina bahaeldini*) and its interactions with the local vegetation, which inhabits the Judean desert in Israel. First, we used a drone to map the vegetation cover in two study areas at a resolution of 3 cm. Next, we collected 81 lizards, measured their fat mass using Dual Energy X-ray Absorptiometry (DEXA), and calculated the percentage of vegetation cover around the collection coordinate of each lizard. Finally, we tested how fat mass is affected by vegetation cover at different radii (1-100m) from the lizard, and by the Julian day. We found that vegetation cover within a 10m radius from each lizard is the best predictor for lizards' fat mass, compared to other radii. Specifically, the fat mass increased with vegetation cover, particularly during the summer. Incorporating the results of the model with other levels of interactions (such as prey abundance) will enable us to estimate the importance of the stability of such ecological interactions in the desert system of lizards and better predict the biological impacts of climate change.

## Joachim Surm

The Hebrew University of Jerusalem

### Dominant toxin hypothesis: Disentangling the evolution of venom as a complex trait

*Joachim M. Surm, The Hebrew University of Jerusalem, Alexander Silberman Institute of Life Sciences, Department of Ecology, Evolution and Behavior, Guy Amir, The Hebrew University of Jerusalem, The School of Computer Science & Engineering, Adi Simhi, The Hebrew University of Jerusalem, The School of Computer Science & Engineering Yehu Moran, The Hebrew University of Jerusalem, Alexander Silberman Institute of Life Sciences, Department of Ecology, Evolution and Behavior, \*These authors contributed equally to this work*

Complex traits are those driven by the expression of many independently inherited genes and can account for significant variation among individuals and populations. These traits are not inherited in a simple Mendelian manner, making it difficult to resolve the contribution of each of their various genetic components to the fitness of an organism. A complex trait hypothesized to be evolving under strong selective pressure is venom because it has essential functional roles related to predation and defense, among others. Using sea anemones as a model to understand the evolution of venom as a complex trait, we employed comparative transcriptomics to quantify and map the expression of 5 functionally characterized toxin families from 28 sea anemone species across three superfamilies. Phylogenetic covariance analysis revealed that the possible combinations of toxin families are not constrained in sea anemones and that the venom phylomorphospace has low dimensionality. This suggests that in sea anemones a single toxin family dominates the venom phenotype of each species. The evolution of the specific dominant toxin family found in each sea anemone species can be highly dynamic, even convergently evolving among distantly related species. Altogether, these results show an unexpected similarity to those reported in the evolution of venom in snakes, a group separated from sea anemones by 600 million years. Thus, our findings provide evidence that venomous animals have convergently evolved a process to generate an optimized venom phenotype dominated by a single toxin family.

## Eran Tauber

University of Haifa

### Seeing the light: Natural Genetic Variation in a Circadian-Clock Photoreceptor Gene

*Mirko Pegoraro, School of Life and Environmental Sciences, University of Liverpool John Moore; Emily Rezek, Department of Evolutionary and Environmental Biology, University of Haifa; Eran Tauber, Department of Evolutionary and Environmental Biology, University of Haifa*

The circadian clock is a molecular and cellular network that creates daily rhythms in the physiology, metabolism, and behavior of organisms. The basic periodicity of the clock is slightly different from 24 hours, but it is synchronized to the circadian cycle by various environmental cues, mainly temperature and light. In many insects (and plants), the dedicated light receptor of the circadian clock is encoded by a gene called cryptochrome (*cry*). A survey of *cry* sequences in wild populations of *Drosophila* reveals a significant difference, the pattern of which indicates the processes of natural selection that operate on this gene. We analyzed different aspects of the day-to-day activity of flies and used association analysis to link single nucleotide polymorphic sites to behavior. We have identified two major haplotypes that differ substantially in their diurnal behavior. This difference has been validated in transgenic flies that carry those haplotypes but otherwise have identical genetic background. Measurement of transcript level produced by each of the haplotypes revealed a significant difference *cry* expression that could drive the behavioral diurnal differences. Overall, this study demonstrates how variation in a single clock gene can lead to rapid adaptation of organisms to their environment.

## Dan S. Tawfik

**Weizmann Institute of Science**

### Protein evolution – from so simple a beginning

*Dan S. Tawfik. Department of Biomolecular Sciences, Weizmann Institute of Science*

The size, structural complexity, and functional perfection of proteins, raise a question for which we so far have no answer: How did the very first protein(s) evolve? Protein synthesis depends on dozens of highly sophisticated proteins in itself, thus presenting a chicken-egg dilemma. The widely accepted scenario is that short and simple polypeptides further expanded in length and complexity to give proteins as we know them today. Can we reconstruct early polypeptide ancestors that are tangibly linked to their modern descents? Can a short polypeptide confer biochemical functions that are reminiscent of modern proteins? I will discuss our most recent findings with respect to the de novo emergence of functional, globular proteins from short and simple polypeptides, including the emergence of the earliest nucleotide binding proteins.

## Viraj Torsekar

The Hebrew University of Jerusalem

### Predation risk disrupts assortative mating in a desert isopod

*Viraj R. Torsekar, Department of Ecology, Evolution, and Behavior, Hebrew University of Jerusalem; Moshe Zaguri, Department of Ecology, Evolution, and Behavior, Hebrew University of Jerusalem; Dror Hawlena, Department of Ecology, Evolution, and Behavior, Hebrew University of Jerusalem*

Assortative mating in species where female size is correlated with fecundity can arise as a consequence of male intrasexual competition for bigger females. Our aim was to examine if and how risk of scorpion predation influences assortative mating in the desert isopods *Hemilepistus reaumuri*. To reveal the underlying behavioral responses, we placed males of disparate size in an arena with a risky and safe burrow holding two females of similar sizes and observed their behavior. To examine the emerging patterns, we dug artificial isopod burrows in the field and established active scorpion burrows near half of them. We monitored the isopods' burrow occupancy, size and reproductive output. We found that larger males spent longer time in and around safe burrows and won most aggressive interactions. Safer burrows were occupied more and by bigger males compared to risky burrows. Furthermore, offspring sired by isopod pairs settled in risky burrows exhibited higher variance in embryo age and size. Our results suggest that predation risk weakens assortative mating by affecting female habitat selection and male competition, with important fitness consequences.

## Liudmyla Vasylenko

University of Haifa

### The power of randomization by sex in multilocus genetic evolution

*Liudmyla Vasylenko, Department of Evolutionary and Environmental Biology and Institute of Evolution, University of Haifa; , Marcus W. Feldman, Department of Biology, Stanford University; Adi Livnat, Department of Evolutionary and Environmental Biology and Institute of Evolution, University of Haifa.*

Many hypotheses have been proposed for how sexual reproduction may facilitate an increase in the population mean fitness, such as the Fisher-Muller theory, Muller's ratchet and others. According to the recently proposed mixability theory, however, sexual recombination shifts the focus of natural selection away from favoring particular genetic combinations of high fitness towards favoring alleles that perform well across different genetic combinations. Mixability theory shows that, in finite populations, because sex essentially randomizes genetic combinations, if one allele performs better than another across the existing combinations of alleles, that allele will likely also perform better overall across a vast space of untested potential genotypes. However, this superiority has been established only for a single-locus diploid model.

We show that, in both haploids and diploids, the power of randomization by sex extends to the multilocus case, and becomes substantially stronger with increasing numbers of loci. In addition, we make an explicit comparison between the sexual and asexual cases, showing that sexual recombination is the cause of the randomization effect.

That the randomization effect applies to the multilocus case and becomes stronger with increasing numbers of loci suggests that it holds under realistic conditions. One may expect, therefore, that in nature the ability of an allele to perform well in interaction with existing genetic combinations is indicative of how well it will perform in a far larger space of potential combinations that have not yet materialized and been tested. Randomization plays a similar role in a statistical test, where it allows one to draw an inference from the outcome of the test in a small sample about its expected outcome in a larger space of possibilities—i.e., to generalize. Our results are relevant to recent theories examining evolution as a learning process.



## Tanita Wein

Weizmann Institute of Science

### The impact of selection regimes on plasmid stability evolution in bacteria

*Tanita Wein\**, Yiqing Wang, Nils F. Hülter, Katrin Hammerschmidt, Tal Dagan

Institute of Microbiology, Kiel University, Kiel, Germany; \*Current address: Department of Molecular Genetics, Weizmann Institute of Science, Rehovot, Israel

Mobile genetic elements are important drivers of bacterial evolution and their evolutionary success depends on positive selection for the genes they encode. Examples are plasmids encoding antibiotic resistance genes that are maintained in the presence of antibiotics. In the absence of positive selection, plasmid survival hinges upon stable persistence in the population. Nonetheless, the transition of plasmids into stably inherited genetic elements remains understudied. We show that positive selection for a plasmid-encoded gene interferes with the evolution of plasmid stability while non-selective conditions favor stable plasmid inheritance. Evolving plasmids under different selection regimes in *Escherichia coli*, we find that antibiotics led to plasmid amplification resulting in plasmid instability. Thus, positive selection promoted the maintenance of suboptimal solutions for plasmid stability and consequently hindered long-term plasmid persistence. Indeed, a survey of *Escherichia* plasmids confirms that antibiotic resistance genes are rarely found on small plasmids. Our results show that a plasmid-mediated advantage for the host may manifest in reduced plasmid evolutionary success. Considering plasmids as autonomously evolving entities holds promise for understanding the factors that govern their evolution.

## Judith Wexler

Hebrew University in Jerusalem

### Reuse of hormone signaling module across developmental and evolutionary time

*Judith Wexler, Hebrew University in Jerusalem; Jessica Hernandez, University of Maryland, College Park; Katie Reding, University of Maryland, College Park; Ariel Chipman, Hebrew University in Jerusalem; Leslie Pick, University of Maryland, College Park*

The redeployment of signaling networks across different developmental times and places is a means of generating phenotypic diversity from a limited genetic toolkit. Hormone signaling networks in particular have well studied roles in multiple developmental processes. In insects, the ecdysone pathway controls critical events in late embryogenesis, such as trachea formation and deposition of cuticle; post embryonically, the pathway directs the timing and type of molts; and in adulthood, ecdysone signaling influences the acquisition of memories. Work from over a decade ago established that one component of the ecdysone signaling network, the nuclear receptor *e75a*, plays a role in segment generation in the milkweed bug *Oncopeltus fasciatus*. Recent work from the harlequin bug *Murgantia histrionica* showed the spatial and temporal expression of *e75a* in germband extension is not restricted to the milkweed bug. Here, we show that these expression patterns are conserved across hundreds of millions of years of insect evolution, from Hemiptera through the two-spotted cricket *Gryllus bimaculatus* and the German cockroach *Blattella germanica*. We also show in the same set of species the expression in similar times and places of a second member of the ecdysone signaling network – the nuclear receptor *ftzf1*. Together, our results suggest that key components of this network could work together to play a role in segmentation, which occurs much earlier than the events previously thought to be the earliest targets of ecdysone signaling.

## Benjamin Yakir

**The Hebrew University of Jerusalem**

### Estimating background genetic similarity from aDNA data

*Benjamin Yakir, Department of Statistics and Data Science, The Hebrew University. , (Joint with Lily Agranat-Tamir and Liran Carmel, The Hebrew University)*

Two randomly sampled haplotypes from a pair of individuals may be identical over a relatively long segment due to inbreeding in the population from which the individuals originated. Hence, the expected number and typical lengths of such intervals may shed light on the level of inbreeding in that population. We propose a simple Poisson-Exponential model for the emergence of such intervals and seek to estimate the parameters of the model from genotypic measurements conducted on samples taken from a population. The estimation task becomes more challenging when DNA samples are extracted from ancient skeletons that are excavated from archeological sites. The quality of genotyping for such samples is typically low leading to difficulties and substantial errors in the determination of the intervals of haplotype identity. In order to mitigate this problem, we use simulation-based models for the errors in the determination of the interval and apply an Expectation-Maximization (EM) algorithm for the computation of the maximum-likelihood estimates of the parameters of interest.

## Shu-Ting You

**Weizmann Institute of Science**

### Protein secretion as a basis of social life in microbes

*Shu-Ting You, Department of Molecular Genetics, Weizmann Institute of Science; Ruthie Golomb, Department of Molecular Genetics, Weizmann Institute of Science; Dvir Schirman, Department of Molecular Genetics, Weizmann Institute of Science; Orna Dahan, Department of Molecular Genetics, Weizmann Institute of Science; Yitzhak Pilpel, Department of Molecular Genetics, Weizmann Institute of Science*

Evolution of cooperation is a major and yet unsolved question in evolutionary biology. Cooperative behavior can be seen even between microorganisms, which is often achieved by secreted proteins to share common goods with an entire community. However, the temptation not to cooperate grows with population growth, resulting in inherent conflicts between interests of individual cells and the community. Studies into this dilemma consider a YES/NO decision, to cooperate or defect. However, different levels of public good sharing can be realized by regulation of protein secretion on a continuous scale. Our lab co-discovered a cis regulatory mRNA motif for protein secretion (SECRete). Here we test whether this motif, alongside the Signal Peptide (SP), may serve as analog knobs governing cellular sociality. Our study explored how both motifs regulate protein secretion and affect cooperation, by using two synthetic yeast libraries. Each library includes various versions of each of the two motifs. All variants were integrated into identical genomic locations driving the secretion of Suc2, a well-characterized public-good yeast protein. Each variant potentially confers a different level of cooperation, attained through public-good secretion. We used pooled competition to measure the population dynamics of cells with various cooperative strategies. We used pooled ER fractionation followed by sequencing to measure ER localization of Suc2 mRNA as a proxy for protein secretion of each variant. We find ER-enriched strains present higher fitness, suggesting that public-good secretion is beneficial, and secretion costs are negligible. We notice fitness values are inconstant throughout the competition, implying that cells present frequency-dependent fitness behaviors. In the SP library high hydrophobicity of the amino acid sequence promotes fitness, presumably by increasing secretion. This system of a continuous range of cooperative strategies together with high throughput measurements of cellular properties enables us to gain a deeper insight into the evolution of cooperation.

## **Posters**

By alphabetic order

### **Yael Admoni**

**The Hebrew University of Jerusalem**

## **microRNA-target complementarity requirements in the sea anemone *Nematostella vectensis***

*Yael Admoni, Arie Fridrich, Yehu Moran*

MicroRNAs (miRNAs) are short RNA sequences with post-transcriptional regulatory roles in animals and plants. miRNAs bind messenger RNA (mRNA) targets via base complementarity and promote downregulation of gene expression. In bilaterian animals (most extant animals), miRNAs frequently bind their targets via a short sequence called “seed” and induce translation inhibition and mRNA degradation. In plants, miRNAs usually match their targets with nearly full complementarity and promote target cleavage. Recent results indicate that miRNAs in Cnidaria (sister group to Bilateria) operate as in plants by nearly full complementarity and target cleavage, although the specific characteristics of this mechanism in cnidarians are still unknown. In this study, we characterize the complementarity requirements between miRNAs and their mRNA targets in the sea anemone *Nematostella vectensis*, a representative cnidarian. We generated a transgenic line, ubiquitously expressing the fluorescent protein mCherry. To target mCherry, we designed short hairpin RNAs (shRNAs), matching the target with different positions. We injected them to transgenic *N. vectensis* embryos and quantified the level of mCherry knockdown (KD). Moreover, we tested the KD of injected mRNA encoding mCherry that contains three seed-match target sites, mimicking the common targeting mechanism of bilaterian miRNA targeting. Our results show that, similarly to plants, miRNAs with only a seed match or seed and supplementary matches to the target, do not knockdown mCherry. Mismatches in positions 10-11, the target cleavage site, also inhibit KD, which demonstrates the importance of target cleavage for cnidarian miRNA activity. Positions 10 or 11 mismatched, result in an intermediate repression, suggesting that naturally occurring targets with positions 10 or 11 mismatches might be selected for weaker repression. Altogether, we expand the knowledge regarding the miRNA regulation mechanism in Cnidaria, revealing more similarities to plants, which support the hypothesis of a common origin to the miRNA-mediated gene regulation in animals and plants.

## Jose Aguilar

The Hebrew University of Jerusalem

### Understanding the evolution of the DEG/ENaC ion channels in animals by their functional analysis in the cnidarian *Nematostella vectensis*

*Jose Maria Aguilar-Camacho, Department of Ecology, Evolution and Behavior, Alexander Silberman Institute of Life Sciences, Faculty of Science, The Hebrew University of Jerusalem, 9190401 Jerusalem, Israel; Katharina Foreman, Institute of Physiology, RWTH Aachen University, Pauwelsstrasse 30, 52074 Aachen, Germany; Reuven Aharoni, Department of Ecology, Evolution and Behavior, Alexander Silberman Institute of Life Sciences, Faculty of Science, The Hebrew University of Jerusalem, 9190401 Jerusalem, Israel; Stefan Grunder, Institute of Physiology, RWTH Aachen University, Pauwelsstrasse 30, 52074 Aachen, Germany; Yehu Moran, Department of Ecology, Evolution and Behavior, Alexander Silberman Institute of Life Sciences, Faculty of Science, The Hebrew University of Jerusalem, 9190401 Jerusalem, Israel.*

The Degenerin/Epithelial Na<sup>+</sup> channel superfamily (DEG/ENaC) includes ion channels with highly diverse activating stimuli and physiological functions. ASICs in vertebrates are gated by acidic pH while ENaCs are constitutively opened. In invertebrates, the degenerins in *C. elegans* and ppKs in *Drosophila* are mechanosensitive while the HyNaCs in the cnidarian *Hydra*, the FaNaC in the mollusk *Helix* and the MGIIC in the annelid *Platynereis* are gated by neuropeptides such as RFamides. This unusual diversity in gating mechanisms masks the ancestral mechanism of action and function of this channel superfamily. To unravel the ancestral state of this family of ion channels, a total of 29 DEG/ENaC (NeNaCs) genes were identified in the genome and transcriptomic datasets from the cnidarian *Nematostella vectensis*. Molecular phylogenetic analysis of the sequences from *N. vectensis* revealed a highly complex evolutionary pattern as the diverse paralogs are dispersed in distinct phylogenetic clades within the DEG/ENaC superfamily that includes members from many other vertebrate and invertebrate species. Some of these ion channels were cloned for performing electrophysiological conductivity measurements and whole mount in situ hybridization (ISH) for the localization of the transcripts in the tissue of this species at three different developmental stages revealing uncertain diverse functions. A behavioral experiment revealed a delay of feeding response in wild type organisms using a DEG/ENaC blocker (diminazene) at different molarity concentrations. In addition, a knock-out line for one of these channels has been generated using the CRISPR-Cas9 technology and is grown and crossed for generating null mutants, which will be characterized.

## Alejandro Alamán-Requena

Bar-Ilan University

### The role of montane isolation in driving lineage formation in three bird species

*Alejandro Alamán-Requena, The Goodman Faculty of Life Sciences, Bar Ilan University, Ramat Gan, Israel, and National Museum of Natural Sciences, Spanish National Research Council (CSIC), Madrid, Spain*

Christophe Thébaud, Université Paul Sabatier, Toulouse, France Borja Milá, National Museum of Natural Sciences, Spanish National Research Council (CSIC), Madrid, Spain

Geographic isolation of populations in remote mountain ranges can lead to evolutionary divergence through genetic drift and natural selection, and potentially to the formation of new species. New Guinea is the largest tropical island and one of the most important biodiversity hotspots in the world, but also one of the least explored. Here, we use a phylogeographic approach to assess the role of montane isolation in driving lineage formation in three bird species: two montane specialists, the Ashy Robin *Heteromyias albispectularis* and the White-faced Robin *Tregellasia leucops*, and a widespread and altitudinal generalist species, the Little Shrikethrush *Colluricincla megarhyncha*. Specifically, we generated mitochondrial DNA sequences from individuals in the Kumawa Mountains, a remote mountain range in the Bird's Neck region of New Guinea, and compared them to other populations across the island. Our results show that the two highland species have similar evolutionary histories, with lineage divergence among the different mountain ranges taking place during the early to middle Pleistocene. In contrast, the broad altitudinal range of the Little Shrikethrush has prevented lineage isolation in the highlands due to ongoing gene flow across lowland areas. According to our results, the New Guinea highlands can be considered a sky-island system of special importance in the process of species formation through the geographic isolation of populations and lineages. Our results have implications for taxonomy and systematics of these species. Phenotypic variation and large inter-lineage genetic divergence within montane species (range: 2.72-5.88%), suggest that diversity could be underestimated in the region. More phylogeographic studies with a wider geographic sampling are needed to properly document the avian diversity of New Guinea and the underlying evolutionary processes that generate and maintain it.

## Or Amar

The Hebrew University of Jerusalem

### Mapping discrepancy between population-genomic estimates of diversity with relation to conservation risk and demographic histories

*Or Amar, The Department of Ecology, Evolution and Behavior, The Alexander Silberman Institute of Life Sciences, The Hebrew University of Jerusalem, Oren Kolodny, The Department of Ecology, Evolution and Behavior, The Alexander Silberman Institute of Life Sciences, The Hebrew University of Jerusalem, Gili Greenbaum, The Department of Ecology, Evolution and Behavior, The Alexander Silberman Institute of Life Sciences, The Hebrew University of Jerusalem*

Genetic diversity is a key concept in conservation biology, as it reflects the evolutionary potential of species and is related to risks of inbreeding. There are several estimators for genetic diversity, such as heterozygosity and allelic diversity, with each estimator expected to behave differently under different conditions and scenarios. In theory, depletion of genetic diversity is expected to be correlated with high-risk conservation status, but there is little evidence of this correlation. One potential explanation for lack of correlation is that the eco-evolutionary processes that maintain genetic diversity are complex, and depend on many factors that vary from species to species and from one conservation risk to another. However, for threatened species, particularly those undergoing sharp demographic declines, it is expected that different genetic diversity estimators would respond differently to extinction-risk trajectories. This difference in responses would generate a discrepancy between genetic diversity estimates. In order to investigate whether extinction risk is related to genetic-estimate discrepancy, we derive effective population size based on different estimators for different species. Effective population size serves as a common ground comparison factor, allowing us to measure and evaluate genetic diversity discrepancy. We investigate the correlation of that discrepancy in many species with different status, based on historic demographic events and types of conservation threats. Investigating the correlation between genetic-estimate discrepancy and extinction risk can help explain unexpected population-genetic patterns, as well as clarify the role of genetic diversity in the context of conservation biology.



## Yotam Ben-Oren

The Hebrew University of Jerusalem

### Asymptomatic carriage of pathogens as a weapon

*Yotam Ben-Oren, The Department of Ecology, Evolution and Behavior, The Hebrew University of Jerusalem; Oren Kolodny, The Department of Ecology, Evolution and Behavior, The Hebrew University of Jerusalem*

Following infection by a pathogen, host organisms often do not clear the infection but rather remain asymptomatic carriers of it. This phenomenon is commonly viewed as a result of a mechanistic constraint: a pathogen adaptation that enables it to evade full clearance by the host immune system. However, we would like to suggest that in some cases, asymptomatic carriage may be adaptive for the host, as the host may thus infect and overcome competing conspecifics that are susceptible to the pathogen. In this study we use spatially explicit agent-based simulations to explore scenarios with 3 types of competitors: susceptible, resistant, and asymptomatic carrier. The susceptible type does not invest in resisting the disease and therefore has the highest fitness of all types when uninfected and the lowest when infected. The two additional types do invest in resisting the disease – one, the resistant, achieves complete resilience and cannot get infected, and the other, the asymptomatic carrier, can get infected but will not develop a disease. Since resistance is costly, the symptomatic carrier and resistant types are inferior to the susceptible type in the absence of the pathogen and it thus may be in their best interest to spread it. While asymptomatic carriers help in the spread of the disease by infecting their neighbors, resistant individual restrict its spread. We find that in a wide range of parameters, asymptomatic carriage of pathogens may be an evolutionary stable strategy, and could even be preferred over complete resilience.

## Gad Degani

**MIGAL – Galilee Research Institute**

### **Blue Gourami (*Trichogaster trichoptreus*) Molecular Variation Gene Markets Model for Labyrinth Fish**

*Gad Degani, MIGAL–Galilee Research Institute, POB 831, Kiryat Shmona 1101602, Israel and Faculty of Sciences, Tel-Hai Academic College, Upper Galilee 1220800, Israel*

The marks of genetic variations among species is important for both apply and basic aspects. In the present revue molecular marker of various genes belong to the blue gourami (*Trichogaster trichoptreus*) fish model for Labyrinth fish suborder Anabantoidei many of them involve in growth and reproduction were revue. The genes that encode hormones described in the present revue are: Kisspeptins (Kiss1 and 2), gonadotropin-releasing hormones (GnRH1, 2 and 3) Growth hormone (GH), Somatolactin (SL), prolactin (PRL), follicle-stimulating hormone (FSH) and the luteinizing hormone (LH), cytochrome b and 12S. We can therefore suggested based the findings of this study that the genetic markers in blue gourami present this revue may represented the marker of suborder Anabantoidei different from other bony fish. In summary, among the genes involved in control growth and reproduction, the most suitable to be genetic markers in the Anabantoidei are in the hypothalamic-pituitary-somatotropic axis (HPS axis), (PACAP and GH) and 12S in the Anabantoidei to separate among the species.

## Koren Erad

The Hebrew University of Jerusalem

### Evolution of genetic diversity in the S-RNase based self-incompatibility S-locus

*Koren Erad and Tamar Friedlander*

Self-incompatibility (SI) is a general name for mechanisms that plants have evolved to avoid self-fertilization. Here we focus on a particular mechanism where outcrossing is ensured by specific molecular recognition between pairs of a female-side and its cognate male-side protein. Both female and male-determinant genes have a large number of distinct alleles population-wide. Each individual is equipped with a single female allele and multiple male alleles that could recognize female alleles different from its own. This unique genomic architecture enables distinction between pollination by “self” and “non-self”.

While experiments in recent years have significantly advanced our understanding of the molecular underpinnings of this mechanism, its evolution is still poorly understood. In particular, the evolutionary patterns and genomic diversity of male and female genes are markedly distinct. Male alleles exhibit significant genetic diversity, which does not necessarily affect their fertilization phenotype, as crossing experiments have shown. Additionally, recent studies revealed a much richer picture than previously thought with unequal number of male and female type-determinants and overlapping recognition scopes between distinct proteins. These genomic hallmarks are unexplained by current models.

To study how the genetic diversity of this locus evolved, we constructed and analyzed a mathematical model of a reproducing haploid population. Each individual is represented by a particular combination of female and male alleles. We then allow for either neutral or deleterious mutations in the male alleles. We use this model to calculate the expected total number of mutant male-side alleles, as well as the expected number of genetic variants at steady state.

## Keren Erez

The Hebrew University of Jerusalem

### The role of biophysical interactions in self-incompatibility evolution

*Keren Erez, Tamar Friedlander, \* The Institute of Plant Sciences and Genetics in Agriculture*

Hermaphroditic plants are at high risk of self-fertilization, which can produce less-fit offspring. To avoid self-fertilization, many plants have developed various mechanisms called “self-incompatibility” (SI). We focus on a particular mechanism, based on specific molecular recognition between proteins of two families: a cytotoxic ribonuclease (SRNase) expressed in female organs and an F-box protein (SLF), expressed in the pollen. The interaction between particular protein pairs determines the possibility of fertilization. The evolution of SI alleles is thus driven by frequency-dependent selection, where the fitness of a particular allele depends on the population frequency of its fertilization partners. Due to these inter-dependencies between S-RNase and SLF alleles at different individuals, it remains unclear how new alleles evolved. In this project, we theoretically study the emergence and maintenance of genetic diversity among SI alleles. We employ a unique theoretical framework, in which we synthesize evolutionary and biophysical models to describe this intriguing system. In our evolutionary model, each diploid individual is represented by two set of S-RNase and multiple SLFs in its S-locus. Each of these genes is represented by the sequence of its recognition domain amino acids. In our biophysical model, the match between particular SLF and S-RNase proteins is determined by the match between their recognition domain sequences. This novel approach allows for a continuum of interaction intensities, unlike previous models, which only enabled two-states: interacting or non-interacting proteins. This in turn will allow a much richer description of the system, which was not possible in previous binary models. We constructed a population level stochastic simulation to study the evolutionary dynamics of this system. We use it to study the evolutionary trajectories for the emergence of new alleles, as well as the emergence of global network connectivity hallmarks, as observed in genomic data.

## Liubov Govta

University of Haifa

### The wheat stripe rust resistance gene Yr15 as a member of the tandem kinase-pseudokinase protein family

*Liubov Govta, Institute of Evolution, University of Haifa, The Department of Evolutionary and Environmental Biology, University of Haifa, Haifa, Israel; Valentyna Klymiuk, Institute of Evolution, University of Haifa, The Department of Evolutionary and Environmental Biology, University of Haifa, Haifa, Israel, Andrii Fatiukha, Institute of Evolution, University of Haifa, The Department of Evolutionary and Environmental Biology, University of Haifa, Haifa, Israel, Tzion Fahima, Institute of Evolution, University of Haifa, The Department of Evolutionary and Environmental Biology, University of Haifa, Haifa, Israel*

Wheat production, as one of the most important food crops for human consumption globally, is affected by different biotic (diseases) and abiotic (natural growth conditions) stresses. Yr15 is a wild emmer wheat (*Triticum dicoccoides*) broad-spectrum stripe rust disease resistance gene. Comparative genomics, chromosome walking, BAC libraries (wild emmer and bread wheat), whole-genome assemblies, EMS mutagenesis, and transgenic approaches enabled us to clone Yr15 and validate its function. Analysis of the protein encoded by Yr15 revealed that it has a putative kinase-pseudokinase structure, designated as Wheat Tandem Kinase 1 (WTK1). WTK1 orthologs and paralogs are found in all group 1 and 6 wheat chromosomes of the available reference wheat genomes Chinese Spring, Svevo, and Zavitan. The unique protein domain architecture of WTK1 was found in 92 putative proteins across the plant kingdom, including the barley RPG1 and a candidate for Un8, suggesting that they are members of a distinct family of plant proteins, termed here tandem kinase-pseudokinases (TKPs). We found that 175 out of 184 kinase/pseudokinase domains of these TKPs were associated with receptor-like kinases (RLKs), suggesting that TKPs are involved in plant defense mechanisms. Further phylogenetic analysis indicated that TKP family members originated from either gene duplication or gene fusion events, suggesting a polyphyletic origin of the TKPs. The decoy role can be proposed as one of the potential models of function of the pseudokinases of TKP family members in the immune response.

## Loren Khatib

University of Haifa

### Genetic Variation in the Circadian Clock of *Drosophila* - What has Changed After 30 Years?

*Loren Khatib, Department of Evolutionary and Environmental Biology, University of Haifa; Battina Fishman, Department of Evolutionary and Environmental Biology, University of Haifa; Martin Kapun, Department of Evolutionary Biology and Environmental Research, University of Zurich; Eran Tauber, Department of Evolutionary and Environmental Biology, University of Haifa*

Polymorphism in phenotypes and their underlying genes are usually maintained by natural selection. When molecular polymorphism is present, and the allele frequency is correlated with the latitude (latitudinal cline), this is taken as evidence for natural selection, since important environmental factors like temperature and day-length vary systematically with the latitude. The gene period (*per*) is a key member of the circadian clock network, a system responsible for creating daily rhythms in a wide range of physiological and biochemical processes of animals and plants. A study conducted in the 1990s in wild populations of *Drosophila* revealed a molecular polymorphism in the *per* gene in a region encoding a tandem repeat of the amino acids threonine and glycine (TG). Wild populations around the world have alleles that harbor a different repeat number, for example the TG17 or TG20 alleles which make up 90% of all alleles in Europe. The frequency of the TG17 and TG20 alleles in Europe follows a latitudinal cline, so that TG20 is more common in northern Europe, while TG17 shows the opposite tendency. A similar gradient has been discovered in Australia, reinforcing the hypothesis that this polymorphism serves an adaptive role. Indeed, further experiments have shown that this polymorphism is adaptive. Recently, the European consortium DrosEU has been conducting genomic sequencing of wild populations across Europe. The availability of these DNA sequences has allowed us to examine whether the geographical pattern of *per* polymorphism has changed during the last thirty years. The results show that the current variance does not show a correlation with latitude and suggests that the pattern of natural selection has changed significantly in recent decades, probably due to extensive environmental changes such as global warming.

## Ayala Polikovsky

Tel Aviv University

### CRISPR-Cas systems in pathogenic *Neisseria* species suggest evolutionary events and possible regulatory roles

*Ayala Polikovsky, The Shmunis School of Biomedicine and Cancer Research; Uri Gophna, The Shmunis School of Biomedicine and Cancer Research*

CRISPR systems provide adaptive immunity against selfish elements in archaea and bacteria. CRISPR arrays consist of short repeats interspaced with spacer sequences that are derived from invasive nucleic acids and mediate their interference. Besides the canonical defense functionality, those systems could limit gene transfer and can reduce the virulence and the antibiotic resistance of pathogenic strains. They could also be directly involved in gene regulation and play important roles in increasing bacterial pathogenesis. Our bioinformatics research includes two *Neisseria* species that are known as human pathogens and focuses on finding evidence for non-defense, regulatory functions of CRISPRs. The data was obtained by classification, filtering and sorting different arrays and CRISPR-related elements from two over 2000 genomes, including >100 newly sequenced and assembled ones. A graph-database was built to store the parameters of different systems, navigating and querying them and expose new relationships. Sequences similarity searches were also performed comparing spacers to the bacterial genomes. Many spacers were matched to chromosomal fragments of core and non-core genes. Those host-derived targets may be the base of the regulation of those genes. In addition, we found unexpected and oftentimes degenerated signatures of CRISPR systems from other bacterial species. Those defective systems could indicate evolutionary events and inter-species transfer of those systems. This extensive examination of *Neisseria* CRISPR systems could provide new insights into the non-defense roles of those systems and help to gain a better understanding of their diverse ecological aspects.

## Animesha Rath

Volcani Center, ARO

### Effect of social interaction on circadian clock on *Tribolium castaneum*

*Animesha Rath (1), Miriam Benita (1,2), Joseph Doron (1) and Daphna Gottlieb (1)*

(1) Department of Food Science, Institute of Post-Harvest and Food Science, TheVolcani Center, ARO, Israel.

(2) School of Zoology, Tel Aviv University

Various behavioral aspects in insects are controlled by an endogenous clock and exhibit circadian rhythmicity. The difference in the circadian rhythmicity may be caused by the influence of environmental parameters and intra-specific social interaction. Especially in the dark cavity-dwelling social animals, circadian clock may have evolved to be entrained by social cues. For example, individuals may rely on information received from group mates that do forage outside their domicile. *Tribolium castaneum* (Herbst), the red flour beetle, is a major pest of food storage facilities. These facilities have very limited light coming in. Thus, we expect social cues to play a role in entraining the circadian clock. Our study examines whether social interaction contributes to entrain circadian clock in both sexes of *T. castaneum*. To explore the circadian clock rhythmicity, we studied the expression patterns of one of the core clock gene i.e. *Tc timeless* for group of eight adults containing either males or females or containing both males and females. The results revealed a bimodal oscillation pattern of the circadian clock in all the groups. However, we do not see any evidence for female-male interaction entraining the circadian clock. These results may suggest that although the species are dark cavity-dwelling social animals, social cues do not play an essential role in the entrainment of the circadian clock.



## Noam Shtolz

Ben Gurion University of the Negev

### The dynamics of mitochondrial genome arrangement throughout metazoan evolution

*Noam Shtolz and Dan Mishmar, department of life sciences, Ben Gurion University of the Negev.*

Mitochondria emerged from an ancient (~2 BYA) endosymbiosis between a free-living  $\alpha$ -proteobacterium and an archaeon. Since then, the mitochondrion and its host developed complete inter-dependence accompanied by the transfer of most of its ancestral genes to the host genome nucleus. It is widely perceived that mitochondrial DNA (mtDNA) gene content remained largely consistent among metazoans; While true for most vertebrates, the extent of such phenomena and the dynamics of mtDNA organization across all metazoans remain unknown. To address this question, we analyzed mtDNA variability across all available metazoan mtDNAs ( $N = \sim 9000$ ), with the goal to identify the evolutionary forces that shaped mitochondrial gene order and content. Our analysis was performed using an in-house pipeline designed to construct a curated metazoan mtDNA database. Cluster analysis based on mtDNA gene content and order revealed strong conservation of mtDNA organization within certain phyla. Accordingly, Chordata and Arthropoda formed a single cluster each, encompassing 99% and 95% of organisms respectively. Unexpectedly, and despite the polycistronic nature of mtDNA transcription, we discovered conservation of long gene orders, such as in Chordata (up to the entire mtDNA's length), that retained the same gene order per mtDNA strand. In contrast, drastic variance in other phyla was observed, such as the six distinct Mollusca sub-clusters. While considering shorter gene orders, we found that certain gene pairs, such as ND4L-ND4 and ATP8-ATP6, remained adjacent in nearly all Chordata and Arthropoda (~99% in both), reflecting strong negative selection. Finally, we found an association between tRNA gene content and codon usage across all tested phyla, implying that mtDNA translation prefers mtDNA-encoded tRNAs. In summary, we found for the first time, that selection acts not only on mtDNA's gene content but also on its organization and order across metazoan evolution, thus having implications towards mitochondrial function and mtDNA regulation.

## Akiva Topper

The Hebrew University of Jerusalem

### Crossing the valley of non-intimidating conspicuousness: evolution of warning colours through the lens of fitness landscapes

*Akiva Topper, Department of Ecology, Evolution and Behavior, The Alexander Silberman Institute of Life Sciences, The Hebrew University of Jerusalem, Edmond J. Safra Campus - Givat Ram, Jerusalem 9190401, Israel; Oren Kolodny, Department of Ecology, Evolution and Behavior, The Alexander Silberman Institute of Life Sciences, The Hebrew University of Jerusalem, Edmond J. Safra Campus - Givat Ram, Jerusalem 9190401, Israel.*

The initial evolution of conspicuous aposematism is a longstanding evolutionary paradox: while the benefits of conspicuousness in aposematic signals have been demonstrated, they rely on predators being familiar with the conspicuous signals and avoiding them. In a system dominated by naïve predators, the appearance of conspicuousness would be expected to increase detection and attack rate by the predators. Hence, it is unclear how such signals could become established in a naïve community. We suggest that this problem may usefully be framed in the terms of “fitness landscapes”, a concept used for visualising the interactions between genotype, phenotype, and fitness. The evolution of conspicuousness can be thought of as a special case of “valley crossing”, which concerns the transition of populations between “fitness peaks”, when such a transition imposes an initial decrease in fitness. Crypsis may be regarded as a local fitness peak, hindering predators’ ability to detect prey; for an unprofitable species, conspicuous aposematism may constitute a higher-still fitness peak, preventing predation attempts altogether and allowing access to niches unavailable to species encumbered by the necessity to remain concealed from predators. However, in order to reach this higher peak, the population must first cross the valley of non-intimidating conspicuousness, in which the prey is conspicuous but the predators are not yet deterred. Using terms borrowed from the concept of fitness landscapes, we categorise several solutions suggested previously in the literature as either negating the existence of the valley, or as illuminating possible “ridges” connecting the two peaks, which emerge from unconsidered dimensions of the fitness landscape. We suggest that considering this question through the lens of fitness landscapes not only facilitates useful categorisation of previously suggested solutions but may also prove useful for thinking about novel ones.

## Beny Trabelsy

University of Haifa

### Gut bacteria disarm the *Ochradenus baccatus* fruits “mustard-oil-bomb”

*Beny Trabelsy, University of Haifa, Department of Evolutionary and Environmental Biology; Ido Izhaki, University of Haifa, Department of Evolutionary and Environmental Biology; Yoram Gerchman, University of Haifa at Oranim, Department of Biology and the Environment*

Plants of the Brassicales order harbor the ‘mustard bomb oil’ mechanism – where damage to plant tissue result in mixing the glucosinolates secondary metabolites with the myrosinase enzyme, and their activation, releasing toxic products such as isothiocyanate. This mechanism protects the plant against herbivores and many pathogenic microorganisms. *Ochradenus baccatus* is a desert plant with juicy fruit. The fruits attracts many animals, to avoid predation of seeds and encourag dispersal, the *O. baccatus* fruit utilize the “mustard bomb oil” in a unique way - the fruit pulp contain high concentration of glucosinolates, while the seeds have the myrosinase enzyme, enabling activation of the system only upon seed and pulp co-consumption. *Pycnonotus xanthopygos* (bulbul) are a major consumer of *O. baccatus* fruits. As birds swallow the whole fruit they are likely to be exposed to toxic products in their digestive system. Hence, the bird feeding on *O. baccatus* fruit exposed to be resistant to such products. This study indicates that glucosinolates and their breakdown toxic products was effect on eating and digestion in bulbuls that expected to be naive to *O. baccatus* fruit compared to birds that regularly feed on *O. baccatus* fruit. There were differences in the amount of eating, food selection and digestibility. *Pantoea vagans* (*P. vagans*) isolate from bulbuls’ droppings feeding on *O. baccatus* fruits shown resistance and even an ability to grow on glucosinolates breakdown products. Enriching the birds naive to *O. baccatus* with these bacteria demonstrated that these bacteria give the birds resistance against the *O. baccatus* toxic breakdown products.

