The 5th meeting of the Israeli Society for Evolutionary Biology

לבוטל ציוד מדעי בע"מ

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ZOTAL Biologicals & Instrumentation

Syntezza

	Sunday 22/9/24	
09:00	Registration, morning coffee	
09:45	***Opening remarks*** **(Feldman A)** Prof. Assaf Friedler - Dean of the Faculty of Math and Sciences, HUJI Prof. Einat Hazkani-Covo - ISEB President Prof. Ariel Chipman - Conference Chair	
10:00	**KEYNOTE: Ruth Hershberg** Dynamics of adaptive variation generation and maintenance under very prolonged resource exhaustion	
11:00	Coffee break	
	Feldman A	**Feldman B**
	Microbial Evolution *(Chair: Jonathan Friedman)*	***Evolution of Brain and Behavior*** *(Chair: Meital Suissa Oren)*
11:30	**Jonathan Friedman**: Reversion to metabolic autonomy underpins evolutionary rescue in a bacterial obligate mutualism	**Meital Suissa Oren**: Sexual adaptation across evolution: the neural basis of female sexual motivation
11:55	**Jonathan Greenbaum**: Balancing infection characteristics underlies cyanophage adaptation in complex environments	**Natasha Shpoliansky**: The links between a cultural foraging tradition and problem solving abilities in black rats
12:10	**Saar Shoer**: Data-driven Approach to Antibiotic Discovery	**Nitzan Alon**: Evolutionary co-option of neural patterning networks to insect segmentation
12:25	**Shira Zion**: *Escherichia coli* adaptation under prolonged resource exhaustion is characterized by extreme parallelism and frequent historical contingency	**Maor Knafo**: *Saccharomyces cerevisiae* cells can utilize reward learning to form new regulatory associations
12:40	**Shu-Ting You**: Mapping genotypes of microbial cooperation	**Tzvi Goldberg**: Inhibitory signaling in collective social insect networks, is it indeed uncommon?
12:55	Poster Session + Lunch Break	
	Organismal Evolution *(Chair: Ariel Chipman)*	***Population Genetics*** *(Chair: Shai Carmi)*
14:30	**Ariel Chipman**: The evolution and development of arthropod tagmata	**Shai Carmi**: DNA of 14th-century German Jews demonstrates genetic heterogeneity and founder event in late medieval Ashkenazi Jews
14:55	**Uri Gat**: Evolutionary developmental studies of chitin synthases in the sea anemone Nematostella - hints to unexpected ancient roles for chitin	**Shirli Bar-David**: Factors affecting female wild ass (*Equus hemionus*) social associations following a change in water-source distribution
15:10	**Ari Meerson**: Transcriptome variation in banded newt (*Ommatotriton vittatus*) during its life cycle and habitat transition	**Sviatoslav Rybnikov**: Combined use of gene drives and pesticides to minimize spillover risk
15:25	**Olga Volovych**: Cuticle biomineralization in the moulting cycle in selected arthropod species	***- Cancelled -***
15:40	Coffee break	
	Evo-Devo *(Chair: Ella Preger-Ben Noon)*	***Evolutionary Theory*** *(Chair: Yoav Ram)*
16:00	**Dale Frank**: Evolution of MEIS Transcription Factor Activity during Metazoan Neural Development – Born to be Wild!	**Ohad Peled**: The effects of habitat fragmentation on population genetic measures
16:15	**Tovah Nehrer**: Conserved pathways, divergent outcomes: The roles of VEGF and ERK in sea urchin skeletogenesis and vertebrate angiogenesis	**Akiva Topper**: Long-distance mimicry: when might allopatric species share aposematic signals?
16:30	**Areej Said Ahmad**: Multiple mechanisms to eliminate enhancer function during morphological evolution	**Yoav Ram**: Cultural transmission, networks, and clusters among Austronesian-speaking peoples
16:45	**Evgenia Propistova**: Eye reduction in cave spiders: Retinal Determination Gene Network dynamics in cave *Tegenaria* Latreille, 1804 (Araneae: Agelenidae) spider embryos	

	Monday 23/9/24	
9:00	Early morning coffee	
	Feldman A	**Feldman B**
	Human Evolution *(Chair: Alon Barash)*	***Molecular evolution & Phylogenetics*** *(Chair: Efrat Regev-Gavish)*
9:30	**Alon Barash**: How did other hominins grow, and why does it matter?	**Efrat Regev-Gavish**: A multidisciplinary approach to study arachnid evolution in Levantine caves
9:55	**Chen Leibson**: Effects of archaic introgression on differential DNA methylation in modern humans	**Itamar Kozlovski**: Induction of apoptosis by double-stranded RNA was present in the last common ancestor of cnidarian and bilaterian animals
10:10	**Nitzan Haim**: How DNA methylation changes shaped recent human evolution	**Dimitry Schepetov**: Driven by glacial cycles: speciation, diversification, and dispersal of Coryphella nudibranchs across the Northern Hemisphere
10:25	Coffee break	
10:55	**Pnina Cohen**: Evaluating the applicability of imputation and kinship analyses for ancient sedimentary DNA datasets	**Hadas Ner-Gaon**: Comparing the use of alternative splicing between human and mouse immune cells
11:10	**Simon Fishilevich**: How monogenic disorders emerge and disappear in evolution	**Erez Levanon**: The evolution of the RNA editing enzyme, ADAR, is dictated by core body temperatures
11:25	**Yotam Ben-Oren**: The invention hourglass: cultural transmission sets the time window for the occurrence of simultaneous inventions	**Daria Aleshkina**: The roles of RdRPs in the antiviral response in Nematostella vectensis
11:40	**Prajjval Pratap Singh**: Genetic History of an isolated tribe of India with an unexpected link with Africa	**Eran Tauber**: DNA Methylation Meets Codon Usage: Exploring the Evolutionary Dynamics of CpG Codon Associations
11:55	Poster Session + Lunch Break	
	Plant Evolution *(Chair: Idan Efroni)*	***Ecology and Evolution*** *(Chair: Michal Segoli)*
13:25	**Idan Efroni**: Identification and evolution of regulatory sequences in flowering plants	**Michal Segoli**: When invasive species carry along their parasites and endosymbionts: the case of the brown widow spider
13:50	**Ayelet Salman Minkov**: Strategies for mining useful alleles for climate change adaptation	**Adrian Jaimes-Becerra**: Functional characterization of venom as a complex trait and elucidation of its contribution to animal fitness
14:05	**David Lerner**: The latitudinal phylogenetic gradient is maintained by a tropical-temperate transitional region	**Amiyaal Ilany**: Microbial strain evolution as a window into animal social interactions and population connectivity
14:20	**Ronen Shtein**: Molecular phylogeny of *Kalanchoe* (Crassulaceae subfam. Kalanchooideae) and the evolution of asexual reproduction	**Lee Koren**: Sperm characteristics reveal rock hyrax mating tactics
14:35	Coffee break	
15:00	**KEYNOTE: Virginie Courtier-Orgogozo (Feldman A)** Examining the mutations to understand evolution, past and future	
16:00	Prizes and concluding remarks	
16:30	***After party***	

Sunday 22/9/24		
Poster #	*Name of presenter*	*Title*
1	Nadav Ben Nun	The Collective Posterior Distribution and Its Application in Simulation-Based Inference from Highly Variable Experimental Replicates
3	Gil Roi	The interaction of population size and species' drift in a simple niche-partitioning model offers a new explanation for biodiversity-productivity relationships
5	Shahar Shemesh	The effect of environmental variation on gene drive dynamics
7	Efrat Beck	Activation of GABA-B Receptor Signaling Affects Cilia Tubulin Post-Translational Modifications in the Sea Anemone *Nematostella vectensis*
9	Shanduo Chen	Deciphering the role of adhesion proteins during sea urchin biomineralization
11	Sharon Warburg	Regards from the Miocene: Ayyalonia- a climatic relict Israeli endemic troglobitic pseudoscorpion genus
13	Elena Naimark	Cambrian Explosion: a Trichoplax perspective
15	Yuval Aharon Shiran	Evolution of cyanophages under different light conditions
17	Nittay Meroz	Evolution in microbial microcosms is highly parallel regardless of the presence of interacting species
19	Reut Shabtai	Microbial Genome Adaptations to Anthropogenic Nutrient Pollution
21	Keith Harris	modelRxiv: a platform for the dissemination and interactive display of models
23	Yonatan Bendett	The war of attrition: a perspective of microbial residents
25	Stav Ratzon	Cultural evolution of prosocial behavior in the Stug-hunt game
27	-	*Cancelled*
29	Gal Frydman	Transcriptomic analysis of novel kidney-related genes in Lesser spotted catshark (*Scyliorhinus canicula*) embryos
31	Srijani Roy	Uncovering the regulatory relationship between the Drosophila Shavenbaby and the Osiris genes
33	Ariel Bar-Lev Viterbo	Unraveling the Complexity of Insect Embryogenesis: Preliminary Insights from Blastoderm Morphology and Evolution
35	Prashant Tewari	PAK4DEV: p21 Activated Kinases Expression, Regulation, and their Roles in Sea Urchin Development and Skeletogenesis
37	Milton Urum	A single-cell view of male genitalia development and evolution

Monday 23/9/24		
Poster #	*Name of presenter*	*Title*
2	Keren Klass	Counterintuitive population genetic patterns across levels of habitat fragmentation
4	Mor Binder	Seed dispersal strategies in response to environmental stress
6	Amit Jangid	Plant collaborative non-self-recognition self-incompatibility systems: facilitating conditions, evolutionary stability, breakdowns, and recovery
8	Saurav Mallik	Co-translational assembly constraints protein oligomeric state evolution upon gene duplication
10	Shira Milo	Differential conservation of classical NHEJ in fungal genomes reveals distinct short genetic variations profiles
12	Yael Klirs	Evolutionary Insights from the Mitochondrial Genome of Oikopleura dioica: Sequencing Challenges, RNA Editing, Gene Transfers to the Nucleus, and tRNA Loss
14	Elya Wygoda	Statistical framework to determine indel-length distribution
16	Ilan Gronau	Inferring complex admixture patterns in the Phoenician Mediterranean world from ancient DNA using F-statistics
18	Dheeraj Chaudhary	Exploring the Pleistocene to Holocene Transition in Central Europe through Sedimentary Ancient DNA
20	Nadav Mishol	Candidate Denisovan fossils identified through gene regulatory phenotyping
22	Omer Ronen	Using saturation mutagenesis to map the evolutionary forces that shaped human regulatory elements
24	David Sayag	The opposing roles of gene exchange in the evolution of self-incompatibility in plants: does it promote or inhibit genetic diversity?
26	Yevgenia Shchitnikov	Pre-existing mitochondrial DNA plasmids escape to the nucleus
28	Michal Tunkel	Inverted repeat extension by template switching in GRE2 promoter affects gene expression through yeast evolution
30	Dan Amichai	Leveraging Evolutionary Insights from the Wright-Fisher Model of Allele Frequency Dynamics to Advance Nature Conservation Strategies
32	Danny Minahan	Anemone flowers produce airborne ultrasounds that may facilitate plant-pollinator interactions
34	Ittai Warburg	Geographical variability of *Messor arenariu* s ants from different regions in Israel

Talk 1:

The roles of RdRPs in the antiviral response in Nematostella vectensis

Daria Aleshkina, Yael Hazan, Yael Admoni, Reuven Aharoni, Yehu Moran

Department of Ecology, Evolution and Behavior, Alexander Silberman Institute of Life Sciences, Faculty of Science, Hebrew University of Jerusalem, Jerusalem, Israel

Examining the antiviral response in basally-branching groups like Cnidaria is essential for understanding the evolutionary origins of immune systems in animals. Invertebrates rely on RNA interference (RNAi) as a key antiviral defense mechanism. RNAi generates small interfering RNAs (siRNAs) that target and silence viral RNAs. In some plants, fungi, and nematodes, the RNAi response is amplified through the production of secondary siRNAs by RNA-dependent RNA polymerases (RdRPs). These secondary siRNAs enhance the initial RNAi response and provide a more robust defense against viral infections. However, in non-nematode animals, RdRPs are either absent or poorly characterized. We found four RdRP homologs in the genome of Nematostella vectensis, a scarlet sea anemone. These homologs are conserved across all sea anemones and stony corals, suggesting they have specialized functions that have been preserved since the divergence of these species about 500 million years ago.

Initial results strongly suggested the absence of secondary siRNAs and RNAi amplification in N. vectensis, leaving the precise role of RdRPs unknown. Upon injection of polyinosinic acid (poly(IC)), which mimics viral infections, three of the Nematostella RdRPs, along with other RNAi-related genes, were significantly upregulated. Moreover, in RdRP knockout mutants of Nematostella, we observed a significant increase in reads mapping to core viruses compared to wild-type individuals.

To gain further insights, we are performing detailed morphological and transcriptomic analyses of RdRP knockout and knockdown mutants. Additionally, we plan to use a reporter gene approach to identify and characterize RdRP-expressing cells. This research aims to illuminate the evolutionary role and functional significance of RdRPs in the animal kingdom, providing valuable insights into the origins of antiviral immune mechanisms. Altogether, this project will shed light on the evolution and function of RdRPs in animals.

Talk 2:

Transcriptome variation in banded newt (Ommatotriton vittatus) during its life cycle and habitat transition

Ari Meerson, Galilee Research Institute (MIGAL) and Faculty of Sciences, Tel Hai college

Gad Degani, Galilee Research Institute (MIGAL) and Faculty of Sciences, Tel Hai college

Israel represents the southern limit of the distribution of the banded newt (Ommatotriton vittatus). The life cycle of O. vittatus includes several distinct phases: eggs, aquatic larvae, a terrestrial phase and an aquatic reproductive phase. We investigated differences in gene expression during the life cycle and transition of banded newts between terrestrial and aquatic habitats using mRNA-seq. We identified ~10 k genes that were differentially expressed (DE) in one of the pairwise comparisons between 3 groups: 1 - terrestrial newts (males and females), 2 - aquatic newts (males and females), 3 - aquatic larvae before metamorphosis. The groups were clearly defined by Principal Components Analysis (PCA). The greatest difference was between aquatic newts (males and females) and aquatic larvae: ~7.4 k DE genes. Of special interest were the ~2.4 k genes DE between the aquatic and terrestrial phenotypes. These included prominent candidates with known roles in kidney function (uromodulin homologs were strongly associated with aquatic lifestyle), tissue structure (keratins), and the thyroid hormone signaling modulator DUOXA1. Additional developmental and metabolic pathways overrepresented among the identified DE genes included “epidermis development”, “nervous system development”, “nucleotide-sugar biosynthesis”. Overall, both metamorphosis and environmental transition of banded newts involve extensive transcriptomic remodeling involving developmental, metabolic, and cellular pathways. Understanding the roles of these pathways and individual genes is instrumental for studies of transition between habitats, especially those affected by climate change. Furthermore, the phenotypic flexibility of the newt and the underlying regulation of gene expression can shed light on the evolution of terrestrial vertebrates. We are currently using Oxford Nanopore direct RNA sequencing to assess changes in RNA modifications during the life cycle and habitat transition of the newt.

Talk 3:

Evolution of MEIS Transcription Factor Activity during Metazoan Neural Development – Born to be Wild!

Dale Frank, Dept. of Biochemistry, Rappaport Faculty of Medicine, Technion

Pavel Fedarenchik, Dept. of Biochemistry, Rappaport Faculty of Medicine, Technion

Antero-posterior body axis formation in bilaterians requires homeodomain transcription factors. TALE and HOX homeodomain proteins interact to induce neural pattern in vertebrates. In the amphibian, Xenopus laevis, the Meis3 TALE-class homedomain protein controls hindbrain and neural crest cell-fate specification. Meis orthologues have two highly conserved regions: (1) a Meis-specific domain and (2) the TALE-class homeodomain. Hox and Meis proteins are expressed in “ancient” metazoans such as radial Cnidarians, Placozoans and Protozoans. Xenopus and Drosophila Meis proteins both efficiently induce posterior neural tissue in Xenopus embryos. We therefore asked the question: When during metazoan evolution did Meis proteins acquire the functional ability to induce vertebrate-specific hindbrain and neural crest tissue structures? By dissecting the Meis protein into various domains, we found that the highly conserved Meis-specific-domain and homeodomain together suffice to induce spinal cord, but not hindbrain. Bilaterian and Cnidarian Meis proteins share a functionally conserved C-terminus transcription activation domain that induces hindbrain. Meis proteins from Placozoan Trichoplax and unicellular protozoan Chlorophyte algae like Chlamydomonas and Volvox induce hindbrain and neural crest in Xenopus embryos. These proteins have a conserved homeodomain, but lack a Meis-specific domain. A truncated Xenopus Meis3 protein lacking the Meis-specific domain that resembles Trichoplax/Chlorophyte Meis proteins also efficiently induces hindbrain. Early in metazoan/eukaryotic evolution, the capacity to induce “vertebrate” structure was intrinsic to Meis protein activity. Thus, the basic building-blocks regulating neural axis formation in the vertebrate embryo pre-date the structures themselves. Early eukaryotes originated with powerful Meis homeodomain proteins that were later recruited during metazoan evolution to create vertebrate specific neural structures, such as hindbrain and neural crest.

Talk 4:

Evolutionary co-option of neural patterning networks to insect segmentation

Nitzan Alon & Ariel D. Chipman

Department of Ecology, Evolution and Behavior, The Hebrew University of Jerusalem.

Insect brains exhibit diverse morphologies, matching the ecological and morphoplogical variety of the group. However, the best studied species are all members of the monophyletic Holometabola, with distinctly different larval and adult brains. That second wave of brain development, happening during the pupa stage, makes the full developmental process of the embryonic to adult brain relatively unexplored. Interestingly, many of the genes involved in the development of the nervous system are also involved in segmentation, suggesting a deep evolutionary connection between the regulatory networks in charge of both processes. We followed the formation of the nervous system in the hemimetabolous insect Oncopeltus fasciatus and created a developmental map, as a comparative base to data from holometabolous species. We use RNA in-situ hybridization staining of pro-neural and neuron-specifying genes as well as canonical segmentation genes. Because the brain of a hemimetabolous insect does not change drastically during its life cycle, it may represent a more ancestral mode of development, and thus provide a better basis for comparing the role of genes in neurogenesis and in segmentation. Our results provide support for the hypothesis that neurogenesis is more ancient than segmentation, and thus neural genes were recruited to the segmentation process.

Talk 5:

Factors affecting female wild ass (Equus hemionus) social associations following a change in water-source distribution

1 - Noa Y. Kan-Lingwood, Mitrani Department of Desert Ecology, Ben-Gurion University of the Negev, Midreshet Ben-Gurion, Israel

2 - Alan R. Templeton, Department of Biology, Washington University, St. Louis, USA

3 - Daniel I. Rubenstein, Department of Ecology and Evolutionary Biology, Princeton University, New Jersey, USA

4 - Amos Bouskila, Life Science Department, Ben-Gurion University of the Negev, Beer-Sheva, Israel

5 - Shirli Bar-David, Mitrani Department of Desert Ecology, Ben-Gurion University of the Negev, Midreshet Ben-Gurion, Israel

Climate change and human activities have increasingly limited the availability of natural water sources, particularly in arid environments. One intervention has been managing artificial water sources, which, while providing essential drinking water, also influence space-use patterns, demography, and reproduction. Therefore, understanding the social structures of species affected by such management is essential. We studied factors affecting females' social associations in Asiatic wild-ass (Equus hemionus) following water-sources management in the Negev Highlands, Israel. Employing a network approach based on genotypes, we correlated sociality, genetic relatedness, and reproductive success and examined the geographical locations of females in relation to water sources. Based on 2,014 fecal samples collected between 2020-2023, we identified 100 unique female genotypes, 57 of which demonstrated strong social ties. The social network revealed a significant correlation between sociality and genetic relatedness across multiple years ($p < 0.001$); however, no correlation was found with reproductive success ($p = 0.831$). Spatial analysis indicated that females with strong social associations tend to revisit similar areas over time. Importantly, the observation of strong social ties among genetically unrelated individuals might play a role in avoiding inbreeding.

Talk 6:

The invention hourglass: cultural transmission sets the time window for the occurrence of simultaneous inventions

Yotam Ben-Oren, Department of Ecology, Evolution & Behavior, The Hebrew University of Jerusalem

Zvi Mintzer, The Institute of Archaeology, The Hebrew University of Jerusalem

Maria M. Martignoni, Department of Ecology, Evolution & Behavior, The Hebrew University of Jerusalem

Maxime Derex, Toulouse School of Economics, Institute for Advanced Study in Toulouse

Erella Hovers, The Institute of Archaeology, The Hebrew University of Jerusalem

Oren Kolodny, Department of Ecology, Evolution & Behavior, The Hebrew University of Jerusalem

The phenomenon of simultaneous inventions – the independent emergence of analogous inventions within a short time frame (e.g., the independent development of evolutionary theory by Wallace and Darwin) – has fascinated scientists and the general public for years. The prevalent explanation for the proximity in time of simultaneous inventions is the Zeitgeist ("Spirit of the age"), suggesting they result from external circumstances making them likely only at a particular period. Drawing from the concept of genetic soft sweeps, we use a simple model to suggest that simultaneous inventions should be explained not only by the conditions that make them possible at a certain timepoint but also by those that make them impossible after a certain timepoint. The diffusion of an invention impedes the emergence of analogous inventions because an individual – by definition – cannot independently invent something they had already learned. Thus, as an invention spreads, the number of naïve individuals who can independently reinvent it decreases. This creates an observation bias: whenever we encounter instances of analogous inventions, it necessarily means their emergence was clustered in time. Furthermore, we suggest that even when the intrinsic probability of invention is uniform across space, a positive association between the location of the simultaneous inventions and their timing is to be expected.

Talk 7:

Evaluating the applicability of imputation and kinship analyses for ancient sedimentary DNA datasets

Pnina Cohen, Department of Anatomy and Anthropology and Department of Human Molecular Genetics and Biochemistry and The Dan David Center for Human Evolution and Biohistory Research, Tel Aviv University

Sarah Johnson, Department of Molecular and Cell Biology, Center for Computational Biology, University of California, Berkeley

Elena I. Zavala, Department of Molecular and Cell Biology, Center for Computational Biology, University of California, Berkeley

Priya Moorjani, Department of Molecular and Cell Biology, Center for Computational Biology, University of California, Berkeley

Viviane Slon, Department of Anatomy and Anthropology and Department of Human Molecular Genetics and Biochemistry and The Dan David Center for Human Evolution and Biohistory Research, Tel Aviv Universit

Ancient DNA (aDNA) analyses— the study of genetic material from individuals that died hundreds or thousands of years ago— have revolutionized the research in human evolutionary genetics. At most archaeological sites dated to the Middle or Late Pleistocene (780,000-12,000 years ago), no human remains have been found. However, recent studies have shown that aDNA can be recovered from archaeological sediments, even in the absence of any skeletal remains, providing an exciting new avenue to learn about our evolutionary past. Despite that, so far only a limited number of studies have successfully recovered, identified and authenticated ancient human DNA from prehistoric sediments. This is due to the complexity of ancient sedimentary DNA datasets, which tend to be composed of small quantities of short and degraded fragments, often representing multiple species and multiple individuals, within an overwhelming background of environmental DNA.

We focus on advancing and developing analytical frameworks to support the study of ancient human DNA from sediments. Here, we evaluate current methods for imputation, phasing and kinship analyses of genetic variants such as Glimpse, Beagle and LinkImpute - testing them for accuracy on both empirical data and on simulated datasets mimicking the characteristics of ancient sedimentary DNA, including very low genetic coverage, restricted relevant reference panels, mixture of individuals within a single sample, and the presence of non-human ancient DNA. Based on this, we propose appropriate filters and parameters for the tested software, when applied to the study of ancient human DNA from sedimentary samples.

Talk 8:

Inhibitory signaling in collective social insect networks, is it indeed uncommon?

Tzvi S. Goldberg, Department of Ecology Evolution and Behavior, Hebrew University

Guy Bloch, Department of Ecology Evolution and Behavior, Hebrew University

Individual entities across levels of biological organization interact to reach collective decisions. Possibly the most extreme form of this are centralized neuronal networks, where competing neural populations commonly accumulate information over time while increasing their own activity, and cross-inhibiting other populations until one group passes a given threshold. Social insects are another useful and well-studied model for the evolution of so-called “swarm intelligence”, as they reach high levels of collective behavior while individuals are functionally self-sufficient, at least in the short term. In these groups, there is good evidence for decisions mediated by positive feedbacks, but we found evidence for similar inhibitory signals only in honey bee (Apis mellifera) stop signals, and Pharaoh’s ant (Monomorium pharaonic) repellent pheromones, with only the former occasionally being used as cross-inhibition, during the colony’s search for new nesting sites. We discuss how these differences likely stem from insufficient research efforts as well as genuine differences across levels of biological organization. Differences in collective decision-making between levels of biological organization is but one example of how comparing the basic mechanisms giving rise to emergent properties between diverse systems can lead to a better understanding of the basic principles in the evolution of these properties across different systems and levels of biological organization.

Talk 9:

Balancing infection characteristics underlies cyanophage adaptation in complex environments

Jonathan Greenbaum, Faculty of Biology, Technion - Israel Institute of Technology

Debbie Lindell, Faculty of Biology, Technion - Israel Institute of Technology

Marine cyanobacteria are abundant primary producers, responsible for roughly a quarter of oceanic carbon fixation. Cyanobacteria-infecting bacteriophages (cyanophages) have massive ecological significance, as they affect the abundance and diversity of the cyanobacterial community. Cyanophages depend entirely on their cyanobacterial hosts for propagation. Therefore, the composition of the cyanobacterial community has the potential to determine the ability of cyanophages to persist, and their evolutionary trajectory. Here, we aim to examine the effect of the cyanobacterial community, consisting of both susceptible and an adsorbable resistant cyanobacteria, on cyanophage evolution. We found that six out of twelve evolved cyanophage populations decreased time to cell lysis compared to the ancestral phage when infecting the original susceptible host. Three of these populations evolved in the presence of a resistant strain. The shorter lysis time indicates a change in at least one infection characteristic, resulting in increased phage fitness. Surprisingly, we found that attachment to both the susceptible and resistant cyanobacterial strains decreased in evolved populations. We hypothesize that this allows cyanophages to limit the amount of futile infections while still maintaining high levels of progeny production. Genomic analysis revealed point mutations in a putative holin in three populations with increased fitness. This mutation has the potential to shorten the phage latent period, hypothesized to be beneficial when a susceptible host is abundant. Our findings suggest that, in order for cyanophages to gain a competitive advantage in complex environments where an adsorbable resistant cyanobacterium is abundant, a balance is maintained between different infection characteristics.

Talk 10:

How DNA methylation changes shaped recent human evolution

Nitzan Haim*, Department of Molecular Genetics, Weizmann Institute of Science; Chengyu Deng*, Department of Bioengineering and Therapeutic Sciences, UCSF; Simon Fishilevich, Department of Molecular Genetics, Weizmann Institute of Science; Nadav Ahituv*, Department of Bioengineering and Therapeutic Sciences, UCSF; David Gokhman*, Department of Molecular Genetics, Weizmann Institute of Science.

* These two authors contributed equally to this work

DNA methylation is a key marker of gene regulation, but its role in human evolution remains obscure. We have previously developed a method to reconstruct full bone DNA methylation maps from extinct organisms and identified thousands of methylation changes that separate modern humans from Neanderthals and Denisovans. Here, we developed a novel method – methylation-based Massively Parallel Reporter Assay (methMPRA) – to systematically test how each of these methylation changes has shaped human gene expression. We compared the expression output in osteoblasts of the methylated and unmethylated states of each sequence and found that methylation affected expression in ~50% of differentially methylated regions between modern and archaic humans. Specifically, we found 1,439 regions where methylation down-regulated expression and, unexpectedly, 454 regions where methylation up-regulated it. We also found that CpG density determined the probability of methylation to up- or down-regulate expression; sequences with higher CpG density were more likely to down-regulate expression. Surprisingly, sequences with a lower CpG density had an almost equal probability of up- and down-regulating expression. We also found that higher CpG density was associated with more extreme down-regulation, but that the level of up-regulation was not affected by CpG density. Overall, our findings suggest that (a) methylation-driven expression changes in human evolution had different underlying mechanisms for down- vs. up-regulating sequences, and (b) evolutionary changes in DNA methylation often resulted in down-regulation, but that a considerable fraction of methylation changes resulted in up-regulation. Our methMPRA method for high-throughput quantification of the effects of methylation changes on expression can be used not only to study human evolution, but also to study the role of methylation changes in cancer and development.

Talk 11:

Functional characterization of venom as a complex trait and elucidation of its contribution to animal fitness

Adrian Jaimes-Becerra [1], Joachim M. Surm [2], Reuven Aharoni [1], Adam M. Reitzel [3] and Yehu Moran[1]

1-Department of Ecology, Evolution, and Behavior at the Hebrew University of Jerusalem.

2-Faculty of Biology, Ludwig-Maximilians-Universität Munich, Munich, Germany

3-Department of Biological Sciences, University of North Carolina at Charlotte,

Charlotte, NC, USA.

Venoms are considered a key innovation underpinning the evolutionary success of many animal lineages. Serving both predation and defense, venom's ecological and functional roles highlight its evolutionary significance despite its metabolic cost, suggesting it evolves under strong selective pressures balancing its fitness impacts. In this work, we proposed to study the contribution of venom to organismal fitness which have been rarely studied experimentally. It now can be directly tested by the genetic manipulation methods available for the sea anemone Nematostella vectensis which inhabits brackish lagoons along the coasts of North America. This cnidarian has become a prominent laboratory model, offering unparalleled insights into venom evolution. Its venom system is multimodal, encompassing both nematocytes and ectodermal gland cells that produce a dynamically changing toxin mixture over its life cycle. Furthermore, the interaction patterns with predators and prey differ across its developmental stages, (eggs, larvae, and adults) reflecting the adaptive nature of the venom system. We generated knockout animals using CRISPR/Cas9 technology for three toxin genes: Nep3 and Nep3-like and NvePTx1. The first two are examples of abundant nematocyte neurotoxins present in the animal from the planula larval stage to the adult and may serve both in defense and in catching prey. NvePTx1 is an ectodermal gland cell toxin restricted to the egg and larval stages, hence used primarily for defense as Nematostella larvae do not feed. Knockout animals were subjected to tests measuring their fitness as well as their ability to catch prey and defend from native Nematostella predators to reveal their organismal function. Our experiments are the first to directly test venom’s effect on animal ecology and its cost, which mirror the evolutionary forces that shape it.

Talk 12:

Induction of apoptosis by double-stranded RNA was present in the last common ancestor of cnidarian and bilaterian animals

Itamar Kozlovski, Department of Ecology, Evolution and Behavior, Alexander Silberman Institute of Life Sciences, Faculty of Science, The Hebrew University of Jerusalem, Jerusalem, Israel

Adrian Jaimes-Becerra, Department of Ecology, Evolution and Behavior, Alexander Silberman Institute of Life Sciences, Faculty of Science, The Hebrew University of Jerusalem, Jerusalem, Israel

Ton Sharoni, Department of Ecology, Evolution and Behavior, Alexander Silberman Institute of Life Sciences, Faculty of Science, The Hebrew University of Jerusalem, Jerusalem, Israel

Magda Lewandowska, Department of Ecology, Evolution and Behavior, Alexander Silberman Institute of Life Sciences, Faculty of Science, The Hebrew University of Jerusalem, Jerusalem, Israel

Ola Karmi, Research Infrastructure Facility, Alexander Silberman Institute of Life Sciences, Faculty of Science, The Hebrew University of Jerusalem, Jerusalem, Israel

Yehu Moran, Department of Ecology, Evolution and Behavior, Alexander Silberman Institute of Life Sciences, Faculty of Science, The Hebrew University of Jerusalem, Jerusalem, Israel

Apoptosis, a major form of programmed cell death, is an essential component of host defense against invading intracellular pathogens. Viruses encode inhibitors of apoptosis to evade host responses during infection, and to support their own replication and survival. Therefore, hosts and their viruses are entangled in a constant evolutionary arms race to control apoptosis. Until now, apoptosis in the context of the antiviral immune system has been almost exclusively studied in vertebrates. This limited phyletic sampling makes it impossible to determine whether a similar mechanism existed in the last common ancestor of animals. Here, we established assays to probe apoptosis in the sea anemone Nematostella vectensis, a model species of Cnidaria, a phylum that diverged approximately 600 million years ago from the rest of animals. We show that polyinosinic:polycytidylic acid (poly I:C), a synthetic long double-stranded RNA mimicking viral RNA and a primary ligand for the vertebrate RLR melanoma differentiation-associated protein 5 (MDA5), is sufficient to induce apoptosis in N. vectensis. Furthermore, at the transcriptomic level, apoptosis related genes are significantly enriched upon poly(I:C) exposure in N. vectensis as well as bilaterian invertebrates. Our phylogenetic analysis of caspase family genes in N. vectensis reveals conservation of all four caspase genes involved in apoptosis in mammals and revealed a cnidarian-specific caspase gene which was strongly upregulated. Altogether, our findings suggest that apoptosis in response to a viral challenge is a functionally conserved mechanism that can be traced back to the last common ancestor of Bilateria and Cnidaria.

Talk 13:

Microbial strain evolution as a window into animal social interactions and population connectivity

Amiyaal Ilany, Faculty of Life Sciences, Bar-Ilan University

Prameek Kannan, Faculty of Life Sciences, Bar-Ilan University

Omry Koren, Faculty of Medicine, Bar-Ilan University

Understanding the intricacies of animal social interactions and population connectivity is crucial for the study of many aspects of social behavior, yet direct observation and genetic analyses often present logistical challenges. We introduce an approach leveraging the strain-sharing of microbes as indirect indicators of social behavior and connectivity among animal populations. By analyzing the microbiomes of individual rock hyraxes from several groups in a population using shotgun metagenomics, we identify shared microbial strains that suggest historical or ongoing social interactions. This microbial fingerprinting allows us to infer patterns of social association and movement across landscapes that are otherwise difficult to document. This approach offers a unique lens through which to view the social and ecological dynamics of animal populations, providing insights into the unseen connections that bind individuals and populations. Our approach has implications for understanding disease transmission dynamics, conservation strategies, and the evolution of social behavior.

Talk 14:

Cultural transmission, networks, and clusters among Austronesian-speaking peoples

Joshua C Macdonald, School of Zoology, Tel Aviv University; Javier Blanco-Portillo, Department of Biology, Stanford University;

Marcus Feldman, Department of Biology, Stanford University; Yoav Ram, School of Zoology, Tel Aviv University

The diverse linguistic and cultural landscape of Austronesia is crucial for studying the forces that drive and preserve cultural diversity. By analyzing publicly available datasets containing four distinct cultural feature classes within Austronesia, we have identified unique cultural clusters. Our findings reveal significant differences in cultural transmission and distinct patterns of cultural variation within each class that cannot be solely attributed to geographical factors. Additionally, our results support the existence of pulses and pauses in the Austronesian expansion, a west-to-east increase in isolation with justifiable exceptions, and a correlation between linguistic and cultural outliers. These findings highlight the potential for analyzing cultural transmission and variation patterns using methodologies inspired by population genetics.

Talk 15:

Effects of archaic introgression on differential DNA methylation in modern humans

Chen Leibson, Hebrew University of Jerusalem

Maxime Rotival, Institut Pasteur, CNRS UMR2000

Etienne Patin, Institut Pasteur, CNRS UMR2000

Lluis Quintana-Murci, Institut Pasteur, CNRS UMR2000

Liran Carmel, Hebrew University of Jerusalem

Ancient admixture between Homo sapiens and archaic humans such as Neanderthals and Denisovans has left a mark on the genomes of many modern human populations. Natural selection, genetic drift, and possible differences in archaic introgression sources resulted in variability in introgression patterns across individuals and populations. There is increasing evidence to suggest that, in some cases, archaic introgression has had functional consequences in contemporary humans, through their effect on gene regulation. Here, we sought to identify such potential regulatory effects in introgressed loci by searching for differential DNA methylation between individuals carrying the introgressed segment and those who do not carry it. Specifically, we investigate the effect of archaic introgression on DNA methylation in a modern cohort, comprised of a thousand healthy western-European individuals from the Milieu Intérieur (MI) consortium.

As expected, we found similar introgression patterns across the entire cohort. When comparing methylation levels at CpG sites in introgressed and non-introgressed individuals, we identified a set of roughly 13,000 CpG positions that show significant differential methylation between the two groups. These sites are underrepresented in CpG island, exons and promoters, and are primarily located in genes enriched for developmental processes, cardiac muscle activity, and basic cellular functions. Using reconstructed methylation maps, we show that the methylation in the introgressed samples in these sites has a slight tendency for consistency with the methylation in archaic humans. This work provides an epigenetic angle to understanding the outcomes of introgression in contemporary humans.

Talk 16:

The latitudinal phylogenetic gradient is maintained by a tropical-temperate transitional region

David Lerner, Plant and Environmental Science, Weizmann Institue of Science

Tamir Klein, Plant and Environmental Science, Weizmann Institue of Science

Gili Greenbaim, Ecology, Evolution & Behavior, Hebrew University of Jerusalem

The present day distribution of species biodiversity is affected by their evolutionary history and driven by the interplay between macroevolutionary forces such as speciation, extinction and colonization. This evolutionary process has generated several biogeographic patterns that align with global latitude. Although efforts to map diversity patterns have been ongoing for over a century, it is still unclear how evolutionary forces lead to their formation. Here, we study the underlying evolutionary histories leading to the distribution patterns of tree species diversity. By compiling an extensive dataset of tree species distributions and their phylogenetic relationships, we use a data-driven approach to delineate global bioregions of similar evolutionary histories, termed phyloregions. We show that phyloregions generally overlap with the three major ecological regions --- tropical, temperate and boreal/tundra; however, we identify a transitional phyloregion between the tropics and the temperate regions, which we termed 'bridge phyloregion'. We identify that the bridge phyloregion has intermediate phylogenetic clustering, between the niche-conserved tropics and phylogenetically over-dispersed temperate, constituting a `phylogenetic latitudinal gradient', and show, using random-forest predictions, weaker association to climatic and environmental variables in this phyloregion compared to the tropical and temperate phyloregions. To understand how the attributes of the bridge phyloregion affect macroevolutionary processes in the formation of the latitudinal phyloregional gradient, we developed a simplistic modeling framework. We show that the global latitude phylogenetic gradient is much more likely to emerge in the presence of a bridge phyloregion, by facilitating the colonization of species between distinct climatic zones. Furthermore, we show that tropical niche conservatism is not a leading cause for the formation of latitudinal diversity gradients. Our study shows how detailed delineation of evolutionary biodiversity can reveal cryptic regions that have important evolutionary roles in the formation of biodiveristy patterns.

Talk 17:

Saccharomyces cerevisiae cells can utilize reward learning to form new regulatory associations.

Maor Knafo, Biomolecular Sciences, Weizmann Institute of Science

Shahar Rezenman, Biomolecular Sciences, Weizmann Institute of Science) (Reinat Nevo, Biomolecular Sciences, Weizmann Institute of Science

Lior Segev, Physics Core Facilities, Weizmann Institute of Science

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Ziv Reich Biomolecular Sciences, Weizmann Institute of Science

Ruti Kapon, Biomolecular Sciences, Weizmann Institute of Science).

Single-cell organisms constantly face challenges – rapidly changing environments, internal malfunctions, and competition – necessitating swift adaptation. While epigenetic mechanisms facilitate these adaptations, a crucial step remains understudied: integrating newly generated solutions (often from random events) into existing regulatory frameworks. This process of sensing stress, generating a response, and committing it to memory could be formally described as learning, yet it is not typically considered in this context.

We set out to check if the induction of feedback on random events can teach populations to transition a protein from its original function to a new stress-alleviating one by turning a glucose-metabolizing protein into a temperature regulator. For this, we constructed a temperature control system whose setpoint is determined by the expression of a specific glucose-metabolizing protein co-expressed with GFP. We have done so by setting up a stress-alleviating feedback loop whereby the ambient temperature progressively shifts to a more favorable one as more proteins, and subsequently, GFP reporters, are produced. The platform used to conduct this experiment is a microfluidic chip incorporating 1024 chambers, each housing ~300 yeast cells, co-expressing GFP for the feedback and RFP as a control, with both fluorophores originally driven by promoters in the glucose metabolism pathway. After setting an initial aversive temperature (39°C), we transfer temperature control to the automatic system and follow the fluorescence of the population at a single-cell level and the temperature it imposes.

Our findings demonstrate that implementing a reward-based learning approach, where stress alleviation is coupled to specific cellular responses, allows an established function to shift towards a new, stress-responsive role. This process facilitates the formation of an association that allows cells to regulate their environment actively, in this case, temperature. These results shed light on a potential learning-like mechanism employed by single-celled organisms and pave the way for further exploration of how environmental information processing might contribute to the evolution of more complex cellular behaviors.

Talk 18:

Conserved Pathways, Divergent Outcomes: The Roles of VEGF and ERK in Sea Urchin Skeletogenesis and Vertebrate Angiogenesis

Tovah Nehrer, Majed Layous, Tsvia Gildor, Smadar Ben-Tabou de-Leon

University of Haifa, Department of Marine Biology

Co-option is a key concept in evolutionary biology where existing biological structures or functions are adapted for new roles. An excellent example of this is the co-option of an ancestral tubulogenesis program which is broadly used for vascularization in metazoans and coopted for biomineralization in the echinoderm phylum. In vertebrates, this program builds a complex vascular network yet, in echinoderms, this program was repurposed to build their skeletons by depositing minerals into a tubular cavity. This raises the question: What aspects of the original program are retained, and what changes when it is co-opted for new functions? Here we studied the interactions between the vascular endothelial growth factor (VEGF) and the extracellular signal-regulated kinase (ERK) pathways during sea urchin skeletal elongation and compared them to those in vertebrate angiogenesis. In vertebrate angiogenesis, VEGF ligand reception activates the ERK pathway triggering delta-notch receptors at the cell junctions between the tip and stalk cells, promoting vascular sprouting. In sea urchins, VEGF signaling is similarly crucial for skeletal elongation, yet all of the skeletogenic cells are fused into a syncytium, eliminating cell junctions between them. We discovered that similar to angiogenesis, VEGF signaling activates ERK in the cells near the tips of the skeletal rods and this activation is essential for proper skeletal elongation. Moreover, ERK activity promotes skeletal elongation in-vivo despite the lack of a localized VEGF signal. However, unlike vertebrate angiogenesis, sea urchin skeletogenesis does not involve delta-notch receptors. Instead, we found that ERK activity alone directs differentiation at the tips of the growing skeletal rods, upregulating gene expression at the tips while downregulating it in the back. In summary, our findings highlight how conserved signaling pathways can be repurposed to generate diverse structural outcomes, illustrating the evolutionary adaptability of developmental processes.

Talk 19:

The Effects of Habitat Fragmentation on Population Genetic Measures

Ohad Peled, Ecology Evolution and Behavior, The Hebrew University of Jerusalem

Gili Greenbaum, Ecology Evolution and Behavior, The Hebrew University of Jerusalem

The persistence of plant and animal populations in the wild is increasingly at risk. Habitat fragmentation, one of the foremost threats to biodiversity, creates small, isolated, and inbred populations, leading to a reduction in both global and local genetic diversity. Genetic monitoring, which involves tracking genetic attributes of populations over time, is a key method used to understand the impacts of fragmentation on population genetics. However, most existing models have employed simplified spatial structures to explore the genetic outcomes of fragmentation. Here, we integrate concepts and methodologies from network science with mathematical and computational techniques from population genetics to examine the relationship between three matrices: the migration matrix, coalescence matrix, and Fst matrix. We designed a framework for modeling and tracking the genetic measures of heterozygosity and Fst along different types of fragmentation. These scenarios are modeled on realistic anthropogenic activities that lead to sequential habitat loss. Our findings reveal significant differences in the rate of genetic measure changes across types of fragmentation, with most processes being non-linear and some indicating a rapid shift in genetic measures, reflecting a qualitative transformation in the structure of population networks. Furthermore, we demonstrate that traditional population genetic assumptions, such as the strong correlation between genetic differentiation and geographical distance, may alter due to fragmentation. Additionally, our results suggest that genetic monitoring can serve as an early warning system to detect population collapses. This framework enables a more nuanced approach to conservation management, taking into account the complexities of real-world connectivity patterns and aiming to preserve the genetic integrity of wildlife populations.

Talk 20:

How monogenic disorders emerge and disappear in evolution

Simon Fishilevich, Molecular Genetics, Weizmann Institute of Science

Nachshon Egyes, Molecular Genetics, Weizmann Institute of Science

Katharina Lange, Molecular Genetics, Weizmann Institute of Science

Nitzan Haim, Molecular Genetics, Weizmann Institute of Science

Ron Moran, Molecular Cell Biology, Weizmann Institute of Science

Mimi Shwartz, Biomolecular Sciences, Weizmann Institute of Science

Dina Listov, Biomolecular Sciences, Weizmann Institute of Science

Sarel Fleishman, Biomolecular Sciences, Weizmann Institute of Science

Georgii Bazykin, Department of Biomedical Informatics, Harvard Medical School

Lukas Kuderna, Universitat Pompeu Fabra Barcelona

Martin Kuhlwilm, Evolutionary Anthropology, University of Vienna

Tomas Marques-Bonet, Universitat Pompeu Fabra Barcelona

David Gokhman, Molecular Genetics, Weizmann Institute of Science

Humans have evolved several exceptional adaptations, including the three-fold increase in our brain size, the transition to upright walking, and our particularly extended maturation and learning phase. Although these adaptations have been pivotal to our success as a species, they have also propelled the emergence of disorders, including Alzheimer's disease, rheumatoid arthritis, bronchial asthma, carcinomas, and more. These disorders are relatively common in humans, but rare or completely absent in our closest relatives, the great apes. To better understand these diseases, it is essential to investigate them not only from a clinical perspective, but also through the lens of evolution. Combining human clinical data with ape whole genome sequencing provides a great opportunity to detect a particularly interesting scenario, where a disease-causing mutation in humans is in fact a reversion to the wildtype ancestral ape allele. This suggests that in apes, who still carry the ancestral allele, there are likely other mechanisms that compensate for the potential deleterious effect of the disease. Here, we leverage databases of human disease-causing mutations and great ape genomes, to generate a catalog of mutations which are disease-causing in humans, but are benign in apes. For each identified mutation, we study the disease mechanism to understand which compensatory mechanisms prevent the disease in apes, such as a paralog gene or an upregulated pathway. Further, we systematically study the shared characteristics of these genes, to understand which genes, pathways and mutation types are more susceptible to human-specific diseases and what could explain the susceptibility and the compensation. This work sheds light on the mechanisms propelling the emergence of human-specific diseases, and the possible compensatory mechanisms attenuating disease deleteriousness.

Talk 21:

Eye reduction in cave spiders: Retinal Determination Gene Network dynamics in cave Tegenaria Latreille, 1804 (Araneae: Agelenidae) spider embryos.

Evgenia Propistsova, The Department of Ecology, Evolution and Behaviour, The Hebrew University of Jerusalem

Ariel Chipman, The Department of Ecology, Evolution and Behaviour, The National Natural History Collections, The Hebrew University of Jerusalem

Prashant Sharma, Department of Integrative Biology, University of Wisconsin-Madison

Efrat Gavish-Regev, The National Natural History Collections, The Hebrew University of Jerusalem

The Retinal Determination Gene Network (RDGN) controls the process of retinal development in various vertebrate and invertebrate eyes including several spider species, such as Cupiennius salei Keyserling, 1877 and Parasteatoda tepidariorum (C. L. Koch, 1841). Functional data for the gene copy soA (sine oculis 1) have shown that it's involved in patterning both principal and secondary eyes in the spider P. tepidariorum and possibly in many other arachnids. Yet, several aspects of this network remain unexplored, including the genes initiating eye formation during embryogenesis and those specifying eye fate in spiders. Species of the genus Tegenaria Latreille, 1804 inhabit caves and present varying degrees of eye development from fully formed eyes to a complete loss of eyes. This makes Tegenaria a good model genus for studying eye loss in cave spiders. In our study, using HCR, we investigated embryonic gene expression in the eye-bearing species Tegenaria pagana C. L. Koch, 1840 and eye-reduced Tegenaria yaaranford Aharon & Gavish-Regev, 2023 in different developmental stages. According to our preliminary data, eye-reduced species lack atonal 1 and sine oculis 1 genes expression in all eye types in later stages of development and Pax2.1 expression in principal eyes comparing to eye-bearing species T. pagana. Our data support the hypothesis of a significant role of sine oculis 1 in the formation and loss of eyes in cave arachnids.

Talk 22:

Reversion to metabolic autonomy underpins evolutionary rescue in a bacterial obligate mutualism

Jonathan Friedman, Institute of Environmental Sciences, Hebrew University

Ignacio Melero-Jiménez, Institute of Environmental Sciences, Hebrew University

Yael Sorokin, Institute of Environmental Sciences, Hebrew University

Ami Merlin, Institute of Environmental Sciences, Hebrew University

Alejandro Couce, Centro de Biotecnología y Genómica de Plantas, Universidad Politécnica de Madrid

Populations facing lethal environmental change can avoid extinction by undergoing rapid genetic adaptation, a phenomenon termed evolutionary rescue. Despite much theoretical and empirical research, evolutionary rescue in the context of communities remains poorly understood, especially in mutualistic ones, where survival is constrained by the less adaptable partner. Here, we explored empirically the likelihood, population dynamics, and genetic mechanisms underpinning evolutionary rescue in an obligate mutualism mediated by reciprocal amino acid exchange in Escherichia coli. We observed that >80% of the communities avoided extinction when exposed to two different types of lethal stresses. Of note, only one of the partners survived in all these cases. Genetic and phenotypic analyses show that the survivor reverted to autonomy by metabolically bypassing the auxotrophy, with little evidence of specific adaptation to the stressors. Crucially, we found that the mutualistic partners were more sensitive to both stresses than prototrophs, so that reversion to autonomy was sufficient to alleviate stress below lethal levels. We observed this increased sensitivity across several other stresses, suggesting that this may be a general property of obligate mutualisms mediated by amino acid exchange. Our results reveal that evolutionary rescue critically depends on the specific genetic and physiological details of the interacting partners, adding rich layers of complexity to the endeavor of predicting microbial community resilience under intense environmental deterioration.

Talk 23:

Combined use of gene drives and pesticides to minimize spillover risk

Sviatoslav R. Rybnikov, Department of Ecology, Evolution & Behavior, Faculty of Science, the Hebrew University of Jerusalem; Institute of Environmental Sciences, the Robert H. Smith Faculty of Agriculture, Food and Environment, the Hebrew University of Jerusalem;

Gili Greenbaum, Department of Ecology, Evolution & Behavior, Faculty of Science, the Hebrew University of Jerusalem;

Adam Lampert, Institute of Environmental Sciences, the Robert H. Smith Faculty of Agriculture, Food and Environment, the Hebrew University of Jerusalem;

Gene drives are artificial genetic constructs capable of rapid propagation in a population due to violation of the standard Mendelian inheritance. Suppression gene drives (those reducing viability and/or reproductive success of their bearers) are believed to become a potent novel biocontrol method, e.g., in combating vector-borne diseases like malaria. However, gene drive alleles may spill over into non-target populations, and this crucial safety concern hinders the development and deployment of the technology. Here, we explore the potential of using gene drives in combination with pesticides, a traditional biocontrol method, to minimize spillover risk. We consider standard suppression gene drives, whose genetic configuration ensures their rapid (~20 generations) spread from rarity to fixation and further extinction of the population due to a negative growth rate of gene drive carriers. We develop an optimal control model to identify the treatment strategy that minimizes the net costs over time, including both the cost of spillover and the cost of pesticide application. We show that, for a given gene drive configuration, the optimal strategy depends on the ratio between the per unit costs of these two types. If the per unit cost of spillover is below a certain threshold, pesticides appear inefficient during the first several generations, while gene drive alleles are still rare and the population recovers quickly, and should therefore be postponed. In contrast, if the per unit cost of spillover exceeds that threshold, pesticides should be used immediately. In both cases, pesticide application should be stopped once the gene drive alleles become abundant enough to govern rapid population eradication by themselves. Our analysis provides a calibration curve that allows estimating the cumulative spillover risk achievable with an available budget for the pesticide treatment.

Talk 24:

Multiple mechanisms to eliminate enhancer function during morphological evolution

Areej Said Ahmad, Noa Shimron, Ela Fainitsky and Ella Preger-Ben Noon.

Department of Genetics and Developmental Biology, The Rappaport Faculty of Medicine and Research Institute, Technion-Israel Institute of Technology, Haifa, Israel

The loss of morphological features or entire organs has occurred repeatedly throughout evolutionary history of life, often driven by sequence changes in tissue-specific enhancers of key developmental genes. Previous studies have mainly focused on the evolution of single enhancers, demonstrating how changes in a single element can lead to loss of gene expression in specific developmental domains. However, many developmental genes possess multiple enhancers with redundant functions, ensuring robust gene expression despite genetic or environmental challenges. How this inherent robustness is overcome to evolve new phenotypes remains unclear, especially as there are few examples of the loss of function across multiple enhancers.

Here, we address these issues by studying the evolved enhancers of the Drosophila shavenbaby gene. Shavenbaby encodes a transcription factor that controls the development of cuticular hair-like projections called trichomes. Trichome patterns have repeatedly evolved in the larvae of the genus Drosophila through changes in the shavenbaby regulatory regions. For example, D. sechellia, a sister species to D. melanogaster, evolved naked larvae through the loss of function of four embryonic enhancers of shavenbaby. We reveal that each of these enhancers lost its activity through distinct mechanisms. Specifically, a 120-nucleotide deletion in the D. sechellia Z1.3 enhancer eliminated most of its embryonic activity. In contrast, the D. sechellia E6, DG2 and A enhancers evolved reduced activities through the accumulation of single nucleotide substitutions that affected transcription factor binding sites. While the E6 enhancer evolved through the loss of activator binding sites and the gain of a binding site for a strong repressor, the DG2 enhancer evolved through loss of activator binding sites, which compromised enhancer robustness to conserved repression, and the A enhancer evolved through the acquisition of long-range repression.

These findings provide new insights into the diverse molecular mechanisms by which redundant enhancer functions are bypassed, contributing to the evolution of novel morphological traits.

Talk 25:

Strategies for mining useful alleles for climate change adaptation

Ayelet Salman-Minkov, Evolution and Ecology; Plant Sciences, UC Davis.

Daniel Runcie, Plant Sciences, UC Davis.

Jeffery Ross-Ibarra, Evolution and Ecology, UC Davis.

Climate change and global warming pose significant challenges to future food security, as elite lines of major crop species are susceptible to heat and drought. A potential solution may lie within traditional varieties. Cultivated by local farmers worldwide for hundreds to thousands of years, traditional varieties possess adaptations to diverse climatic conditions. We would like to leverage these adaptations, identify alleles beneficial in future environments, and integrate them into the elite lines of crop species.

Our objective is to determine the most effective strategy for identifying and incorporating valuable alleles into elite lines, utilizing both geo-referenced and genomic data. To represent diverse, realistic genetic architectures, we utilize simulated genomic data representing populations evolving across various demographies and landscapes. We evaluate three breeding approaches: 1) environmental GWAS (envGWAS) followed by marker-assisted selection (MAS), 2) genomic prediction of local adaptation combined with QTL mapping in a simulated future environment followed by MAS, and 3) genomic prediction of local adaptation combined with genomic selection in a simulated future environment. We anticipated that the envGWAS approach would be effective when there are common alleles with large-effect sizes, but the QTL mapping approach might be more effective when the population has many large-effect alleles, but all are rare. We found that the envGWAS approach was rarely better than the alternatives, while the QTL approach was best in nearly 50% of scenarios, regardless of genetic architecture. This suggests that the QTL approach may be the preferred choice for mining beneficial alleles.

Talk 26:

Data-driven Approach to Antibiotic Discovery

Saar Shoer, Department of Computer Science and Applied Mathematics, The Weizmann Institute of Science

Yitzhak Pilpel, Department of Molecular Genetics, The Weizmann Institute of Science

Eran Segal, Department of Computer Science and Applied Mathematics, The Weizmann Institute of Science

Antibiotics played a pivotal role in transforming human health by providing a powerful tool to combat bacterial infections. Nevertheless, the emergence and spread of antibiotic resistance among bacterial populations pose substantial challenges. We developed a method to conduct Genome-Wide Association Study (GWAS) in bacteria. The unique nature of bacterial genetics poses new analytic challenges that have not been resolved by previous GWASs. For example, we have to deal with a much more complex population structure than in humans. By conducting GWAS on bacterial abundance, we learn about species' evolution and ecology. In this process, models are generated to predict which of the billions of bacterial Single Nucleotide Polymorphisms (SNPs) have a significant effect on bacterial growth, in cohorts of thousands of individuals from Israel and the Netherlands. This effect can then be validated experimentally and utilized for the development of new probiotic and antibiotic treatments. Our results suggest species carry genetic variations that are beneficial for themselves and harmful to other species, resonating with evolutionary theories. As an example, we find variations in ribosomal, cell wall and membrane proteins that facilitate antibiotic resistances.

Talk 27:

DNA Methylation Meets Codon Usage: Exploring the Evolutionary Dynamics of CpG Codon Associations

Eran Tauber, Department of Evolutionary and Environmental Biology and Institute of Evolution, University of Haifa

Leo Creasey, Department of Evolutionary and Environmental Biology and Institute of Evolution, University of Haifa

While research on CpG sites the targets of DNA methylation has traditionally concentrated on non-coding regions, especially promoter regions, recent studies suggest that methylation within coding regions may also play a crucial role. This study examined the occurrence of codon pairs (NNC-GNN) forming CpG sites. Through a comprehensive analysis of 261 orthologous genes from eutherian mammals, we investigated the distribution and conservation of these CpG codon dyads. Genes exhibiting a high density of CpG codon dyads were found to be associated with homeobox domains and RNA polymerase II transcription factors while those with a low density were associated with DNA damage repair and mitosis. Our findings indicate a bias towards the start of the coding sequence in the distribution of CpG codons (NCG) and codon dyads (NNC-GNN). Notably an increase in the presence of CpG-containing genes during embryonic development suggests their involvement in gene regulation at critical developmental stages. Analysis of DNA methylation sequencing datasets revealed that a significant number of CpG codon dyads undergo methylation. Phylogenetic analysis uncovered intriguing evidence suggesting that the frequency of CpG dyads is influenced by the evolutionary relationships among mammalian orders. We highlight the functional significance of CpG codon dyads in DNA methylation and gene expression emphasizing their coevolution with consecutive codons and their impact on codon usage bias.

Talk 28:

Comparing the use of alternative splicing between human and mouse immune cells

Hadas Ner-Gaon, Tal Shay

Department of Life Sciences, Ben-Gurion University of the Negev, Beer-Sheva, Israel

Mouse is the most common model organism in biology in general and in immunology in particular. The genomes of the human and the mouse share a lot of similarities and orthologous genes between the human and the mouse have been defined. However, orthology at the level of exons, transcripts and junctions is not well defined, and the use of alternative splicing events in similar cell types has not been compared between the species.

A mapping of one-to-one orthologous exons and junctions was done between human and mouse. Based on this mapping, the ratio of the use of orthologous alternative splicing events was compared between human and mouse immune cells.

Of the 3,144 human-mouse orthologous alternative splicing events, ~500 events are expressed in human and mouse immune cells. Surprisingly, many of those events displayed significantly different use ratio between human and mouse.

Mapping alternative splicing events between human and mouse and identifying differences in the use ratio of alternative splicing events in immune cells between both species allows us to identify changes in protein functionality between the species.

Talk 29:

The evolution of the RNA editing enzyme, ADAR, is dictated by core body temperatures

Erez Levanon, Adi Avram-Shperling, Kobi Shipra, , Renana Drummer, Itamar Twersky, Shay ben-Aroya, Eli Eisenberg

RNA editing alters genetic information at the RNA-level. The most common type of RNA editing is the conversion of adenosine (A) to guanosine (G), which can lead to protein diversification beyond the genomic DNA blueprint. A-to-G editing is catalyzed by members of the highly conserved ADAR protein family. ADARs substrate recognition mainly depends on a duplex RNA secondary structure surrounding the target adenosine, which is recognized by ADARs' dsRNA Binding Domains. dsRNA secondary structure is affected by the ambient temperature, as one generally expects tighter dsRNA structures at lower temperatures. Thus, editing is expected to depend on temperature. Accordingly, maintaining editing at the desired level may require adaptation of the editing substrate to the ambient temperature through mutations that modify the RNA structure stability. In parallel, homoeothermic species could also adapt the editing enzymes to their body temperature, changing their dsRNA binding and the catalytic activity to compensate for inter-species differences in body temperatures. We therefore suggest that species that evolved to live with higher core body temperatures have developed ADAR enzymes that target weaker dsRNA structures and would, therefore, be more potent than other ADARs (compared at equal temperatures). To explore this hypothesis, we used the baker yeast Saccharomyces cerevisiae as an editing-naïve system. We exogenously expressed a range of heterologous ADARs and identified the hummingbird and primarily mallard-duck ADARs, which evolved at 40–42°C, as two exceptionally potent editors. Our results indicate that species that evolved to live with higher core body temperatures have developed ADAR enzymes that target weaker dsRNA structures and would, therefore, be more effective than other ADARs. Such potent ADAR enzymes cam also serve as a starting point for the development of novel base editors technologies.

Talk 30:

The links between a cultural foraging tradition and problem solving abilities in black rats

Natasha Shpoliansky, Alex Dorfman, Pazit Zadicario, Noa Truskanov

Cultural traditions can lead to the preservation of useful skills in natural populations. It is often suggested that such traditions are associated with enhanced cognitive capacities. Intraspecific comparisons of individuals from different knowledge backgrounds can shed light on this claim, but such comparisons are rarely feasible. Here, we focus on a tradition that occurs in black rats (Rattus rattus) and involves the transmission of an efficient extractive foraging technique termed pinecone-opening. We tested individuals from pine tree habitats that exhibit the pinecone-opening technique, and naive rats lacking this skill in a battery of tests. We hypothesized that pinecone-opening rats would be better at solving unfamiliar foraging problems and more capable of delaying rewards (an ability that was previously suggested to be important for learning this skill). Our preliminary findings revealed a non-significant trend according to which rats with prior experience in opening pinecones performed better in a novel extractive-foraging task. Conversely, there are no differences at the delaying rewards task. Our findings suggest that previous knowledge in extractive foraging, might come in handy while encountering novel problems, but could affect on other abilities. These results highlight the complexity of the links between cultural and cognitive evolution in animals.

Talk 31:

Molecular Phylogeny of Kalanchoe (Crassulaceae subfam. Kalanchooideae) and the Evolution of Asexual Reproduction

Ronen Shtein, School of Plant Sciences and Food Security, Tel Aviv University

David-Paul Klein, Albrecht Daniel Thaer-Institute of Agricultural and Horticultural Sciences, Humboldt University of Berlin

Claudia Simon, Systematik, Biodiversität & Evolution der Pflanzen, Ludwig-Maximilians Universität München

Gudrun Kadereit, Systematik, Biodiversität & Evolution der Pflanzen, Ludwig-Maximilians Universität München

Tal Pupko, The Shmunis School of Biomedicine and Cancer Research, Tel Aviv University

Itay Mayrose, School of Plant Sciences and Food Security, Tel Aviv University

Dorothée Huchon, The Steinhardt Museum of Natural History, and School of Zoology, Tel Aviv University

Kalanchoe is one of the largest genera in Crassulaceae, containing nearly 200 described species. Most species are Malagasy endemics, while others are from continental Africa and parts of Asia. Kalanchoe species exhibit great morphological diversity and occupy a variety of ecological habitats. Moreover, species in this clade exhibit several distinct asexual reproduction modes, each at various degrees of complexity and specialization. Several species gained significant economic importance in the horticultural industry, while others serve as a model for Crassulacean Acid Metabolism photosynthesis, invasion biology, and medical research. Yet, a stable classification for Kalanchoe has been lacking and the evolution of traits such as different asexual reproduction modes remains unexplored. In this work, we provide the most up-to-date phylogeny of this genus, based on whole genome raw read sequencing, plastomes, and internal transcribed spacer (ITS) data for 30, 34, and 161 taxa, respectively. The resulting nuclear, plastome and ITS trees are not fully congruent, suggestive of ancient hybridization events. Additionally, these reconstructions allowed us to examine the evolution of asexual reproduction in this clade. Four modes of asexual reproduction, which are virtually unique to the genus, are recovered as derived traits, appearing in four distinct monophyletic Malagasy lineages, while other forms are plesiomorphic or arose convergently. Reversals in specialization degree in one mode could be attributed to a tradeoff between asexual and sexual reproductive success. Further, our biogeography analysis support Madagascar as the origin of Kalanchoe, with a single dispersal event out of Madagascar, and possibly two events into Asia.

Talk 32:

Evolutionary developmental studies of chitin synthases in the sea anemone Nematostella - hints to unexpected ancient roles for chitin

Uri Gat, Life Sciences Institute, Hebrew University

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The sea anemone Nematostella vectensis (Nv) is a basal cnidarian animal model, a close sister clade to bilaterian animals. Our studies aim to elucidate the origin of gene families that are important to establishing the body structure of Nv during its development and upon whole body regeneration (WBR). The evolutionary relation between the body structure and shape of cnidarians and bilaterians is not clear as well as the remarkable WBR process in cnidarians and its relation to embryonic development.

In order to investigate the WBR process in Nv, we performed a transcriptional screen, in which we defined the genes which respond in their expression pattern during the time course of regeneration. Besides well-known developmental pathways that were previously shown to regulate these processes such as the Wnt pathway, surprisingly, one of the most conspicuous differentially expressed groups were chitin related genes. Thus, we defined the chitin synthase (CHS) genes and mapped three paralogues on Nv chromosome 3.

The expression patterns of the CHS genes were explored on mature Nv polyps body parts as well as along the developmental and WBR time courses. CHS genes are dynamically expressed and do not display an expression pattern consistent only with a structural role in the animals' body wall. Chitin staining revealed a unique population of positive cells starting from the mid larva stage which eventually populate the mesenteries (inner tissue folds) of the polyps. This data together with evidence from the recent single cell Nv RNA-Seq project suggest a cell labelling and branding function which we can hypothesize to represent a more ancient role for chitin which may have remained in cnidarian animals but does not occur or was undetected in bilaterians.

Talk 33:

Sperm characteristics reveal rock hyrax mating tactics

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Reproduction in males has been linked to testosterone levels, which are related to morphological, physiological, and behavioral features, including social status and roles. However, variance in reproductive parameters such as sperm characteristics and testosterone, also plays a pivotal role in shaping mating tactics, including the development of alternative reproductive tactics and sperm competition, leading to diverging life-histories. In the polygynandrous rock hyrax (Procavia capensis), there are three male classes: residents, bachelors, and late-dispersers. Across three field seasons we obtained sperm and hair samples pre and post the breeding season from males and found that although there were no differences in copulation success between bachelor and resident males, sperm motility decreased and structural mutations increased post breeding only in residents. We also found that whereas residents with higher testosterone levels had lower sperm quality, in bachelors it was the opposite. Our findings shed light on the diverse mechanisms and trade-offs that are available for male rock hyrax adopting different reproductive tactics and enhance our understanding of the evolutionary forces that drive sperm competition.

Talk 34:

Driven by glacial cycles: speciation, diversification, and dispersal of Coryphella nudibranchs across the Northern Hemisphere.

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Nudibranch mollusks from genus Coryphella are widely distributed and species-rich gastropod group lacking fossil record and displaying a complex distribution across both Southern and Northern hemispheres. Our study has facilitated the development of detailed hypotheses on the evolutionary history of the genus Coryphella, which has proven to be more complex and intricate than previously thought. We estimated of divergence times between species, an ancestral distribution, and population structure of widely distributed trans-Arctic species Coryphella verrucosa to investigate the evolution, phylogeographic patterns and reconstruct possible historical routes of oceanic dispersal. Working with a larger sample size and five molecular markers (COI, 16S, H3, 28S and 18S) we revealed a complex evolutionary history of Coryphella, shaped by transgression, vicariance, and dietary shifts, and overall driven by the pervasive effect of glacial cycles. We also revealed the presence of previously undetected cryptic diversity, which suggests that further sampling may produce additional species discovery in this group of nudibranchs. Divergence estimation indicates the genus Coryphella originates in the middle Miocene in the Pacific Ocean and the early divergence within this group also occurred in different regions of the North Pacific. The ancestral area reconstruction inferred five independent instances of transgression from the Pacific Ocean to the Atlantic via different migration routes, including the Panamanian seaway and the Bering Strait. Among them, we identified three cases of successful transition to the Arctic waters from the North Pacific via the Bering Strait, associated with interglacial conditions of middle Pleistocene. Consequently, Pleistocene glacial cycles likely prompted pulses of boreal faunal elements to disperse southwards followed by range disjunction and temporary isolation of distant populations and resulting in allopatric speciation. Evidence from the population structure of contemporary trans-Arctic species suggests an independent recolonization pathways of Arctic waters from both southernly and northern refugia after the Last Glacial Maximum.

Talk 35:

Genetic History of an isolated tribe of India with an unexpected link with Africa

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South Asia has several isolated tribal populations which are still practicing hunting-gathering lifestyles. Studying such isolated tribal populations may help to understand the genomic architecture of ancient hunting-gathering populations. Therefore, in our quest to find the ancient genomic signatures of these hunter-gatherers, we have analyzed an isolated tribal population living in the Southern Indian State of Karnataka. Our extensive cultural expedition revealed that this population live in remote, and isolated regions maintaining their social and cultural isolation. We have genotyped over half a million autosomal markers for this population to deduce its intra and inter-population history. To our surprise, we observed a significant ~5% of African ancestry among Koraga tribal populations. Our further investigation revealed substantial gene flow from the Siddi population, who lived apart at a distance of nearly 400 km. The haplotype-based analyses suggested that the Koraga population received large amounts of genomic chunks from the Siddi population and made a tight cluster with them. Thus, in spite of the fact that strict endogamy is omnipresent in South Asia, porosity is more common among tribals than the caste populations.

Talk 36:

The role of aneuploidy in the evolution of cancer drug resistance

Remus Stana, School of Zoology, Faculty of Life Sciences, Tel Aviv University

Uri Ben-David, Department of Human Molecular Genetics and Biochemistry, Faculty of Medicine, Tel Aviv University

Daniel B. Weissman, Department of Physics, Emory University

Yoav Ram, School of Zoology, Faculty of Life Sciences, Tel Aviv University

Evolutionary rescue is the process by which a population is able to survive a sudden environmental change which initially causes the population to decline towards extinction. A prime example of evolutionary rescue is the ability of cancer to survive being exposed to various treatments. We are interested in the mechanisms through which a population of cancer cells are able to adapt to chemotherapy, and in particular, the role played by chromosomal instability (aneuploidy). Cancer cells which have aneuploidy are hypothesized to have a higher fitness in an environment altered by anti-cancer drugs as they have incomplete pathways which drugs activate in order to kill the cells. Aneuploidy is highly prevalent in tumours and certain drugs which attempt to combat cancers through increasing chromosomal instability. As a result, the question we wish to answer is how aneuploidy impacts the fate of the population of cancer cells. We propose to model evolutionary rescue with the help of multi-type branching processes to obtain the probability that cancer will survive.

Talk 37:

Long-distance mimicry: when might allopatric species share aposematic signals?

Akiva Topper, Yotam Ben-Oren, Oren Kolodny

Department of Ecology, Evolution & Behavior, The Hebrew University of Jerusalem

The establishment of an aposematic signal such that predators avoid it often renders it beneficial for other species to display the same signal, in a phenomenon known as mimicry. A recurring assumption in mimicry theory is that all species participating in a mimicry system must be sympatric. This is because the predator must encounter both model and mimic, in Batesian mimicry, or all co-mimics, in Müllerian mimicry, in order to confuse them. While it has been suggested that mimicry may occur between allopatric species through the mediation of migratory predators, this possibility has remained unexplored both theoretically and empirically. As a first step towards exploring this matter theoretically, we used computer simulations to model the population dynamics expected to occur in the relatively simple scenario of two populations of unprofitable aposematic prey connected by migratory predators. Each population in the simulation is affected by both local predators, which do not migrate and are therefore not directly affected by the foreign signal, and by migratory predators, which are affected by the signals in both populations. We demonstrate that while local predators select against the establishment of allopatric mimicry, migratory predators may be sufficient to drive the evolution of allopatric mimicry in certain conditions. The idea of mimicry occurring between allopatric species opens up the possibility for numerous long-distance interactions between species, of which we may be completely unaware, and highlights the importance of exploring this matter further, both theoretically and empirically.

Talk 38:

Cuticle biomineralization in the moulting cycle in selected arthropod species

Olga Volovych, The Department of Ecology, Evolution and Behavior, The Alexander Silberman Institute of Life Sciences

Ariel D. Chipman, The Department of Ecology, Evolution and Behavior, The Alexander Silberman Institute of Life Sciences

Reinforcement of the cuticle with minerals is widely reported across the arthropods. A shining example is the incorporation of calcium as an indispensable step of cuticle maturation in crustaceans. In addition to calcium, several other inorganic elements are notably concentrated in the mouthparts, as observed in spiders, scorpions, and ants. It is hypothesized that these elements, such as zinc and copper, enhance the properties of the cuticle, imparting it with increased hardness. The elemental composition of other arthropod groups remains poorly understood. Additionally, the fate of many incorporated minerals during the moulting cycle is still unspecified for all arthropods. For this study, we selected representatives of three arthropod subphyla, Chelicerata, Myriapoda, and Crustacea, to explore the elemental composition of the cuticle with special attention to mouth appendages. For this analysis we selected three species: Scutigera coleoptrata (Myriapoda), Holocnemus pluchei (Chelicerata), and Porcellionides pruinosus (Crustacea). Analytical HR-SEM with elemental mapping was performed on individuals during intermoult and on shed exuviae. The cuticle of S. coleoptrata showed little to no mineralization. Trace metals, such as sulfur, calcium, chlorine, phosphorus, and magnesium in sum comprise less than 1 atomic % across the entire body. The mouth appendages have a negligible quantity of copper, without specific localization patterns. Similarly, the cuticle of H. pluchei has a low atomic % of elemental abundance except for the chelicerae fang, which contains up to 20 atomic % of zinc. The cuticle of P. pruinosus is heavily calcified cuticle typical for crustacean species. Other elements, such as magnesium, phosphorus, sulfur, and chlorine comprise less than 5 atomic % combined. The mouth apparatus doesn't show any other elements, stiffness is achieved through calcification agents alone. Finally, an elaborate comparison with the data from the exuvia allows us to reveal the element reabsorption events that occur in preparation for ecdysis.

Talk 39:

Mapping genotypes of microbial cooperation

Shu-Ting You1, Ruthie Golomb1, Dvir Schirman2, Gabriela Lobinska3, Orna Dahan1, Yitzhak Pilpel1

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Cooperation introduces complexities into microbial evolution. In the absence of cooperation, individuals focus solely on their own survival. Conversely, cooperative individuals invest in the well-being of the community, often at their own expense. Cheaters, who exploit the communal benefits without contributing, pose a significant threat to both cooperators and the community. Despite this, cooperation remains prevalent in nature. Traditional studies often use a binary YES/NO approach to measure cooperation, typically based on the secretion of public good proteins. However, cooperative strategies can vary continuously due to the regulation of protein production and secretion. Our lab has co-discovered a cis-regulatory mRNA motif involved in protein secretion, termed SECReTE. In this study, we examine SECReTE alongside Signal Peptide (SP) motifs to better understand the genetic basis of cooperation. We created two synthetic yeast libraries, each containing thousands of variants of these motifs, to investigate their effects on the secretion of Suc2, a well-characterized public good protein. After 60 generations of competition, both libraries showed a reduction in Suc2 secretion capacity, indicating a decreased ability for nutrient utilization. Notably, cooperator sub-populations, including SUC2 synonymous mutants and SUC2 wild-type variants in the SP library, increased in prevalence during competition. This suggests that these cooperator sub-populations may help sustain the community when nutrient availability decreases, highlighting the role of dynamic community composition in the survival of cooperative groups. Additionally, by examining thousands of SECReTE sequence variants, we identified specific RNA localization patterns for SUC2 mRNA. Our findings indicate that the localization of RNA to the ER negatively correlates with its stability and translation efficiency. We are currently investigating how these new sequence features relate to secretion behaviors and competitive success.

Talk 40:

Escherichia coli adaptation under prolonged resource exhaustion is characterized by extreme parallelism and frequent historical contingency

Shira Zion, Rapport Family Faculty of Medicine, Technion - Israel Institute of Technology

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Like many other non-sporulating bacterial species, Escherichia coli is able to survive prolonged periods of resource exhaustion, by entering a state of growth called long-term stationary phase (LTSP). In July 2015, we initiated a set of evolutionary experiments aimed at characterizing the dynamics of E. coli adaptation under LTSP. In these experiments populations of E. coli were allowed to initially grow on fresh rich media, but were not provided with any new external growth resources since their establishment. Utilizing whole genome sequencing data obtained for hundreds of clones sampled at 12 time points spanning the first six years of these experiments, we reveal several novel aspects of the dynamics of adaptation. First, we show that E. coli continuously adapts genetically, up to six years under resource exhaustion, through the highly convergent accumulation of mutations. We further show that upon entry into LTSP, long-lasting lineages are established. This lineage structure is in itself convergent, with similar lineages arising across independently evolving populations. The high parallelism with which adaptations occur under LTSP, combined with the LTSP populations' lineage structure, enable us to screen for pairs of loci displaying a significant association in the occurrence of mutations, suggestive of a historical contingency. We find that such associations are highly frequent and that a third of convergently mutated loci are involved in at least one such association. Combined our results demonstrate that LTSP adaptation is characterized by remarkably high parallelism and frequent historical contingency.

Poster 1:

The Collective Posterior Distribution and Its Application in Simulation-Based Inference from Highly Variable Experimental Replicates

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Bayesian inference produces a posterior distribution over model parameters, which is the probability of model parameters θ given an observation X, P(θ|X). However, when a collection of observations is assumed to arrive from the same distribution, such as in repeated biological experiments, we are provided with more information that could be used for collective conclusions. Given a model, we could use an axiomatic approach to form P(θ|X_1,...,X_n), a collective posterior distribution for model parameters θ, conditioned on the entire collection of observations X_1,...,X_n. In this project, we used a state-of-the-art neural-network simulation-based inference algorithm, Neural Posterior Estimation, to estimate the posterior distribution of experimental evolutionary observations. The data consists of time series describing the proportion of adaptive mutants in yeast populations of four different genetic backgrounds (28 series total) in a nutrient-limited environment over 116 generations. We then implemented and applied the collective posterior distribution to each genetic background, leading to a between-group comparison that considers the high within-group variance that is exhibited in repeated evolutionary experiments. Our results demonstrate the potential of the collective posterior distribution in Bayesian inference from repeated biological experiments.

Poster 2:

Counterintuitive population genetic patterns across levels of habitat fragmentation

Keren Klass, HUJI

Forest loss and fragmentation can alter dispersal patterns, which may lead to small, isolated, genetically depauperate animal populations at risk of extirpation. We examined whether gene flow and population genetics of endangered black howler monkeys (Alouatta pigra) inhabiting a landscape with increasing levels of forest fragmentation conformed to the predictions of the common theoretical paradigm, that increasing fragmentation leads to a reduction in dispersal across the matrix, gene flow, and local genetic diversity; and an increase in inbreeding and population genetic structure. We extracted host-enriched fecal DNA from 158 monkeys sampled from 37 forest fragments and Palenque National Park (fragments=130, PNP=28) and generated a dataset of 9,567 SNPs using ddRAD sequencing. Observed heterozygosity was higher in the fragments than in PNP, while inbreeding was lower. Population structure analyses clearly showed PNP forming one cluster, while the fragmented forest showed more genetic structure in the southern, less fragmented area, and more admixture with less discernible structure in the northern, more fragmented area. EEMS-derived maps of spatial variation in gene flow showed higher gene flow in the northern part of the fragmented landscape, and lower gene flow in and around PNP. Contrary to the theoretical paradigm that habitat fragmentation restricts movement and creates isolated sub-populations, our results showed that increasing levels of forest fragmentation force black howlers to move through the landscape more, not less. Black howlers may prefer to remain and reproduce in larger, higher-quality forest patches when possible (i.e., PNP and to a lesser extent the fragments in the southern part of the study area), whereas individuals in small, more isolated fragments (i.e., fragments in the northern area) are obliged to disperse across the matrix to seek reproductive opportunities. Our results highlight the complex behavioral and genetic consequences of forest fragmentation for arboreal primates.

Poster 3:

The interaction of population size and species' drift in a simple niche-partitioning model offers a new explanation for biodiversity-productivity relationships

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Philip Lazos, Sapienza University of Rome

Prof. Amos Korman, Department of Computer Science, University of Haifa

Prof. Yossi Yovel, Department of Neurobiology, Tel-Aviv University

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Niche partitioning among species is a fundamental organizing principle of ecological communities and is a powerful perspective for explaining species' richness in them: species that compete for a very similar niche cannot stably co-exist, as opposed to species whose niches are separate, even if partially overlapping. How different must two species' characteristics be, i.e. how much niche separation is necessary, to allow co-existence? We explore this question in a simple model of population dynamics and find that the answer depends on the characteristic sizes of the species' populations, dictated by the available resources. When populations are large, the impact of stochastic processes is diminished, and even slight niche differences between similar species result in coexistence. When populations are small, species' drift takes place among species that occupy similar niches, leading to recurrent extinctions and to reduced species' richness. This offers a new explanation to the unresolved empirical link between species' richness and bioproductivity.

Poster 4:

Seed dispersal strategies in response to environmental stress

M. Binder, E. Zinger, B. Bashir, L. Hadany, N. Ohad

Sessile organisms such as plants disperse their offspring through seeds, spores, pollen, or other reproductive units away from the parent organism. This process is crucial for the survival and proliferation of plants, as it allows them to colonize new habitats, reduce competition with parent and sibling plants, and maintain genetic diversity. According to Fitness Associated Dispersal (FAD) theory, less fit individuals are expected to disperse further in comparison with fitter individuals. Dispersal will allow the individual's genes to escape the mal environment as well as their mal genotype (through outcrossing with less related individuals). Lamium amplexicaule is a cleistogamic annual herb, that can generate two types of flowers simultaneously: Chasmogamic flowers (CH) are open and allow cross pollination, and Cleistogamic flowers (CL) are smaller, with a closed petal structure, and perform only self-pollination. Plasticity in cleistogamy rates enables variation in pollen dispersal, as only CH flowers allow it. We present results regarding the dispersal strategies of L. amplexicaule plants under two growth treatments: Salt stress population, and Control Non-stress population. Each population was under one irrigation regimen (stress/nonstress) for a duration of two generations. The results presented here focus on F2 seed traits, and their association with F1 reproduction strategy (CH vs. CL). Our results show that F2 seeds produced under stress are lighter, longer, and less covered, with smaller Eliosomes compared to the control, thus more adapted for dispersal. In addition, the parent plant CH rate was negatively correlated with seed size and cover percentage. We also found that under stress, heavier seeds were later to sprout, and developed into selfing plants, which produced wider, more covered seeds. Dispersal is a fundamental aspect of ecology and evolution. Understanding dispersal dynamics is critical for conservation biology, as it helps in predicting how species will respond to environmental changes, habitat fragmentation, and climate change.

Poster 5:

The effect of environmental variation on gene drive dynamics

Shahar Shemesh, Gili Greenbaum, EEB department, The Hebrew University of Jerusalem

Gene drive is a CRISPR-based technology which can generate super-Mendelian inheritance, in which an engineered gene cuts out the homologues cite and replicate itself in place of the wild-type allele. Such a genetic construct can rapidly spread in a population even if it significantly reduces the fitness of the individuals carrying it. This technology could provide an efficient solution for suppressing harmful species such as pests, invasive species, and disease-vectors. However, gene drives pose substantial risks, and application should be done with caution after investigating expected outcomes. Specifically, because environmental factors influence evolutionary processes, and laboratory experiments do not reflect the complexity of nature, it is important to understand the effect of environmental variation on gene drive spread. I aim to understand this effect by designing models that incorporates environmental changes over time and space. Using analytic mathematical analysis and simulations I found that temporal variation and spatial variation may have different effects on the gene drive evolutionary dynamics - temporal environmental variation is expected to reduce the gene drive success rate, whereas spatial variation accelerates the gene spatial spread. I will generalize the model to include both temporal and spatial variation, as well autocorrelation of the variation, to provide a broad perspective on the potential use of gene drives, incorporating a consideration of the ecological context.

Poster 6:

Plant collaborative non-self-recognition self-incompatibility systems: facilitating conditions, evolutionary stability, breakdowns, and recovery

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Self-incompatibility evolved to avoid self-fertilization among hermaphroditic plants, which could lead to inviable offspring, (‘inbreeding depression’). Self-incompatibility relies on specific molecular recognition between highly diverse proteins of two families: female and male determinants, such that the combination of genes an individual possesses determines its mating partners. While self-incompatibility has the benefit of avoiding inbreeding depression, it bears the cost of limiting the number of mating partners and could break down under various mutations conferring self-compatibility. Indeed, population surveys found self-compatible genotypes, and evolutionary transitions between self-compatibility and self-incompatibility are thought to occur. Here we focus on the plant collaborative-non-self recognition self-incompatibility system, found in the Rosaceae and Solanaceae families. We study the evolutionary conditions facilitating the emergence and stability of self-incompatibility in this system and the conditions under which it breaks down. We construct a novel theoretical framework, that crucially affords interaction promiscuity and multiple distinct partners per protein, as is seen in empirical findings. We find three behavioral regimes of the system. In the first regime, we demonstrate spontaneous self-organization of the population into distinct 'classes' with full between-class compatibility and a dynamic long-term balance between class emergence and decay. In the second regime, the population is fully self-compatible, namely all individuals are capable of self-fertilization. In between, we find a third mixed regime with both self-compatible and self-incompatible individuals in dynamically unstable proportions. The choice of either regime depends on the extent of promiscuity and inbreeding depression, and hence in most regimes, the transitions to self-compatibility are reversible. Our work highlights the important evolutionary role played by promiscuous molecular recognition. Promiscuity was found in additional systems suggesting that our framework could be more broadly applicable.

Poster 7:

Activation of GABA-B Receptor Signaling Affects Cilia Tubulin Post-Translational Modifications in the Sea Anemone Nematostella vectensis.

Efrat Beck, Tamar Lotan, The Leon H. Charney School of Marine Sciences, University of Haifa

The cilium is a highly conserved organelle present in most eukaryotic cells. The motile cilia are important for the locomotion of fluids and the movement of aquatic organisms. The cilia consist of microtubules, primarily made from α and β tubulin dimers, which undergo post-translational modifications (PTMs) such as acetylation, glycylation, polyglutamylation, and tyrosination. PTMs affect cilia's length and stability, flexibility, motility, degradation rate, and ciliary beating. Defects in cilia can cause different illnesses and syndromes in humans, termed 'ciliopathies'. Here, we used the sea anemone Nematostella vectensis as a model organism to study ciliogenesis. At the larval stage, the planulae are covered by motile cilia that facilitate locomotion in the aqueous medium. We demonstrate that planula ciliogenesis is affected by GABA-B receptor signaling. The addition of GABA-B agonist baclofen caused a reversible arrest of planula mobility, development, and metamorphosis. Comparative transcriptomic profiling of baclofen-treated and untreated control planulae revealed changes in the expression of genes associated with ciliary structure and transport. Further analysis using specific antibodies against tubulin modifications demonstrated that the expression level of certain PTMs is altered when treated with baclofen. We suggest N. vectensis as an evolutionary model for studying cilia development and modifications leveraging its phylogenetic position in Cnidaria as a sister group to Bilateria.

Poster 8:

Co-translational assembly constraints protein oligomeric state evolution upon gene duplication

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Introduction. Oligomeric proteins are central to life and duplication and divergence of their genes is a key evolutionary driver. Gene duplications often yield very different outcomes. Given a homomeric ancestral protein, duplication can yield two paralogs that form two distinct homomeric complexes, or a heteromeric complex comprising both paralogs. However, the biological basis for the emergence of these different oligomeric fates remains unknown.

Results. Here we used a phylogenomic approach to trace the duplication of genes encoding homomeric proteins across the eukaryotic tree of life. These duplications have gradually complexified the eukaryotic interactome by introducing homo- and heteromeric paralogs. We show that heteromeric paralogs typically originate from mutational biases intrinsic to random genetic drift, whereas homomeric paralogs arise under purifying or positive selection scenarios. Purifying selection primarily includes each paralog retaining the co-translational homomeric assembly of the pre-duplication ancestor. Such an assembly mechanism disfavors their heteromeric interaction by driving each paralog to be synthesized as kinetically stable homomers. Positive selection scenarios include accumulation of evolutionary changes in the two paralogs that disfavors their heteromeric interactions. These changes include insertion/deletions at their oligomeric interfaces, changes in their subcellular localizations, and divergence of their gene expression profiles away from spatiotemporal co-expression. Once fixed in the genome, heteromeric paralogs remain functionally coupled over evolutionary time and diverge in sequence at similar rates primarily in the neutral regime. In contrast, homomeric paralogs continue to divergence in function and tend to evolve asymmetrically in the adaptive regime.

Conclusion. These results establish a fundamental connection between the mechanism of protein complex assembly and the divergence of the oligomeric state upon gene duplication. We show that co-translational assembly explains much of oligomeric fates after gene duplication events across the eukaryotic tree of life and across almost all protein functional classes across the human genome.

Poster 9:

Deciphering the role of adhesion proteins during sea urchin biomineralization

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Biomineralization is a process that developed during the evolution of the five kingdoms of life, enabling living organisms to produce minerals for various functional purposes, such as teeth, shells, skeletons, and bone. A common feature of biominerals is their high stiffness, that exceeds the stiffness of any other organic tissue. Cells can sense the stiffness of the extracellular matrix (ECM) and respond to it through the formation of focal adhesion and the activation of cytoskeleton remodeling. Integrins are transmembrane proteins and Talin is an intracellular protein; together, they initiate focal adhesions crucial for cellular mechanical sensing, but their role in biomineralization remains largely unknown. Here I use the sea urchin larval skeletogenesis to address this gap in knowledge. The embryonic sea urchin's larval skeleton consists of two calcite spicules formed by the skeletogenic lineage, through deposition of mineral into an internal cavity. I used single-cell RNA sequencing data to identify integrin related genes expressed in the skeletogenic cells. I used whole mount in-situ hybridization to study the expression of genes encoding Talin, Integrin-Alpha and the Integrin ligand, Npnt. Specifically, npnt is enriched in the sea urchin skeletogenic cells at early and late gastrula stage and also pluteus stage. I tested the function of npnt by downregulating its expression using morpholino antisense oligo nucleotide (MASO). The two npnt MASOs have significantly decreased both the length of body and post-oral skeletal rods and induced ectopic spicules and branching phenotypes at pluteus stage. These findings suggest that Npnt activity is essential for sea urchin skeleton elongation. This research will hopefully promote the understanding of the roles of Integrins in the formation mechanosensing in biomineralization and illuminate the molecular regulation of Metazoan biomineralization.

Poster 10:

Differential conservation of classical NHEJ in fungal genomes reveals distinct short genetic variations profiles

Shira Milo, Einat Hazkani-Covo

Fungi are the most diverse group of organisms. DNA repair plays a role in fungal development and is important for fungal genome integrity and survival. Thus, factors affecting the conservation and efficiency of pathways used to repair DNA may contribute to the general mutation burden in fungal organisms and their ability to emerge and adapt to changing environments. We surveyed the conservation of double strand break (DSB) repair pathways in hundreds of non-Ascomycete fungal organisms. We found that a group of early diverging fungi, Zoopagomycota, completely lacks the non-homologous end joining (NHEJ) pathway. In addition, we confirmed that a subdivision in Basidiomycota, the Ustilaginomycotina, lacks Ligase IV (LIG4), a DNA ligase that is essential for NHEJ. We hypothesized that the absence of NHEJ, which is the most common DSB repair pathway, is reflected in the genomic sequence. To test our hypothesis, we developed NHEJScan, a comparative genomic pipeline that detects and classifies insertions and deletions as potential genomic signatures of different DSB repair mechanisms. We found that genomes that either completely lack NHEJ or only LIG4 show significantly larger proportion of events that are classified as potential results of unequal crossing over, SSA, replication slippage and alternative-EJ whereas groups that are predicted to maintain NHEJ activity display more events that potentially resulted from NHEJ. We show that for both deletions and insertions, the flanking regions tend to be longer when NHEJ components are absent. Furthermore, NHEJ-deficient genomes show larger proportion of longer microhomology (MH) (5-10 bp) compared to NHEJ- and LIG4-conserved genomes, whereas the latter show significantly shorter MH (2-4 bp) compared to the former. We did not, find a significant difference in the proportions of 0-1 bp length MH between the groups, suggesting that the fundamental activity of NHEJ exist, at least to some extent, in genomes lacking NHEJ.

Poster 11:

Regards from the Miocene: Ayyalonia- a climatic relict Israeli endemic troglobitic pseudoscorpion genus

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The evolution of obligate cave-dwelling species can often be explained by the Climatic Relict Hypothesis (CRH) suggesting that climatic changes lead to vicariant speciation of subterranean populations. While the surface is susceptible to climatic and environmental changes, subterranean ecosystems can preserve stable conditions for very long periods, enabling a refugium for relict species while their epigean ancestor becomes extinct. Some species evolve morphological adaptations to the hypogean environment (troglomorphism) such as eye loss, elongated appendages, and loss of pigmentation, which increase reliance on the cave environment, and lead to a loss of migration between epigean and hypogean populations. These evolutionary processes may cause high genetic partitioning, fragmented distributions, and consequently multiple speciation events of separate subterranean troglobitic relictual populations restricted to their caves. In this scenario of CRH, troglobitic sister species can be found in remote caves, while their epigean ancestors underwent extinction, as known from spiders, scorpions and pseudoscorpions. In a survey of the subterranean arachnid fauna in Israel, many unidentified pseudoscorpion morpho-species, mostly from the family Chthoniidae, were discovered, including new species of Ayyalonia. The only previously described Ayyalonia species, Ayyalonia dimentmani, was found only in the unique, previously sealed, chemoautotrophic Ayyalon cave, which it invaded during the mid-Miocene ~14 Mya. During the Miocene the Levant has endured a dramatic aridification. Phylogeny based on the genomic analysis Ultra Conserved Elements of the first ever DNA sequences of Ayyalonia species revealed three new micro-endemic highly troglomorphic Ayyalonia species, each found only in a single cave in a different region of Israel: Arak Na'asane (Eastern Samaria), Ayyalon (Shfelat Yehudah), Sha'at (Western Samaria), and Yir'on (Galilee). All these caves are deep, highly isolated, hypogene, phreatic caves with elongated tunnels. The large geographic distance between close phylogenetic species is an indication of the evolutionary process explained by CRH.

Poster 12:

Evolutionary Insights from the Mitochondrial Genome of Oikopleura dioica: Sequencing Challenges, RNA Editing, Gene Transfers to the Nucleus, and tRNA Loss

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Sequencing the mitochondrial genome of the tunicate Oikopleura dioica is a challenging task due to the presence of long poly-A/T homopolymer stretches, which impair sequencing and assembly. Here, we report on the sequencing and annotation of the majority of the mitochondrial genome of O. dioica by means of combining several DNA and amplicon reads obtained by Illumina and MinIon Oxford Nanopore Technologies (ONT) with public RNA sequences. We document extensive RNA editing, since all homopolymer stretches present in the mitochondrial DNA correspond to 6U-regions in the mitochondrial RNA. Out of the 13 canonical protein-coding genes, we were able to detect eight, plus an unassigned ORF that lacked sequence similarity to canonical mitochondrial protein-coding genes. We show that the nad3 gene has been transferred to the nucleus and acquired a mitochondria-targeting signal. In addition to two very short rRNAs, we could only identify a single tRNA (tRNA-Met), suggesting multiple losses of tRNA genes, supported by a corresponding loss of mitochondrial aminoacyl-tRNA synthetases in the nuclear genome. Based on the eight canonical protein-coding genes identified, we reconstructed maximum likelihood and Bayesian phylogenetic trees and inferred an extreme evolutionary rate of this mitochondrial genome. The phylogenetic position of appendicularians among tunicates, however, could not be accurately determined.

Poster 13:

Cambrian Explosion: a Trichoplax perspective.

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My experiments on fossilization of soft bodied organisms aimed to deeper understanding of the metazoan diversification event around the Precambrian/Cambrian boundary. These experiments showed that the fossilization of soft bodied organisms required the fast deposition of preservative ions AL and/or Si on the surface of a dead body. Meanwhile, unicellular metazoan ancestors in comparison with multicellulars did not deposit AL on their surface. For example, in colonial amoeba Dictyostelium discoideum, the unicellular stage did not bind Al on the cell surface while the multicellular stages did. This difference was explained by the expression of cell adhesion molecules in the multicellular stages of D. discoideum as well as in all metazoans. These molecules have a high affinity to charged preservative agents. Thus, multicellularity itself inevitably triggers formation of the metazoan fossil record, but at the same time, unambiguous unicellular relatives of Metazoa are hardly known.

In Placozoa, the simplest group among Metazoa, the cell adhesion complex is incomplete, but their dead bodies did adsorb Al-ions on their surfaces. However, Trichoplax adherens demonstrated a phenomenon which precluded the preservation of a Trichoplax-like body. Immediately after death (2-10 mins), the body of Trichoplax disintegrated into single cells and quickly scattered away. This is insufficient time for preservation to start.

Such fast postmortem disintegration is possibly related to the reduction of a basement membrane in recent Placozoa. This membrane underlies an epithelium and provides the entity of cell layers for some time after the death of an animal. Therefore, to preserve a soft body in the fossil record, a basement membrane is required. The “basement membrane” hypothesis suggests a new insight on the Cambrian diversification event related to the development the basement membrane in various metazoan linages. Importantly, this hypothesis can be tested on other animals with the reduced basement membrane.

Poster 14:

Statistical framework to determine indel-length distribution

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Insertions and deletions (indels) of short DNA segments, along with substitutions, are the most frequent molecular evolutionary events. Indels were shown to affect numerous macro-evolutionary processes. Because indels may span multiple positions, their impact is a product of both their rate and their length distribution. An accurate inference of indel length distribution is important for multiple evolutionary and bioinformatics applications, most notably for alignment software. Previous studies counted the number of continuous gap characters in alignments to determine the best fitting length distribution. However, gap-counting methodsare not statistically rigorous, as gap blocks are not synonymous with indels. Furthermore,such methods rely on alignments that regularly contain errors and are biased due to theassumption of alignment methods that indels lengths follow a geometric distribution. In this study, we aimed to determine which indel length distribution best characterizes alignments using statistical rigorous methodologies. To this end, we reduced the alignment bias using a machine-learning algorithm and applied an Approximate Bayesian Computation methodology for model selection. Moreover, we developed a novel method to test if current indel models provide an adequate representation of the evolutionary process. We found that the best fitting model varies among alignments, with a Zipf length distribution fitting the vast majority of them.

Poster 15:

Evolution of cyanophages under different light conditions

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Marine cyanobacteria from the genera Prochlorococcus and Synechococcus are very abundant, widespread and contribute much to primary production in the ocean. The cyanobacteria serve as hosts to cyanophages, marine viruses that infect them. Environmental conditions such as light intensity can affect the phage infection cycle. However, it remains unclear whether cyanophages undergo adaptation to different light intensities on an evolutionary scale, and what genetic changes are responsible. Moreover, we don't know whether acquisition of auxiliary metabolic genes, such as the photosynthetic gene psbA, contributes to this adaptation. Here, we investigate whether cyanophages can adapt to light intensity, and aim to determine the genotypic consequences of such adaptations. We simulated an evolutionary process using semi-batch cultures of 3 Syn9 strains (Syn9 WT, mutant with partial deletion of psbA gene, and a mutant with whole deletion of psbA gene) at two light intensities. The evolutionary experiment showed a significant change in plaque size and host lysis between the evolved and ancestral strains. This indicates higher fitness of the evolved populations. No reacquisition of the gene psbA was detected at the end of the experiment. However, sequencing of evolved populations showed mutations in a total of 29 genes. Six of the genes had mutations that were unique for high light evolved populations, and one gene had mutations only in low light evolved populations. Furthermore, the majority of mutations were nonsynonymous for each light and strain treatment. These findings suggest that the cyanophage mutations are not due to genetic drift and result from adaptation.

Poster 16:

Inferring complex admixture patterns in the Phoenician Mediterranean world from ancient DNA using F-statistics

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Ancient DNA has emerged as a powerful resource in the past decade for expanding our knowledge on human evolution and history. The few thousands of ancient human individuals that have been sequenced in the past decade have allowed us to begin to piece together a rich history of human population interactions and migrations. F-statistics, which have been shown to be very powerful in resolving relationships between divergent populations, are also commonly used when analyzing ancient DNA. However, when analyzing ancient DNA these methods are challenged by the small number of sampled individuals and limited choice of ancient populations to use as reference. I will present these challenges and solutions we found for them in a recent study we conducted on Phoenicians in the Mediterranean.

Phoenicians established an unprecedented maritime trade network originating in the Levant beginning in the 2nd millennium BCE. During the 1st millennium BCE, Phoenicians expanded to the central and western Mediterranean and established Carthage as a major center. The extent to which the spread of their culture across the Mediterranean was propelled by migrations of people or the adoption of ideas has remained unclear in the absence of systematic ancient DNA evidence. Together with colleagues, we generated and analyzed genome-wide data for 196 individuals originating from 14 Phoenician sites in the Levant, North Africa, Sicily, Sardinia, and Iberia. We used these genomes to study the population history of Phoenicians in the Mediterranean and address two key open questions in their history:

* To what extent is the Levantine cultural origin of Phoenicians reflected in genetic ancestry?

* How did the expansion of Carthage impact the genetic make-up Phoenician settlements under its influence?

We show how addressing these questions with current methods based on F-statistics is challenging and present solutions to these challenges.

Poster 17:

Evolution in microbial microcosms is highly parallel regardless of the presence of interacting species

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Evolution often follows similar trajectories in replicate populations, suggesting that it may be predictable. However, populations are naturally embedded in multispecies communities and the extent to which evolution is contingent on the specific species interacting with the focal population is still largely unexplored. Here, we study adaptations in strains of 11 different species experimentally evolved both in isolation and in various pairwise co-cultures. While partner-specific effects are detectable, evolution was mostly shared between strains evolved with different partners; similar changes occurred in strains' growth abilities, in community properties, and in about half of the repeatedly mutated genes. This pattern persisted even in species pre-adapted to the abiotic conditions. These findings indicate that evolution may not always depend strongly on the biotic environment, making predictions regarding coevolutionary dynamics less challenging than previously thought.

Poster 18:

Exploring the Pleistocene to Holocene Transition in Central Europe through Sedimentary Ancient DNA

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The shift from hunting and gathering to a sedentary lifestyle and the beginning of the domestication of plants and animals represents a pivotal transformation in human history, which profoundly influenced our demography, culture, genetic diversity, and interactions with the environment. Our study leverages recent developments in sedimentary ancient DNA (sedaDNA) research to investigate this transition in Central Europe. Seventy-six sediment samples were collected from two archaeological sites in southern Poland: Perspektywiczna Cave and Poręba Dzierżna. In a pilot study on 16 samples, we extracted DNA fragments from the sediments, converted them to single-stranded DNA libraries, and performed targeted enrichment for mammalian mitochondrial DNA – all using laboratory protocols tailored to the characteristics of short and highly-degraded ancient DNA. Sequencing data analysis included taxonomic identification at the biological family level and authentication of ancientness based on the presence of specific damage patterns known to accumulate post-mortem in DNA fragments over time. Five samples from Perspektywiczna Cave displayed good preservation of ancient DNA fragments, pertaining to 10 different mammalian families. We note that the families identified match with the known zooarchaeological record of the site. Interestingly, the presence of mixed Pleistocene and Holocene taxa in some samples suggest potential post-depositional mixing of sediment and/or DNA. This may have implications on our understanding of the cave's depositional history, and also of processes leading to potential post-depositional movement of sedimentary ancient DNA in archaeological cave sites. DNA analysis of the remaining samples are currently in progress. We anticipate that in combination with ongoing luminescence dating of the sediments and an in-depth analysis of the archaeological, geological and zoological contexts, these data will help to better characterize human-environment interactions across a major transitional time in prehistory.

Acknowledgments: This study is funded by the United States-Israel Binational Science Foundation (Grant 2021219 to MF and VS)

Poster 19:

Microbial Genome Adaptations to Anthropogenic Nutrient Pollution

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The rapid intensification of human activities, particularly in agriculture, has caused significant alterations in global biogeochemical cycles, which are essential for Earth's resilience and health. While microorganisms play crucial roles in these cycles, the evolutionary consequences of nutrient pollution on microbial communities remain underexplored. Previous studies suggest that anthropogenic factors may influence amino acid and codon usage in bacteria, but the mechanisms driving these changes are not fully understood. This study aims to investigate the adaptations of microbial genomes within an environmental microbiome to varying ambient conditions, focusing on the influence of human-driven nutrient availability. We use 367 freshwater metagenomic samples and computational methods to assess the elemental composition of bacterial proteins in environments across human interference gradients. Our approach involves analyzing cross-study metagenomic data from samples exposed to varying levels of nutrient pollution and human activity at the taxon level. This taxa-based analysis allows us to identify and quantify the human impact. Through this research, we aim to determine whether the effect of human impacts is taxa-based, meaning interference selects for specific bacteria; adaptive, meaning the same taxon exhibits different elemental compositions depending on the environment; or function-based, meaning bacteria responsible for specific functions, like sulfur oxidation, have genes with higher sulfur content than other bacteria in the same environment. This study is expected to contribute to our understanding of the broader ecological impacts of human activity on microbial communities globally.

Poster 20:

Candidate Denisovan fossils identified through gene regulatory phenotyping

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Denisovans are an extinct group of humans whose morphology is mostly unknown. The scarcity of verified Denisovan fossils makes it challenging to study their distinct anatomy, and how well they were adapted to their environment. We previously developed a genetic phenotyping approach to gain insight into Denisovan anatomy by detecting gene regulatory changes that likely altered Denisovan skeletal morphology. Here, we scan Middle Pleistocene skulls for unclassified or disputed specimens that match predicted Denisovan morphology and thus might be related to Denisovans. We found that Harbin, Dali, and Kabwe 1 show a particularly good match to the predicted Denisovan profile. We conclude that our genetic phenotyping approach could help classify unidentified specimens, and that Harbin, Dali, and Kabwe 1 likely belonged to individuals closely linked, or anatomically similar, to the Denisovan lineage

Poster 21:

modelRxiv: a platform for the dissemination and interactive display of models

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Integrating the conclusions of complex eco-evolutionary models can be challenging, especially when models are developed in different frameworks; this can introduce technical hurdles into reproducing model results and preclude meaningful crosstalk between modelers working in the same field. Crosstalk is particularly important when model conclusions can directly influence decision-making on matters pertaining to conservation, such as in the rapidly developing field of gene drive modeling. Gene drives are genetic constructs that can rapidly spread deleterious alleles in wild populations, potentially leading to population collapse within a number of generations. Despite their immense potential in biocontrol of disease vectors and agricultural pests, the release of gene drives into the wild could have far-reaching detrimental effects on multiple ecosystems. Our knowledge of gene drive dynamics is limited to caged lab experiments that lack many complexities that are present in wild populations, and the field currently relies primarily on mathematical and computational modeling to study how these complexities could affect gene drive dynamics in order to design safe deployment programs. However, it is challenging to provide regulators with a coherent overview of currently published models. To address this challenge, we developed an interactive repository of models, called modelRxiv, which provides a web-based platform for interacting with models developed in many different frameworks. By incorporating state-of-the-art AI LLMs (large-language models) that assist in model integration, we have made the platform language-agnostic and suitable for many different types of models. A unified resource of published and unpublished gene drive models could help establish an interface between modelers and regulators. For modelers, it can provide a comprehensive view of current models and highlight overlooked parameters that have yet to be considered. Using as examples a number of gene drive models that we developed, I will demonstrate the potential of modelRxiv as a platform for eco-evolutionary modeling.

Poster 22:

Using saturation mutagenesis to map the evolutionary forces that shaped human regulatory elements

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Adaptation via natural selection is the process by which the incredible fit between species and their environment has evolved. However, despite the good understanding of evolutionary adaptation at the phenotypic level, we have a limited understanding of the genetic changes that made us human. Particularly, we are still far from understanding how adaptation presents itself at the molecular level. This task is even more difficult in the noncoding parts of the genome, where most adaptations occur.

Saturation mutagenesis is an approach that allows researchers to compare true evolutionary changes to the full spectrum of possible mutations. We apply it using massively parallel reporter assays (MPRAs), allowing us to generate the largest saturation mutagenesis library of regulatory regions in the human genome, consisting of 500 diverse regulatory elements. To identify signatures of selection, we leveraged and expanded classical evolutionary tests, such as the McDonald-Kreitman test, to apply them to noncoding regulatory elements. We also developed meta-analysis approaches to gain insight not only into specific regions, but also into classes of regulatory elements.

We identified signals of positive and negative selection in various elements, and discovered specific variants that have likely driven human-specific phenotypes, e,g., in IRF4, a key transcription factor that affects pigmentation and skin diseases.

This work allowed us to study how selection has shaped human noncoding regulatory elements, and to shed light on the role of key substitutions in human adaptations.

Poster 23:

The war of attrition: a perspective of microbial residents

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The “war of attrition” model is a foundational framework in evolutionary game theory, used to analyze conflicts where individuals compete over a resource by enduring costs for as long as possible. This model has significantly contributed to the understanding of costly persistence in biological contexts. Microbes play crucial roles in host health and behaviour, often influencing competitive dynamics. By extending the war of attrition model to include both the hosts and their microbes, we uncover how these microorganisms may affect the outcomes of such conflicts. Our analysis reveals that microbes can alter the cost-benefit landscape of the contestants, leading to novel equilibrium strategies and deviations from classical genes dynamics. We further consider the effect of host stress on the results. Our results raise the possibility that changes in the microbial composition within individuals can affect the nature of competitive interactions, and suggest a richer and more comprehensive perspective on the dynamics of biological conflicts.

Poster 24:

The opposing roles of gene exchange in the evolution of self-incompatibility in plants: does it promote or inhibit genetic diversity?

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Self-incompatibility (SI) evolved to avoid self-fertilization among hermaphroditic plants, which could lead to inviable offspring, ('inbreeding depression'). Self-incompatibility relies on specific molecular recognition that distinguishes between self and non-self-pollination and enables fertilization only by the latter. This recognition is implemented by specialized proteins of two families, expressed in male and female reproductive organs. Since the combination of genes an individual possesses determines its mating partners, and in particular ensures it is incapable of self-fertilization, this combination is preserved via genetic linkage.

Despite the tight linkage between these genes, a low rate of gene conversion was detected. Yet its evolutionary consequences remain controversial. Gene conversion was proposed to promote the establishment of new specificities but also to decrease allelic diversity, which should have the opposite effect. A third possible effect is the accidental formation of self-compatible individuals. So far, these effects have been considered separately, and a unified model accounting for the overall contribution of gene conversion is still lacking.

We constructed a population-level evolutionary-biophysical simulation that allows the assessment of the various implications of gene conversion altogether. Each protein is represented in our model by its protein interaction domain, which could evolve via point mutations. Each individual in the population is represented by its protein combination, and proteins can be transferred between individuals, representing gene conversion. Our framework affords interaction promiscuity and multiple distinct partners per protein, as found empirically. Our model exhibits a spontaneous organization of the population into distinct mating specificities, as observed in nature.

Our preliminary results show that in the regime of gene conversion lower than the mutation rate, a higher gene conversion rate increases the population proportion of self-compatible individuals and the number of mating specificities, but decreases allelic diversity. In the extreme of a high gene conversion rate the class structure breaks down.

Poster 25:

Cultural evolution of prosocial behavior in the Stug-hunt game

Stav Ratzon, department of zoology, Tel Aviv university

Cooperative behavior has been a focus of study for evolutionary theory. Traditionally, the prisoner's dilemma has been the standard model for investigating such phenomena. However, because the prisoner's dilemma is not a coordination game and does not account for the benefits of collective cooperative action, it may not fully represent real-world scenarios such as cooperative foraging and hunting. In this study, we propose an evolutionary model based on the stag-hunt, a coordination game, as well as both vertical and non-vertical transmission. We examined scenarios leading to the fixation of cooperation, fixation of defection, unstable polymorphism, and stable polymorphism, depending on various parameters in the model. Our analysis focused particularly on the relative influence of non-vertical versus vertical transmission, the impact of the payoff from reciprocal cooperation, and the differences between our findings and those derived from a previous model based on the prisoner's dilemma. Our results highlight the critical importance of the reciprocal cooperation payoff in determining evolutionary outcomes, contrasting with models where this factor is not considered.

Poster 26:

Pre-existing mitochondrial DNA plasmids escape to the nucleus

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Mitochondrial DNA transfer to the nucleus is an ongoing event in all eukaryotes. Yet, the mechanism of the transfer is unknown. Thirty years ago, Thorsness and Fox established a genetic system to track events of escape of DNA from the mitochondrial genome to the nucleus. The system is based on inserting the TRP1 gene into the mitochondrial genome while deleting it from its native location. Under these conditions the cells are auxotroph for tyrosine, but if the TRP1 gene escapes the mitochondria and migrates to the nucleus they become prototroph. While it was known that the TRP1 was episomal within the nucleus how and where those episomes were formed was unknown. We tested the hypothesis that broken mitochondrial DNA escapes the mitochondria and circularized by double strand break repair mechanisms. Consequently, we expected that the rate of DNA escape will increase upon exposure of yeast cells to ethidium bromide that damages mitochondrial DNA but in fact the rate of escape decreased. In addition, we expected that in double strand repair mutant the rate of escape will decrease but it hardly changed in NHEJ deficient cells or in HR deficient cells and what somewhat decreased but was not eliminated in a double mutant. We sequenced the plasmids replicated in the nucleus. One of the plasmids was probably generated by a crossover event within the mitochondrial genome because it included an inversion of the TRP1 gene. We found several types of plasmids, almost all of them showed short homology at the breakpoint. Surprisingly, we were able to identify some of these events in tryptophan auxotroph cultures. Our results suggest that plasmids can be naturally formed and maintained within the mitochondria; these plasmids are more likely to be transferred to the nucleus than broken linear DNA fragments.

Poster 28:

Inverted repeat extension by template switching in GRE2 promoter affects gene expression through yeast evolution

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Inverted repeats (IRs) are sequences with internal symmetry that can form non-canonical DNA structures. DNA polymerase template switching between IR arms can expand IR arm size. Here we tested the hypothesis that IR expansion in promoters can modify gene expression through short term evolution.

We used a bioinformatical pipeline to identify recent template switching events in in S. cerevisiae strains resulted in extended prefect IRs in promoters at locations potentially associated with expression. Out of hundreds of potential events, we focus on two genes (ETR1 and GRE2) with long extended IRs (24-25 bp) compared to the reference lab WT strain. We tested the effect of IR elongation on gene expression in the reference lab WT strain. The mutants (long IR) and WT (short IR) strains were grown in different media and their growth rates were measured. ERT1 mutant didn't show a coherent effect of the long IR. On contrast, the GRE2 mutant has a severe growth defect. GRE2 is a 3-methylbutanal reductase and NADPH-dependent methylglyoxal reductase is shown as an important factor in bioethanol production. This is specifically interesting as GRE2 IR expansion was identified in a strain used in bioethanol production. RNA sequencing shows that the GRE2 expression is 4 times higher than the WT. GRE2 overexpression potentially activated different pathways: including methyl-citrate cycle, amino acids synthesis, transporters, mitochondrial genes and cell cycle genes which maintain G1 arrest. One possible reason for this change in expression might be a transcription factor such as CIN5 which binds to both IR arms. Expanding of IR can change the affinity of transcription factors to the promoter, here by increasing length between recognition sites, and thus the expression of genes. Further study of IR expansion on GRE2 promoter expression may be used to improve ethanol fermentation.

Poster 29:

Transcriptomic analysis of novel kidney-related genes in Lesser spotted catshark (Scyliorhinus canicula) embryos

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Many studies were published along the years suggesting novel regulatory pathways guiding vertebrate kidney morphogenesis and transition between its different developmental forms. However, much less is known about the pronephros (primary vertebrate kidney) field formation and organogenesis. Here, we show the results of a transcriptomic analysis of pronephros formation in early Gnathostome organism, the catshark Scyliorhinus canicula. By separating embryonic tissues that give rise to the formation of the pronephros, before and during the process, from other incompetent anterior tissues, we were able to identify potential novel pronephric genes. Using temporal and spatial differential expression, we next verified few potential genes by RNA In situ hybridization. Eventually, we aim to find and characterize novel regulators and signaling pathways responsible for the vertebrate primary kidney morphogenetic field.

Poster 30:

Leveraging Evolutionary Insights from the Wright-Fisher Model of Allele Frequency Dynamics to Advance Nature Conservation Strategies

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The Wright-Fisher model is a foundational tool for predicting allele frequency dynamics in populations, particularly when one allele confers a slight disadvantage. This model highlights the critical role of population size, where smaller populations experience weakened natural selection and enhanced influence of neutral processes. As a result, slightly deleterious alleles may become fixed more easily in small populations, with an increased likelihood of fixation for more harmful alleles as population size decreases.

In this study, we use the Wright-Fisher model as an analogy to examine the dynamics between two competing species, analogous to alleles at a single locus, where one species exhibits a slight competitive disadvantage. Specifically, we focus on conservation scenarios where the weaker species is the target for preservation or reintroduction, while the stronger species represents an invasive or disruptive competitor. We employed a spatially explicit, grid-based simulation to model isolated habitat patches, with annual migration events between these patches. The key processes influencing population dynamics in the model include interspecies competition, which occurs during the breeding season and/or throughout the year, singular or recurrent reintroduction of the target species into patches, and migration between patches.

Our findings indicate that when managing species under competitive pressure, reintroductions may benefit from being strategically targeted at small, isolated patches rather than larger mixed-species communities. This approach leverages the reduced impact of competition in smaller, isolated populations, compared to the impact of stochastic processes, thereby increasing the chances of successful establishment and persistence of the target species. These results have significant implications for conservation, particularly in efforts to reintroduce or maintain species in environments where they face competition from invasive or otherwise dominant species.

Poster 31:

Uncovering the regulatory relationship between the Drosophila Shavenbaby and the Osiris genes

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Gene transcription is an intricate process governed by the interplay between transcription factors and their target genes, forming complex regulatory networks. This dynamic mechanism is largely directed by the cis-regulatory modules of the genes. Studies show that differences in gene regulation contribute to differences in morphology, physiology and behaviours observed in animals.

The Drosophila Shavenbaby is a master control gene that is expressed in the embryonic epidermis, and encodes a transcription factor (SVB) that orchestrates the development of cuticular trichomes, by activating downstream genes controlling cell differentiation and morphogenesis. Our previous cell type-specific transcriptomic analyses revealed that embryonic svb expressing cells are enriched in the genes of the Osiris (Osi) complex- a conserved insect-specific group shown to be involved in tissue plasticity, cuticle formation and olfaction in insects. Furthermore, ChIP-seq analyses identified SVB binding at intergenic regions within the Osiris complex, these regions were also enriched in enhancer-associated chromatin modifications in svb expressing cells.

Based on these findings, we hypothesize that SVB regulates the expression of Osi genes in the embryonic epidermis of D. melanogaster. To investigate this, we identified 10 putative enhancer elements in the Osiris complex, and assayed their expression using a LacZ reporter system. Our results reveal, 5 enhancer elements surrounding Osi6, Osi7, and Osi14 drive their expression epidermally in embryonic stage 14-16. The spatial and temporal expression of the enhancer elements surrounding Osi6 and Osi7 are consistent with the embryonic expression of svb, suggesting a regulatory linkage between the svb and Osi genes

Poster 32:

Anemone flowers produce airborne ultrasounds that may facilitate plant-pollinator interactions

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Plants produce flowers with characteristics attractive to their pollinators to entice floral visits. Visual and olfactory characteristics of flowers are known to be used by flower visitors seeking rewards. Recent results revealed that plants also produce airborne ultrasounds, especially when stressed. Here we examined whether the petal movement of flowers produces airborne ultrasounds, focusing on Anemone (Anemone coronaria) flowers. Anemone flowers open and close following a circadian rhythm, but also in response to changes in light and temperature. We recorded the sound of Anemone petal movements from 10cm, and found that petal movement, full or partial, is associated with airborne ultrasounds, with the highest energy frequencies between 35 – 60kHz. These results suggest that other organisms – possibly including pollinators or nearby flowers – may have evolved to respond to these sounds. Specifically, pollinators of these plants may use these sounds in their decision to visit a specific plant, while other Anemone flowers could use these sounds for synchronizing their flowering time.

Poster 33:

Unraveling the Complexity of Insect Embryogenesis: Preliminary Insights from Blastoderm Morphology and Evolution

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Insect embryogenesis is a remarkably complex process with considerable variation across different taxa. Nevertheless, like all arthropods, insects share a highly conserved developmental milestone known as the arthropod phylotypic stage: the germband. The shared conservation is evident in morphological characteristics and genetic traits, namely the segment polarity network. While segmentation and germband formation have garnered considerable attention, the earlier blastoderm stage has remained relatively overlooked and poorly understood. Temporal constraints from both sides of the developmental process influence the blastoderm stage. The shape of the egg, determined by reproductive ecology, directly impacts the characteristics of the blastoderm, thereby setting the “developmental stage” for subsequent events. Ultimately, the blastoderm must execute the segmentation cascade to culminate in the definitive germband morphology, effectively engineering developmental events in reverse. The blastoderm, acting as a central orchestrator, drives the intricate processes leading to the emergence of the distinct germband structure, making it a pivotal stage in insect embryogenesis. New data from roaches and an extensive literature review combined with contemporary methods are used to map known blastoderm characters onto a phylogenetic tree. This enables the tracing of their evolutionary history and the identification of any emergent patterns.

Poster 34:

Geographical variability of Messor arenarius ants from different regions in Israel

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Messor arenarius ants are distributed mainly in deserts or sandy areas of the Middle-East and North-Africa. In Israel, those ants are inhabited in the Negev Desert, as well as in sandy areas along the Mediterranean Coastal Plain. In this work, several locations in the Coastal Plain of Israel were checked also for surface activity of M. arenarius ants, in different occasions between May 2020- March 2021. Ant lengths were measured from the fore-edge of their mandibles to the hind-edge of their abdomen; ant mandible widths were measured from the right edge of their right mandible to the left edge of their left mandible. In this work it was found, that lengths of M. arenarius ants from southern parts of the Coastal Plain of Israel, between Tel-Aviv and Ashkelon (12.32mm±1.68mm; N=37), are significantly bigger than lengths of those ants from northern or central parts of this Coastal Plain between Tel-Aviv and Rosh-Haniqra (11.46mm±1.83mm; N=63) (t=2.3463; S.E.=0.368; D.F.=98; P=0.0210 in a bilateral t-test). It was also found, that mandible widths of M. arenarius ants from southern parts of the Coastal Plain of Israel, between Tel-Aviv and Ashkelon (2.216mm±0.630mm; N=37), are mostly significantly bigger than mandible widths of those ants from northern or central parts of this Coastal Plain, between Tel-Aviv and Rosh-Haniqra (1.746mm±0.530mm; N=63) (t=3.9910; S.E.=0.118; D.F.=98; P=0.0001 in a bilateral t-test). The finding, that M. arenarius ants from the southern parts of this Coastal Plain, are bigger than those ants from the northern or the central parts of this Coastal Plain, seems to be an adaptation to desert conditions, because their ratio of body surface area to body volume is smaller than in those ants from those northern areas. The southern parts of this Coastal Plain, are usually hotter than the northern or the central parts of the Coastal Plain of Israel.

Poster 35:

PAK4DEV: p21 Activated Kinases Expression, Regulation, and their Roles in Sea Urchin Development and Skeletogenesis

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p21-activated kinases play an evolutionary conserved pivotal role in cell signalling from amoeba to humans and serve as the main downstream effector proteins for the small Rho GTPases, Rac and CDC42. Two main functions of PAKs are the regulation of cytoskeletal remodelling and the phosphorylation of MEK in the RAS/MEK/ERK pathway, both crucial mechanisms in morphogenesis. During neurogenesis, PAKs play a conserved role in axonal guidance from humans to fruit flies (D. melanogaster) and nematodes (C. elegans). However, little is known about the regulation and role of PAKs in marine invertebrate development. To fill this knowledge gap, here we investigated the expression, regulation, and role of PAKs in sea urchin embryogenesis using the Mediterranean Sea urchin, Paracentrotus lividus (P. lividus). There are two PAK genes in the P. lividus genome, Pl-pak1/3 and Pl-pak4 and both are dynamically expressed during sea urchin development. Inhibition of both PAK activities using a broad PAK inhibitor interferes with gut development and skeletal growth. F-actin polymerization is enriched around the skeletal rods, yet, PAK inhibition does not visibly hinder F-actin enrichment. During sea urchin development, ERK is active in the skeletogenic cells near the tips of the skeletal rods, and in the ciliary band neurons. PAK inhibition reduced the pERK signal in the skeletogenic cells and in the ciliary band region, implying it plays a role in neurogenesis. Pl-pak1/3 expression is enriched in the skeletogenic cells and its genetic perturbation by morpholino antisense oligonucleotides (MASO) results in a reduction in skeletal elongation. Our finding portrays the role of PAK proteins in sea urchin skeletal, and gut development, and supports an evolutionary conserved role in neurogenesis. Altogether, this study provides insight into the role of PAKs in marine invertebrate development and illuminates conserved cellular and molecular mechanisms across species.

Poster 37:

A single-cell view of male genitalia development and evolution

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One of the major challenges of evolutionary biology is uncovering the molecular mechanisms underlying morphological divergence. To address this question, we employ a model system with significant interspecific variety: the Drosophila male terminalia (genitalia and analia). Male genitalia rank among the most diverse and rapidly evolving organs in the animal kingdom, probably due to sexual selection. This trend extends to the model organism D. melanogaster and its close relatives, which display dramatic morphological differences.

To gain insights into the developmental processes diversifying male genitalia across evolution, we monitored pupal terminalia development in twelve Drosophila species using confocal microscopy. We uncovered multiple morphogenetic events generating a wide variety of unique genital substructures. Next, we delved into the genetic pathways involved in the development and diversification of genital structures in two of these species. We performed a single-cell RNA sequencing on the pupal terminalia of D. melanogaster and D. simulans at three developmental time points. By combining unsupervised cell-clustering with gene expression pattern data, we obtained transcriptomes for each anatomical substructure of the pupal terminalia across development. This approach enabled us to elucidate the network components operating in particular genital structures and to compare their expression between the two species.

Focusing on the posterior lobe, a substructure unique to the D. melanogaster species group, we identified new genes involved in posterior lobe development and diversification. These data will allow us to uncover the regulatory networks that contributed to the morphological differences between species.