	Tuesday 10/2/26	
09:00	Registration, morning coffee	
09:30	***Opening remarks*** **(Zonnenfeld Auditorium)** Prof. Raz Jelinek - Vice president and Dean of R&D, BGU Prof. Eyal Privman - ISEB Vice President Prof. Shimon Bernstein - Conference Chair	
10:00	**KEYNOTE: Philipp Messer** Eco-evolutionary dynamics of engineered gene drives	
11:00	Break	
	Auditorium 1, Building #35	**Auditorium 2, Building #35**
	Microbial Evolution *(Chair: Shimon Bershtein)*	***Evolution of Behavior*** *(Chair: Noa Truskanov)*
11:30	**Shimon Bershtein:** Metabolite correlation networks as complex phenotypes of adaptation-driving mutations	**Noa Truskanov:** Culture, cognition, and social dynamics in a rat foraging tradition
11:55	**Jonathan Friedman:** When does coevolution matter in microbial communities?	**Amiyaal Ilany:** Bacterial and viral transmission capture different temporal scales of rock hyrax social networks
12:10	**Darar Bega:** The evolution of longevity from the microbiome perspective	**Aviad Heifetz:** What about male quality? A model to predict male investment in a single female
12:25	**Yael Baranovitch:** Indirect evolutionary rescue in an obligate bacterial mutualism	**Eya Wolfson:** A latent drive: How evolution silenced (and can restore) female sexual behavior
12:40		**Yael Lubin:** Mothers build fortresses: Parsing the costs of egg sac construction in two widow spider (*Latrodectus*) species
12:55	Poster Session + Lunch Break	
	Evo-Devo and Evolutionary Innovation *(Chair: Idan Frumkin)*	***Population Genetics*** *(Chair: Eyal Privman)*
14:30	**Idan Frumkin:** Simulating gene birth in the lab: Insights into orphan genes from random sequences	**Eyal Privman:** Evolution of supergenes: lessons from social chromosomes
14:55	**Doron Lancet:** Darwinian origin of life	**Batel Attias:** Genomic ancestry of remains from Herod's mausoleum shows links to local populations
15:10	**Shany Barkan Zaslavsky**: Immune activation of symbiotic Hexacorallia induces algae expulsion	**Ohad Peled:** Tracing historical disease transmission using F_{st}
15:25	**Adi Livnat:** De novo rates of a Trypanosoma-resistant mutation in two human populations	**Moran Gershoni:** Flipping a coin or playing with genes? Genetic mechanisms behind male-biased offspring in mammals
15:40	Coffee break	
	Cancer Evolution *(Chairs: Nir Yosef, Ofir Cohen)*	***Evolutionary Theory*** *(Chair: Oren Harman)*
16:00	**Nir Yosef:** Single cell phylogenetics: Toward spatiotempotal analysis of tumor growth	**Oren Harman:** Metamorphosis: A natural and human history
16:25	**Leeat Keren:** Phenotypic, microenvironmental, and genetic crosstalk shapes pancreatic cancer organization	**Yotam Lifschytz:** Geometry of high-dimensional fitness landscapes leads to deterministic epistatic dynamics
16:40	**Ido wolf:** The evolutionary logic of metastatic tropism	**Tami Yosef:** Evolution of menopause: the mama's boy hypothesis
16:55	**Yuval Tabach:** Cancer as an evolutionary process: How It begins, escapes cures, and how evolution can guide new treatments	**Yoav Ram:** Copying the popular mimics drift in social learning

	Wedensday 11/2/26	
09:00	Early morning coffee	
	Auditorium 1, Building #35	**Auditorium 2, Building #35**
	Molecular Evolution & Phylogenetics *(Chair: Yehu Moran)*	***Ecology and Evolution*** *(Chair: Tamar Keasar)*
09:30	**Yehu Moran:** Selection on molecular combinations: asymmetric constraints in the evolution of venom systems	**Tamar Keasar:** Morphologically complex flowers from a pollinator's perspective
09:55	**Sinai Sacharen:** HLA escape and exposure: A balancing act in viral evolution	**Keren Klass:** Divergent effects of forest fragmentation on endangered black howler monkey population genetics and gut microbiomes
10:10	**Itamar Kozlovski:** Functional characterization of specialized immune cells in a cnidarian reveals an ancestral antiviral program	**Lachan Roth:** Pre-zygotic dynamics shaping inter-specific fertilization in reef invertebrates
10:25	Coffee break	
10:55	**Eran Tauber:** Do protein networks constrain or enable molecular evolution?	**Michal Segoli:** What limits the lifetime reproductive success of fig wasps?
11:10	**Benyamin Rosental:** Applying biomedical tools in ecological research - Immunity and stem cell transplantation for corals	**Talia Borofsky:** Coupled dynamics of predator group formation and prey populations
11:25	**Amir Sapir:** The evolution of sterol metabolism in mosquitoes: cholesterol as a driver for nectar-to-blood feeding transition	**Hadas Hawlena:** Can pathogen ecology and evolution within vertebrate hosts explain wildlife epidemiology? A case study of Bartonella bacteria in rodents
11:40	**Evgeni Bolotin:** Genes that are used together are more likely to be fused together in evolution by mutational mechanisms	**Justine Boutry:** The legacy of past heatwaves on 'off-host' parasite stages: Reduced infection risk and costs in the Daphnia-Pasteuria system
11:55	Poster Session + Lunch Break	
	Plant Evolution *(Chair: Tamar Friedlander)*	***Human Evolution*** *(Chair: Yoav Ram)*
13:25	**Tamar Friedlander:** Reconciling conflicting selection pressures in the plant self-incompatibility system	**David Gokhman:** A genome-wide atlas of Neanderthal and Denisovan regulatory activity
13:50	**Ronen Shtein:** GRANDMA: An iterative phylogenomic framework for inferring nested and multiple allopolyploidization events	**Keith D. Harris:** Genomic signatures of increasing disease burden in recent prehistory
14:05	**Evgenii Potapenko:** Genome size variation is attributed to adaptive transposable elements silencing efficiency	**Nachshon Egyes:** Ape genomes reveal natural protection mechanisms against human diseases
14:20	**Guy Horev:** A chromosome-level assembly of the endemic species *Trifolium israeliticum* reveals recent transposon expansion	**Nadav Mishol:** Uncovering the regulatory changes that shaped human skeletal evolution
14:35	Coffee break	
15:00	**KEYNOTE: Nathalie Balaban (Auditorium 1, Building #35)** The two archetypes of growth arrested cells under stress: evolutionary and clinical consequences	
16:00	Prizes and concluding remarks	

Poster ID	Presenter	Title
1	Sharon Moscovitz	Parthenogenic crayfish invasion in Israel, adaptivity aspects, and a possible biocontrol approach
2	Gad Degani	Variation in Coloration and Ecological Adaptation of Amphibians Across Israel's Climatic Gradient
3	Monika Almozlino	Epitranscriptomic variation in banded newts (Ommatotriton Vittatus) across life stages and sexes in the semi-arid habitat in Northern Israel
4	Yael Klirs	Hypomethylation in Oikopleura dioica genome
5	Noam Shtolz	Programmed mtDNA ribosome frameshifting is selectively constrained across 17,530 metazoan species
6	Ori Sharon	tSNP: A dimensionality reduction algorithm for genetic data
7	Noa Yaffa Kan	Changes in relatedness between mating pairs in the Asiatic wild ass (Equus hemionus) population following a water source management in the Negev Highlands
8	Kobi Shapira	A-to-I editing generates unparalleled complexity in the neural proteome of cephalopods
9	Yoav Livne	Sympatric speciation in killer whales may be driven by mother's curse and mito-nuclear compatibility
10	Erez Weisberg	Bacterial Secretion Systems as Drivers of Ecological Adaptation: A Pan-Genomic Analysis Reveals Niche-Specific Evolutionary Patterns
11	Ester Notarius	Changes in heritability of autoimmune diseases in the last 12,000 years
12	Aleksandra Panyutina	What a Functional Morphologist Can Learn About Bat Evolution from a Rodent and a Tongue
13	Amit Jangid	Volatile but persistent co-existence of self-compatibility and self-incompatibility in plants
14	Alona Azarov	Heat Stress Activates Hexacorallia Immune Cells and Inhibits Endo-Symbiosis
15	Shira Zion	Increased survival of low-frequency lineages during fluctuations in resource abundance
16	Gal Bodek	The effect of variants in cis-regulatory elements on divergent gene expression
17	Eliya Sultan	Discovery and functional characterization of cytotoxic cells in planarians
18	Guy Ben Zvi	A Transposable elements vantage on wheat domestication
19	Itai Fein	Exploring Heteropteran genomes: New insights from Oncopeltus homeoboxes
20	Daria Aleshkina	Role of RdRps in the cnidarian model Nematostella vectensis
21	Mor Lurie-Weinberger	A mixed clonal-plasmid outbreak of KPC-carrying Enterobacterales, simultaneously driven by an E. coli ST6448 clone and an IncN plasmid carrying an NTEKPC-Y element
22	Sviatoslav Rybnikov	Density dependence introduces new types of gene drive dynamics
23	Adrian Lehvy	Eco-Evolutionary Cross Talk in Multiple-Species Biofilm
24	Asaf Pinhasi	CORAL: large-scale read-based inference of lineage-specific mutation rates, spectra, and signatures across eukaryotes
25	Michael Sheinman	Bayesian inference of demographic history from the distribution of distances between heterozygous sites
26	Rakan Haib	Evolutionary graph pangenome of the order Poales from chloroplast genome assemblies highlight phylogenetic inconsistencies
27	Noga Ben-Sira	Genomic characterization of bulbous barley (Hordeum bulbosum) an untapped source of adaptive alleles
28	Nadav Ben Nun	Segmental copy number amplifications are stable in the absence of selection
29	Shani Talice	Isolation and transplantation of candidate stem cells in Hexacorallia: a model for coral cell therapy
30	Ziv Ben-Moshe	Saccharomyces Boulardii Rapidly Evolves to Improve Histidine Degradation and Production of Beneficial Metabolites
31	Elizaveta Miticheva	Impact of Horizontal Gene Transfer on population dynamics and outcomes of adaptation of Acinetobacter baylyi ADP1
32	Amir Bar	Cross-Species Atlas of Bacterial RNA 3′ Ends Reveals Termination Mechanistic Signatures and Evolutionary Patterns
33	Tanya Rachel Shanthakumar	Evolutionary Tradeoff Between Co-translational folding/assembly and Chaperone Dependency in Bacterial S-adenosyltransferases (MATs)
34	Yonatan Cohen	Antibiotic Exposure Dynamics Shape Evolutionary Trajectories and Fitness Costs of Ampicillin Resistance in E. coli
35	Meydan Cohen	Candidate stem cell isolation and transplantation in Hexacorallia
36	Gavriel Minor	Investigating C/EBPB as a novel candidate regulator of mitochondrial and nuclear gene expression
37	Sefi Weinstein	Predicting complex phenotypes from ancient genomes
38	Giulia Di Crosta	Ancient DNA analysis of early Levantine farmers from Motza, Israel

Talk 1
Metabolite correlation networks as complex phenotypes of adaptation-driving mutations

Sharon Samuel, Weronika Jasinska, Ezra Sternlicht, Matvey Nikelshparg, Daniel Kleiner, Shai Pilosof and Shimon Bershtein

Ben-Gurion University

Living organisms are organized into hierarchical levels of increasing complexity. As mutational effects propagate through these levels, multiple phenotypes are produced. However, identifying which phenotypes influence fitness and drive selection remains a key challenge in understanding genotype-phenotype-fitness relationships. Here, we demonstrate that mutation-induced structural changes in metabolite correlation networks, an organizational level with emergent properties shaped by the cumulative effects of multiple biochemical reactions and regulatory mechanisms, constitute complex phenotypes linking mutations to bacterial fitness. We engineered a metabolically suboptimal *E. coli* strain by replacing the *metK* gene encoding methionine adenosyltransferase (MAT) with an ortholog from *U. urealyticum* and subjected it to laboratory evolution. Analysis of correlation networks constructed from 2,118 untargeted metabolites revealed that adaptive mutations enhanced the strain's fitness by reducing network density, removing node hubs, and extensively rewiring connectivity. These changes yielded smaller, more cohesive, and better-interconnected network clusters. Moreover, evolution shifted the node representing S-adenosylmethionine (SAM), the product of the MAT-catalyzed reaction, from a peripheral role to a key connector between network clusters with a significantly increased centrality. None of the accumulated mutations potentially driving this transition directly influenced MAT activity or SAM metabolism, indicating that the shift in SAM's role is an adaptive phenotype emerging from the metabolic system's complexity. Targeted metabolomics of key nodes displaying similar network transitions unveiled additional metabolites involved in SAM-related pathways. We propose the construction and analysis of metabolite correlation networks as an experimental and analytical framework for mapping genotype-phenotype-fitness relationships and exploring the mechanisms of metabolic adaptation.

Talk 2
Culture, cognition, and social dynamics in a rat foraging tradition

Noa Truskanov

School of Zoology, Tel Aviv University

Cultural traditions, socially learned behaviors that persist within groups, can shape how animals interact with their environment, with potential consequences for cognition, ecology, and evolution. A classic example is pinecone opening in black rats (Rattus rattus), a complex extractive foraging skill that is vertically transmitted from mothers to offspring and enables exploitation of planted pine forest habitats. This system provides a rare opportunity to examine the implications of cultural experience in a natural foraging tradition. In this talk, I present work examining whether experience with the pinecone-opening tradition affects problem solving in other contexts, and how social interactions shape the social setting in which this behavior is expressed. Comparing rats from a pinecone-opening population with naïve rats in novel extractive foraging tasks, we found no general cognitive advantage of cultural background. Instead, cultural experience biased how individuals approached novel problems, producing task-specific effects rather than an overall enhancement in performance. Examining the social interactions surrounding pinecone opening in semi-natural captive colonies, we found pronounced individual differences in initiation and proficiency. Although adults typically open pinecones solitarily, the behavior is embedded in frequent visiting and scrounging interactions that are biased toward more proficient individuals. These interaction patterns may help explain why horizontal transmission of the skill is limited, while also highlighting social dynamics that allow access to pinecone resources without direct skill acquisition. Taken together, the problem-solving outcomes do not point to the emergence of enhanced cognitive performance, and the social setting of the tradition is unlikely to drive the evolution of enhanced cognition; instead, it may weaken selection on traits related to skill learning and promote cognitive polymorphism. By integrating cognitive testing with analyses of social behavior, this work provides novel insights into the potential evolutionary consequences of cultural traditions and on how culture and cognition interact in animal societies.

Talk 3
When does coevolution matter in microbial communities?

Nittay Meroz, Tal Livny, Yael Sorokin, Jonathan Friedman

Institute of Environmental Science, Hebrew University

Evolutionary dynamics in laboratory microbial populations are often repeatable across replicates, suggesting they may be predictable. However, in natural settings, species evolve within complex communities, and the extent to which such biotic contexts shape evolutionary outcomes remains unclear. To investigate this, we evolved 11bacterial species alone and in diverse pairwise co-cultures. While some partner-specific effects occurred, evolutionary outcomes were largely independent of co-culture identity—even for species already pre-adapted to the abiotic environment. To explain this robustness to community context, we developed a theoretical model capturing the boom-and-bust dynamics imposed by serial passaging in experimental evolution. The model shows that selection acts mainly early in the growth cycle, when population densities are low and interspecific interactions are weak, limiting the influence of co-cultured species on adaptive trajectories. These results suggest that under typical experimental conditions, biotic context may play a surprisingly limited role in shaping evolution. This decoupling may help explain the consistency of microbial evolution and could simplify predictions of evolutionary outcomes in both laboratory and natural microbial communities experiencing intermittent growth.

Talk 4

Bacterial and viral transmission capture different temporal scales of rock hyrax social networks

Amiyaal Ilany, Prameek Kannan, Asaf Tamam, Tomer Oron, Adi Stern, Sondra Turjeman, Omri Koren, Nicola Segata

School of Zoology, Tel Aviv University

Animal social networks have profound effects on fitness, yet they are difficult to observe and quantify in the wild. Here, we show that microbial transmission can be used to reconstruct the social networks of wild rock hyraxes (Procavia capensis) across multiple temporal scales. We collected fecal samples from marked individuals and performed shotgun metagenomic sequencing. From these data, we assembled microbial genomes, identifying a high proportion of previously undescribed bacterial taxa. For bacterial species present in multiple individuals, we reconstructed phylogenetic relationships and inferred cases of strain transmission, revealing long-term social associations. For example, a male that had dispersed from its natal group continued to share most of its bacterial strains with members of its previous group. Applying a similar approach to DNA viruses instead captured short-term transmission patterns: the same male predominantly shared viral strains with members of its current group. Together, these results demonstrate that different classes of microbes capture distinct temporal layers of animal social networks. More broadly, they highlight a central role for social interactions in structuring microbiomes at the levels of individuals, groups, and populations, with important implications for ecology and evolution.

Talk 5
The evolution of longevity from the microbiome perspective

Darar Bega, Yonatan Bendett, Lilach Hadany

Life Science, Tel-Aviv University

How natural selection shapes organisms' pattern of senescence is a fundamental evolutionary question. Most theories that deal with the evolution of senescence focus on the aging individual or its genes. Here, we propose considering not only the host and its genetic makeup, but also the microbes it hosts. A conflict between host genes and microbes in the context of senescence is expected: the individual serves as a vehicle for spreading its genes as long as it reproduces or helps its relatives, but serves as a vehicle for microbial transmission whenever it interacts with other individuals, regardless of kinship. As a result, selection acting on microbes that affect host senescence may differ from selection acting on host genes with similar effect. Here we construct mathematical models and consider different microbial effects on host senescence, as well as the possible costs associated with such effects. We find that selection tends to favor microbes that slow senescence under wider conditions compared to genes with similar effects. This result may shed light on several phenomena such as menopause and the increased longevity of social species, suggesting that microbes may benefit from extended host lifespan even when host genes do not.

Talk 6
What about male quality? A model to predict male investment in a single female

Aviad Heifetz, Yael Lubin, Jutta Schneider, Michal Segoli

Management and Economics Department, Open University of Israel

Monogyny, a rare, little-understood mating system, contradicts conventional sex roles, as the male puts his effort into mating with a single female, while the female may mate multiple times. Previous mathematical models suggested that monogyny is likely to evolve in cases where there is a male-biased sex ratio, which is typical in species with extreme female-biased sexual size dimorphism (eSSD). While previous models mainly consider the species level, potential individual strategies have received little attention. Here we use a game theory approach, considering the interplay between male and female decisions, to address how variation in male quality (e.g., size or body condition) affect the monogynous male mating strategy. The model was based on the biology of widow spiders, where males exhibit extreme mating investment including prolonged courtship, mate guarding, genital damage and even self-sacrifice, but can be relevant to other species with eSSD. The results of the model confirm previous predictions and point to a novel, testable, and somewhat surprising prediction: unless females are extremely rare relative to males, and/or male survival prospects are very slim, the highest quality males would avoid extreme investment and rather set out to look for additional females to mate with. This is because high-quality males face a lower risk that the female will not use their sperm, and they are also likely to be accepted by subsequent (even already mated) females. Future studies could test this hypothesis experimentally by comparing the tendency of males of varying qualities to invest in a current mate under different demographic and ecological conditions.

Talk 7
A latent drive: How Evolution Silenced (and Can Restore) Female Sexual Behavior

Eya Wolfson, Shachaf Shapira, Rizwanul Haque, Mattia Morandi, Elena Fidel, Shifra Ben-Dor, Gil Stelzer, Neta Regev-Rudzki, Meital Oren-Suissa

Brain Sciences, WIS

Across the animal kingdom, reproductive strategies drive the propagation and evolution of species. In sexually reproducing species, sexual behavior is subjected to selection and affects fitness. In the Caenorhabditis genus, androdioecy has evolved independently in C. elegans and two other species from a common dioecious ancestor, resulting in a substantial shift in the evolutionary forces exerted upon the species. However, the ways in which changes in the mating strategy affect the behavioral patterns and the underlying neuronal mechanisms remain mostly unexplored. Strikingly, we found that, while C. elegans hermaphrodites remain largely passive and often avoid males, females of the gonochoristic C. afra, C. japonica, C. brenneri and C. inopinata exhibit a pronounced sex drive towards males, actively engaging in and initiating mating. Despite the lack of any obvious anatomical changes in their sensory neurons compared to hermaphrodites, C. afra females exhibit a clear attraction to male-emitted cues that is mediated by a distinct neuronal activation pattern, absent in hermaphrodites. Importantly, we found that under induced reproductive pressure across generations, sperm-deficient C. elegans hermaphrodites switch to female-like behaviors, suggesting the existence of a suppressed neuronal mechanism. This change is accompanied by the emergence of attraction to male cues and female-like neuronal activity. We compared the transcriptomes of 1st- and 20th- generation pseudofemales (F0, F20), and C. afra females, and identified downregulation of neuropeptides as a key modulator of female mating behavior. Importantly, knockdown of specific neuropeptides in hermaphrodites was sufficient to induce female sexual behaviors, while their overexpression in C. afra females suppressed sexual drive. Together, our work offers an opportunity to explore the origins of female sexual attraction, and how it can be evolutionarily silenced yet retained in neural circuits, providing a framework to study how nervous systems adapt to shifting reproductive strategies and evolutionary pressures.

Talk 8
Indirect evolutionary rescue in an obligate bacterial mutualism

Yael Baranovitch

Plant Pathology and Microbiology, The Hebrew University of Jerusalem

Evolution is a fundamental force shaping biological systems, yet most experimental studies focus on single species evolving in isolation. In nature, however, species live in communities, where evolution in one species can affect the persistence of others. In antagonistic interactions such as predator–prey systems, rapid evolution in one species has been shown to either lead to the extinction of its partner or indirectly rescue it from extinction, a process known as indirect evolutionary rescue (IER). Whether IER can occur in other types of interactions, particularly mutualisms, remains largely unexplored. Here, I investigate how evolution in one species affects its partner within a microbial mutualism. I developed an experimental system that allows one species to evolve while its interacting partner is maintained in an ancestral state. Using this system, I (co)evolved a pair of Escherichia coli strains that exchange essential amino acids and form an obligate mutualistic interaction. I find that IER can occur in bacterial mutualisms only when both species evolve together. When coevolution was prevented, mutualistic populations frequently went extinct. Under coevolution, persistence was driven by adaptation in one strain that indirectly rescued its partner from extinction. This rescue was associated with mutations in metabolic pathways that reduced amino-acid requirements and increased population growth, thereby enhancing partner survival. These results demonstrate that coevolution can be essential for preventing extinction in mutualistic interactions by enabling IER and promoting long-term community persistence.

Talk 9

Mothers build fortresses: Parsing the costs of egg sac construction in two widow spider (Latrodectus) species

Yael Lubin, Malay Pandey, Oded Berger-Tal, Michal Segoli

Desert Ecology, BGU

In oviparous species, maternal protection of eggs enhances offspring survival but incurs costs to mothers. These costs may include the expenditure of energy, time, or materials devoted to defense against natural enemies and protection from environmental stressors. Spiders protect their eggs by enclosing them in silk egg sacs. The brown widow spider, Latrodectus geometricus (Theridiidae), additionally constructs spike-like silk projections on the outer surface of its egg sacs. These structures have been shown to reduce parasitism by the wasp Philolema latrodecti relative to the smooth-surfaced egg sacs of a congener, the white widow spider, L. pallidus. Here, we examined the additional costs to mothers associated with producing these spike-like structures. We documented the behavioral sequences involved in egg sac construction and compared maternal investment in L. geometricus and L. pallidus in terms of silk expenditure, construction duration, and the rate of silk deposition. We predicted that L. geometricus would exhibit greater maternal investment across these measures. When scaled to maternal body mass, the total mass of silk invested in egg sac covering did not differ between the two species. However, L. geometricus females spent more time constructing each egg sac and showed a higher rate of silk-dabbing activity. This increased allocation of time and effort may reflect the additional cost of producing the spike-like silk structures characteristic of the brown widow spider. Overall, our results suggest that the two species employ distinct egg sac construction strategies, potentially shaped by the different environmental pressures experienced during their evolutionary histories.

Talk 10

Simulating gene birth in the lab: Insights into orphan genes from random sequences

Idan Frumkin

Tel Aviv University

Orphan genes, genes with no detectable homologs in other lineages, represent a major source of evolutionary novelty. Many are thought to arise de novo from previously non-coding DNA, yet the mechanisms by which random sequences acquire biological function remain poorly understood. How does a non-functional stretch of DNA become a gene? To address this question, we experimentally simulate gene birth in the laboratory using large libraries of synthetic random DNA sequences that are designed to be transcribed and translated in bacteria. These libraries model newly emerging genes and allow us to observe evolutionary processes that would normally unfold over millions of years. In previous screens, we identified random sequences that confer fitness advantages, including protection against toxins and bacteriophages, demonstrating that functional genes can emerge from sequence space without prior evolutionary history. Building on this, we now combine high-throughput fitness assays with experimental evolution to quantify the distribution of fitness effects of expressing random sequences in bacteria. This effort also reveals toxic variants that inhibit cellular growth, which we use to probe how new molecular toxicities arise. Together, this framework provides a controlled experimental platform to uncover fundamental principles governing de novo gene birth and evolutionary innovation.

Talk 11
Evolution of supergenes: lessons from social chromosomes

Eyal Privman

Institute of Evolution, University of Haifa

Supergenes are large genomic regions with suppressed recombination that determine complex polymorphic traits. "Social chromosomes" harbor supergenes that determine colony structure in polymorphic ant species, which form either monogyne (single queen) or polygyne colonies (with multiple queens). Two analogous supergenes evolved independently in two diverged ant lineages – Solenopsis fire ants and Formica wood ants. In both cases, the monogyne form is associated with one supergene haplotype (M) and the polygyne form is associated with the other (P). We discovered a third such system in the desert ant Cataglyphis niger, by reduced-representation genomic sequencing (RAD-seq) of 20 individuals from each of 30 nests. Our analyses identify a large chromosomal region of suppressed recombination between the M and P haplotypes, at least 6Mbp long, which is associated with the social structure. Surprisingly, the Cataglyphis social chromosome is homologous to the Solenopsis chromosome, even though these lineages diverged more than 90 million years ago. We suggest that this ancient chromosome harbors an ancestral genetic toolkit that was reused for the repeated evolution of sociobiological traits across diverse ant species. The repeated evolution of supergenes (in Solenopsis and Cataglyphis) on an ancient social chromosome present excellent opportunities for the study of evolution and maintenance of genomic architectures underlying adaptive complex polymorphisms.

Talk 12
Darwinian origin of life

Roy Yaniv, Doron Lancet

Molecular Genetics, Weizmann Institute

There is no widely accepted path from early protocells to the Last Universal Common Ancestor (LUCA), precursor of all species on planet Earth. It is accepted that protocells must have been simple enough to assemble spontaneously from the primordial soup, but at the same time sufficiently complex to undergo Darwinian evolution. The two wide-open questions are: 1) what could constitute such protocells, and 2) what their hereditary mechanism was. A quarter of a century ago, our group proposed that this could be heterogeneous nanoscopic lipid micelles that form spontaneously [1], in the realm of Lipid First. Our Graded Autocatalysis Reproduction domain (GARD) model, proved by rigorous kinetic computer simulations, suggests that the chemical composition of micelles harbor a mutually catalytic network [2], reaching a capacity to self-reproduce upon cycles of growth and fission. These micelles portray the physical property of dynamic attractors, strongly enhancing the odds of reproduction, mutations, natural selection, potentially leading to Darwinian evolution at a very early stage [3]. Micelles are strong candidates for being very early protocells, as they constitute excellent catalytic reactors, supporting the emergence of mutually catalytic networks (early metabolism) in a stable spatial volume [3]. Finally, combinatorics of typical micelles with 100-300 lipids, appearing in a soup owning tens of thousands of lipid types, each micelle will have a different composition, powerfully supporting natural selection [4]. With the abovementioned accumulated evidence, it seems highly plausible that micellar protocells could seed origin of life, as they undergo Darwinian evolution all the way to LUCA [5].

Talk 13

Genomic ancestry of remains from Herod's mausoleum shows links to local populations

Batel Attias, Roi Porat, Anna Belfer-Cohen, Shai Carmi, Benjamin Yakir, David Reich

Department of Genetics, The Hebrew University of Jerusalem

The Roman era was a period of profound transformation marked by imperial expansion and cultural exchange across the Mediterranean and Near East. Yet, the genetic composition of individuals from this period remains largely unexplored. Our study addresses this gap by presenting the first Roman-period genomes from Judea, recovered from Herodium – one of the most historically and archaeologically significant landmarks in the early Roman southern Levant. Constructed by Herod the Great around 30 BCE, Herodium functioned as a fortified palace and administrative center and remained an important seat of power for two centuries. Over time, it hosted a cosmopolitan mix of rulers and occupants, including Hasmonean and Roman elites, and later Jewish rebels during the First Jewish–Roman War and the Bar Kokhba Revolt. It is also renowned as the final resting place of King Herod, as described by Flavius Josephus. We recovered and analyzed ancient DNA from four male individuals excavated from distinct monuments within the Herodium complex. Genomic analyses yielded two key findings. First, kinship reconstruction revealed no close familial ties among the individuals up to the second degree. Second, population modeling indicated strong genetic similarity across all individuals, clustering with Late Bronze Age Levantine groups (Canaanites) from the Mediterranean coast. Despite the site's cosmopolitan character, these individuals exhibit continuity with earlier local populations. These results provide the first genomic insight into Roman-period Judea and establish the Herodium genomes generated in this study as a valuable reference for future genetic and archaeological research in the region.

Talk 14
Immune Activation of Symbiotic Hexacorallia Induces Algae Expulsion

Shany K. Barkan Zaslavsky, Alona Azarov, Shani Talice, Grace A. Snyder, Orly Gershoni-Yahalom, Nikki Traylor-Knowles, Benyamin Rosental

Microbiology, Immunology, and Genetics, Ben Gurion University

Rising seawater temperatures have increased coral bleaching events worldwide, an event in which the coral's symbiotic algae is expelled. This bleaching effect is detrimental for coral reefs. Previous research on coral heat stress induced bleaching found that different immune genes were differentially regulated and suggested immune activation. This led to the assumption that the immune response is a consequence of bleaching. Previously, we discovered phagocytic immune cells in Hexacorallia, a subclass containing stony corals and sea anemones. Furthermore, these immune cells increased their activity when we exposed them to heat stress. We then aimed to separate the two processes of phagocytosis vs. algae intake for symbiosis. To test this, we have used a Hexacorallia model system: the sea anemone Exaiptasia diaphana – which can be reared with and without symbiotic algae. We developed a cellular algae intake assay to test the effects of heat stress on symbiosis. We saw that while exposure to heat stress increases phagocytic activity, that same stress reduces algae intake. We then asked whether activation of the immune system could lead to algae expulsion. To this end, we injected immune activators into whole polyps and measured algae expulsion. We found that immune activation on its own might cause algae expulsion similar to that of heat stress. Hence, our data provides the basis for further study into heat induced immune activation in corals and sea anemones. We aim to elucidate the mechanisms in which immune activation leads to the destruction of symbiosis between the host and their symbiotic algae.

Talk 15
Tracing historical disease transmission using FST

Ohad Peled, Keith D. Harris, Gili Greenbaum

Hebrew University

Diseases induce some of the strongest selection pressures on our genomes. These immune-related selection pressures shape genetic variation at the central component of the immune system, the major histocompatibility complex (MHC). The MHC is the most diverse genomic region in our genomes due to the long-term balancing selection generated by disease burden on populations. While genome-wide patterns of genetic differentiation are often explained by geography and demographic history, it remains unclear whether the MHC follows similar trajectories or whether pathogen-mediated selection produces distinct signatures. To address this, we quantified population differentiation in the MHC and compared it to genome-wide expectations using a normalized measure of genetic differentiation (FST). We applied this framework to 54 populations from the Human Genome Diversity Project (HGDP). We observe that, overall, the pairwise FST values in the MHC are lower than the genomic background, suggesting higher immune-related similarity between populations than expected by processes not related to disease burden. However, several population pairs, many involving East Asian populations, showed comparatively higher MHC differentiation, indicating that MHC patterns are not uniform across populations. We further found that MHC class II, often associated with bacterial or fungal recognition, showed the strongest deviation from genome-wide patterns and the weakest correlation with genome-wide FST , implying partially distinct selective and demographic patterns within the MHC. To understand which cultural and ecological drivers are driving these patterns, we used an extensive database of such factors related to disease burden that was assembled for this purpose, DisECCO, in a multivariable analysis framework. Extent and timing of animal domestication, and the timing of transition to urbanized societies emerged as strong contributors to explaining MHC differentiation patterns across populations. Together, these results indicate that MHC differentiation is shaped by evolutionary forces that are tied to cultural innovations. Furthermore, our analyses pinpoint populations and subregions where historical disease transmission coupled with human gene flow have had a strong impact on how immune-related variation is shaped.

Talk 16
De novo rates of a Trypanosoma-resistant mutation in two human populations

Adi Livnat, Daniel Melamed, Revital Shemer, Evgeni Bolotin, Michael B. Yakass, Dorit Fink-Barkai, Edem K. Hiadzi, Karl L. Skorecki

Institute of Evolution, University of Haifa

Mutation rates have long been measured as averages across many genomic positions. Recently, a method to measure the rates of individual mutations was applied to a narrow region in the human hemoglobin subunit beta (HBB) gene containing the site of the hemoglobin S (HbS) mutation as well as to a paralogous hemoglobin subunit delta (HBD) region, in sperm samples from sub-Saharan African and northern European donors [Melamed et al., Genome Res. 32, 488–498 (2022)]. The HbS mutation, which protects against malaria while causing sickle-cell anemia in homozygotes, originated de novo significantly more frequently in the HBB gene in Africans compared to the other three test cases combined (the European HBB gene and the European and African HBD gene). Here, we apply this approach to the human apolipoprotein L1 (APOL1) gene containing the site of the G1 1024A→G mutation, which protects against African sleeping sickness caused by Trypanosoma brucei gambiense while causing a substantially increased risk of chronic kidney disease in homozygotes. We find that the 1024A→G mutation is the mutation of highest de novo origination rate and deviates most from the genome-wide average rate for its type (A→G) compared to all other observable mutations in the region and that it originates de novo significantly more frequently in Africans than in Europeans—i.e., in the population where it is of adaptive significance. The results are unexpected given the notion that the probability of a specific mutational event is independent of its value to the organism and underscore the importance of studying mutation rates at the individual-mutation resolution.

Talk 17
Flipping a Coin or Playing with Genes? Genetic Mechanisms Behind Male-Biased Offspring in Mammals

Moran Gershoni

Volcani Institute

In mammals, offspring sex is determined by the sex-chromosomal content of the fertilizing sperm. While the expected sex ratio is ~1:1, deviations are frequently observed, suggesting a role for genetic mechanisms that challenge classic Fisherian expectations. In livestock, particularly dairy cattle, such skew has major economic implications, as female calves are preferred for milk production. We analyzed over 800,000 insemination, calving records, and pedigree data from 1,300 Israeli Holstein bulls. GWAS identified 3 paternal X-linked loci (QTLs) significantly associated with a male-biased sex ratio. Genome -based kinship analysis revealed two multi-generation lineages with a heritable pattern of progenies male bias. Whole-genome sequencing of one lineage identified a polymorphism in SPZ1, a transcription factor expressed specifically in post-meiotic spermatids and known to activate genes on the otherwise silenced X chromosome that are important to the completion of sperm maturation. Co-expression analysis of SPZ1 and testis-specific genes identified X-linked spermiogenesis post-meiotic genes located adjacent to the GWAS QTLs, linking the population and pedigree-level results and suggesting a possible post-meiotic regulatory impairment in SPZ1- or QTL-carriers. In support, functional assays demonstrated semen from SPZ1-variant bulls have normal X:Y ratios in raw ejaculates but Y-enrichment after swim-up challenge, indicating impaired motility or viability of X-bearing sperm. IVF experiments with SPZ1-variant sperm yielded an excess of male embryos. Furthermore, SPZ1-variant bulls exhibited fewer sperm with intact acrosomes, a hallmark of sperm maturation, suggesting physiological deficits associated with disrupted post-meiotic gene activation. This work provides evidence for an X-linked regulatory mechanism that biases sperm function and offspring sex, representing a rare example of post-meiotic sex-ratio distortion in mammals. These findings challenge the assumption of random sex determination, highlight a role for selection acting at the gamete level, and open the door for evolutionary and agricultural applications in sex ratio management.

Talk 18
Geometry of high-dimensional fitness landscapes leads to deterministic epistatic dynamics

Yotam Lifschytz, Yitzhak Pilpel, Ariel Amir

Physics, Weizmann institute of science

Evolutionary trajectories of asexual populations are fully characterized by the distribution of fitness effects (DFE), which represents the maximal information available about future stochastic evolutionary dynamics. Here, we analyze and compare DFEs emerging from three of the most widely used fitness landscape models -- the Sherrington-Kirkpatrick spin-glass model, the NK model, and Fisher's Geometric Model -- to identify common behavior and the origin of some empirically observed phenomena. We find that all three models exhibit similar evolution of the DFE which is deterministic on the distribution scale, as well as other key qualitative DFE dynamics observed in asexual evolution experiments. Specifically, recent studies of LTEE populations have shown that the fitness effects of individual mutations rapidly lose autocorrelation over evolutionary time. We find that this behavior is reproduced across all three fitness-landscape models and arises from long-term epistatic dynamics that are deterministic on the genome-wide scale. Furthermore, we find that local fitness peaks reached by adaptive walks in all three models are "sharp", lacking neutral and near-neutral mutations. Together, these behaviors arise generically across distinct fitness-landscape models and follow from the geometry of high-dimensional fitness landscapes and their accessible peaks, suggesting a universality that is independent of organism and environment details.

Talk 19
Evolution of Menopause: the Mama's Boy Hypothesis

Tami Yosef, Liran Samuni, Yoav Ram

School of Zoology, Tel Aviv University

Menopause is characterized by a prolonged post-reproductive lifespan. It is an evolutionary puzzle and is rare among mammals, well-documented only in humans and a few toothed whale species (e.g., killer whales). Previous studies suggest that the evolution of menopause can be explained by kin selection, particularly the “grandmother hypothesis,” in which post-reproductive females increase inclusive fitness by helping their descendants. Menopause may have evolved via two evolutionary pathways: "live long" (extended lifespan with unchanged reproductive duration) or "stop early" (shortened reproductive duration). We developed an evolutionary, age- and sex-structured mathematical model that incorporates life-history, social structure, and demography to test whether a menopause-inducing allele can invade a non-menopausal population when post-reproductive females increase the survival and/or fecundity of younger kin within their social group. We parameterized the model using data from humans, chimpanzees, baboons, elephants, sperm whales, and killer whales. Our model’s predictions align with empirically observed post-reproductive representation values: it predicts menopause at empirically plausible ages only in species with menopause, under both evolutionary pathways. Consistent with prior work identifying male philopatry as a driver of increased female relatedness to the social group, we find that the selection for menopause is driven mostly by post-reproductive female help that increases male survival. We therefore propose an update to the grandmother hypothesis, which we term the “mama’s boy hypothesis”: menopause evolves when post-reproductive help increases the survival of philopatric sons and grandsons, who contribute disporportionately to maternal inclusive fitness.

Talk 20
Copying the popular mimics drift in social learning

Yoav Ram

School of Zoology, Tel Aviv University

Social learning strategies such as payoff-biased learning, conformity, and prestige bias are thought to shape behavioural traditions in group-living animals, including humans. However, the evolutionary consequences of prestige bias—when learners preferentially copy individuals who are already widely copied—remain unclear . Using analytical and simulation models of finite populations, we study role-model choice based on success and prestige bias. Success bias consistently favours higher-payoff traits and acts like directional selection. In contrast, prestige bias generates rich-get-richer dynamics analogous to genetic drift: initially common traits are more likely to spread and fix, even when neutral or mildly maladaptive. Strong prestige bias in highly social groups therefore promotes rapid cultural change and arbitrary divergence in behavioural traditions between animal groups.

Talk 21
Selection on molecular combinations: asymmetric constraints in the evolution of venom systems

Yehu Moran

Ecology, Evolution and Behavior, The Hebrew University of Jerusalem

Complex molecular systems are often composed of multiple components whose individual effects are weak or difficult to detect in isolation, while system-level function emerges from interactions among components. This raises a fundamental evolutionary question: how does selection act on molecular elements whose fitness effects depend on specific partners rather than on standalone activity? Animal venoms provide a tractable context for addressing this question. Although venoms are chemically complex mixtures, their ecological effects are frequently dominated by a small number of highly potent toxins. Using sea anemones as a model system, I argue that part of venom complexity may reflect selection acting on combinations of components rather than on individual toxins alone. In the sea anemone Nematostella vectensis, a single dominant peptide toxin, Nv1, largely determines predator interactions but is metabolically costly and subject to strong trade-offs. Within this system, we identified an additional venom peptide, Nve910, which shows extremely weak standalone toxicity yet strongly potentiates the effect of Nv1 when the two are combined. Nve910 is co-expressed with Nv1 in the same venom gland cell type, tightly co-regulated under stress, and phylogenetically restricted, despite having no sequence or structural similarity to Nv1. These observations suggest that some venom components may not be selected to function independently but instead evolve as interaction-dependent modifiers whose evolutionary trajectories are constrained by preexisting partners. More broadly, this logic is consistent with a form of asymmetric molecular canalization, in which historical molecular architectures bias the evolution of new components toward conditional, partner-dependent roles. I intend to discuss the roles of drift, linkage, and other historical constraints in shaping such interaction-dependent components and explore whether selection on molecular combinations may represent a more general principle extending beyond venoms to other complex molecular systems.

Talk 22
HLA Escape and Exposure: A Balancing Act in Viral Evolution

Sinai Sacharen, Alison Tarke, Alba Grifoni, John Sidney, Alessandro Sette, Tomer Hertz

Microbiology Immunology and Genetics, Ben-Gurion University of the Negev

The escalating arms race between pathogens and host immune systems represents one of nature's most compelling examples of coevolutionary dynamics. While viral immune escape has long dominated our understanding of pathogen evolution, emerging evidence suggests that the relationship between host genetics and viral mutation is far more nuanced. Previous work has demonstrated that viral mutations can lead to escape from both antibodies and T-cells. The Human Leukocyte Antigen (HLA) system presents short peptides on the surface of cells that can activate T-cells. We developed HEX (HLA Escape and Exposure), a computational framework that predicts the effects of viral mutations on HLA presentation. Using HEX we identified a previously underappreciated mechanism in host-pathogen evolution: the simultaneous occurrence of immune escape and immune exposure events due to viral mutations. By analyzing observed mutations across time in influenza A/H1N1, SARS-CoV-2, and HIV-1, three viruses with distinct transmission and persistence strategies, we demonstrate that viral mutations frequently generate novel HLA-peptide interactions alongside traditional escape variants. Our analysis of temporal dynamics across three decades shows that escape and exposure trajectories are highly correlated ($r > 0.94$), suggesting a balanced evolutionary strategy. Critically, we discovered that mutations driving escape from antibodies are significantly enriched for HLA exposure, indicating coupling between humoral and cellular immune pressures at the molecular level. Population-level analysis of the 27 most common HLA alleles (>97% global population coverage), reveals striking differences in escape-to-exposure ratios across HLA types. Alleles associated with severe COVID-19 outcomes exhibited significantly higher escape/exposure ratios, while those linked to favourable disease outcomes showed elevated exposure frequencies. Furthermore, the genome-wide escape/exposure ratio correlated strongly with global SARS-CoV-2 mortality ($r = 0.66$), suggesting this metric may predict pathogenic potential and epidemic severity. These findings challenge the escape-centric paradigm and suggest that human populations maintain polymorphic HLA alleles, in part, to balance immune evasion and exposure, highlighting a fundamental principle of coevolution in rapidly evolving pathogens and with implications for understanding how population genetic variation shapes disease outcomes globally.

Talk 23

Divergent effects of forest fragmentation on endangered black howler monkey population genetics and gut microbiomes: insights from molecular data

Keren Klass, Sarie Van Belle, Julie Teichroeb, Eva Wikberg, Gwen Duytschaever, Hadjira Hamou, Maria-Luisa Savo Sardaro, Ohad Peled, Adriana Marcela Morales-Guerrero, Anthony Di Fiore, Katherine Amato, Amanda Melin, Gili Greenbaum

Ecology, Evolution, and Behavior, Hebrew University of Jerusalem

Habitat loss and fragmentation are urgent threats to biodiversity. Molecular data can be informative regarding the effects of fragmentation on wild populations. For endangered black howler monkeys (Alouatta pigra) inhabiting a landscape with increasing levels of fragmentation in Chiapas, Mexico, we sequenced 9567 SNPs from 158 fecal samples to test the hypothesis that their population genetic patterns conform to the classic theoretical paradigm: increasing fragmentation reduces gene flow and local genetic diversity, and increases inbreeding and population genetic structure. In addition, we sequenced 9472 microbial ASVs from 307 fecal samples to test the hypothesis that black howler gut microbiome diversity decreases and heterogeneity increases with increasing fragmentation. Using LASSO variable reduction and multiple regression analyses, we identified the specific habitat and demographic variables that shaped each of these aspects of black howler biology. While gut microbiome patterns conformed to our predictions, population genetic patterns did not: With increasing fragmentation, heterozygosity increased while inbreeding decreased, and population genetic structure decreased. A gene-flow mapping analysis (EEMS) showed that gene flow was highest in the most fragmented part of the landscape. Taken together, our results indicate that, surprisingly, increasing forest fragmentation forced black howlers to move across the matrix more, not less. This highlights fragmentation's variable effects on different aspects of a single population's biology, and the importance of understanding these myriad impacts for effective conservation.

Talk 24

Functional characterization of specialized immune cells in a cnidarian reveals an ancestral antiviral program

Itamar Kozlovski, Ton Sharoni, Shani Levy, Adrian Jaimes-Becerra, Shani Talice, Hee-Jin Kwak, Daria Aleshkina, Reuven Aharoni, Xavier Grau-Bové, Ola Karmi, Benyamin Rosental, Arnau Sebe-Pedros, Yehu Moran

Microbiology, Immunology, and Genetics, Ben-Gurion University

Examining early-branching animal phyla can help reconstruct the evolutionary origins of immune cells. Here, we characterized immune-related cell programs in embryos of the sea anemone Nematostella vectensis, a model of Cnidaria, which diverged ~600 million years ago from other animals. Using a transgenic Nematostella reporter line expressing mCherry under the RLRb antiviral promoter, we identified a morphologically and transcriptomically distinct cell population activated by the viral mimic poly(I:C). These cells upregulate immune effector and regulator genes and show increased phagocytic activity. Bulk RNA sequencing of RLRb expressing cells and single-cell transcriptomics revealed gene regulatory programs expressed in specialized immune cells under basal conditions and upon activation. Comparing Nematostella's immune expression profile with that of stony corals treated with the immunostimulant 2′3′-Cyclic GMP-AMP demonstrated a conserved immune response across Hexacorallia. This study uncovers a novel cnidarian immune cell type involved in antiviral immunity, providing insights into the evolutionary history of innate immunity.

Talk 25
Pre-zygotic dynamics shaping inter-specific fertilization in reef invertebrates

Lachan Roth, Gal Eviatar, Yarden Freund, Omri Bronstein

Zoology, Tel-Aviv University

Inter-specific breeding, i.e., reproduction between individuals of different species, is often avoided to prevent the formation of low-fitted hybrids and maintain genetic diversity. However, the biological mechanisms underlying inter-specific breeding avoidance are poorly understood in marine invertebrates. Broadcast spawning is a widespread sexual reproduction strategy in marine invertebrates that involves shedding gametes into the water column, where external fertilization occurs. However, this process significantly increases the potential for inter-specific gamete encounters. Motility of benthic marine invertebrate species is often limited. As a result, pre-copulation behavior and mate-choice control are significantly challenged, and sperm transport relies primarily on sperm kinematics and water movement. Here, we examine whether inter-specific breeding avoidance is driven by differential sperm behavior. We tested the effect of egg derivatives from six sea urchin species (Echinodermata: Echinoidea) and two fire coral species (Cnidaria: Hydrozoa) on sea urchin sperm kinematics. We used Computer-Assisted Sperm Analysis (CASA) to accurately measure sperm motility parameters (e.g., velocity) and examined the sperm behavior in the presence of female derivatives of all eight species. Our results reveal that sperm was effectively activated by signals from all eggs lineages, regardless of species assignment - implying an equal sperm activation potential, regardless of phylogenetic distance. Nevertheless, sperm velocity analysis revealed a stronger signal within conspecifics, rather than across species boundaries. These findings provide new insight into the ecological and evolutionary processes shaping gamete interactions in reef invertebrates. Moreover, our results highlight the potential of CASA systems to be applied within marine invertebrates to elucidate the fundamental mechanisms underlying sexual reproduction at sea. Such insights can, in turn, enhance breeding efficiency and support sustainability in marine resource management.

Talk 26
Do Protein Networks Constrain or Enable Molecular Evolution?

Eran Tauber, Leo D. Creasey

Evolutionary and Environmental Biology, University of Haifa

Understanding how biological networks change through evolutionary time is essential for explaining the emergence and adaptation of complex traits. Protein interaction networks balance structural conservation with evolutionary plasticity, allowing organisms to adjust to shifting environmental conditions. We investigate these dynamics using the circadian clock of Drosophila as a model system. Drawing on data from the recently released 101 Drosophilidae Genomes Project, we examined patterns of evolution and co-evolution among 11 core circadian clock proteins across 65 species representing roughly 60 million years of divergence. Analysis of coding sequences with a sliding window approach uncovered pronounced variation in nucleotide divergence among genes, with Clk and per showing rapid evolution, while Pdp1 and sgg remained highly conserved. We further analyzed coordinated amino acid changes across proteins and detected 67 pairs of co-evolving sites, most frequently involving interactions between CLK and PER, CLK and CWO, and SGG and PER. Codon-based evolutionary models identified signatures of positive selection in four genes, namely cwo, jet, per, and sgg. Given the multifunctional roles of several clock components, we evaluated whether pleiotropy constrains their evolutionary rates. Using multiple measures of pleiotropy, we found no meaningful association between pleiotropic breadth and non-synonymous substitution rates across 440 Drosophila proteins, including those involved in circadian regulation. Together, these results indicate that the circadian clock network allows considerable evolutionary freedom among its components, potentially supporting lineage-specific tuning of clock function while accommodating their diverse biological roles.

Talk 27
What limits the lifetime reproductive success of fig wasps?

Michal Segoli, Manasa Kulkarni, Saskya van Nouhuys

Ben-Gurion University

The lifetime reproductive success of female insects may be constrained either by the availability of mature eggs or by the availability of suitable oviposition sites, including the time required to locate and exploit them. Disentangling the relative importance of these contrasting limitations and linking them to environmental conditions is notoriously difficult. Fig wasps offer a unique opportunity to address this problem because females complete their entire reproductive lifespan and die within a single fig. In a field experiment, we allowed 1, 5, or 9 female fig wasps to enter a fig and opened the fig 24 hours later, when all females had died. We dissected the females and counted the eggs remaining in their bodies. Females entering figs singly were egg-limited, exhausting their egg supply before death. In contrast, when multiple females entered a fig, many were unable to lay all of their eggs, indicating limitation by time or by the availability of suitable oviposition sites (i.e., fig flowers) rather than by egg supply. This constraint became increasingly pronounced as the number of founding females increased. In a parallel treatment, pollen was removed from females prior to fig entry. Females deprived of pollen tended to retain more eggs; however, this effect was not statistically significant, suggesting that the time required for pollination does not further constrain oviposition success. Together, these results indicate that under conditions of high intraspecific competition, selection may favor reduced investment in egg production relative to other biological functions, such as body maintenance or energy reserves. More broadly, this study highlights how different ecological constraints shape lifetime reproductive success in insects and underscores the value of fig wasps as a model system for addressing fundamental ecological and evolutionary questions.

Talk 28
Coupled dynamics of predator group formation and prey populations

Talia Borofsky, Erol Akçay, Daniel Rubenstein, Gili Greenbaum, Simon Levin

High Meadows Environmental Institute, Princeton University

Cooperative hunting can help predators capture large prey that is unattainable otherwise, and may select for predator group-living. However, many cooperatively hunting predators hunt in groups that exceed the size maximizing food intake. One explanation (Clark and Mangel 1984 Am Nat) is that predators behaving adaptively should continue to join a group until the fitness achieved in the group is the same as being alone. However, it is unclear whether large hunting groups should form in systems with multiple predator groups and depletable prey, nor how cooperative hunting alters the coexistence between big and small prey. We thus develop a theoretical model coupling the dynamics of predator group sizes to the population dynamics of predators hunting two types of prey: big prey best hunted cooperatively and small prey that can be caught alone. Individual predators adaptively join or leave groups based on fitness payoffs. This full model is compared to submodels in which either group size or population sizes are fixed. We find that while abundant large prey favors the formation of predator groups, those groups do not grow large. Although individuals should join groups until they exceed the group size maximizing individual fitness, instead group sizes generally end up at or below this optimum. Group size is constrained by slow growth of large prey and by high encounter rates among solitary individuals, which favor pair formation over joining large groups. Thus, synergies among multiple social mechanisms, such as territoriality, rather than the benefits of cooperative hunting alone, may be required to explain the evolution of large predator groups. Furthermore, accounting for dynamic group sizes leads to ecological predictions not found by models that fix predator group size; sometimes the dynamic model yields a bimodal distribution of group sizes that generates apparent facilitation, rather than competition, between prey types.

Talk 29

The evolution of sterol metabolism in mosquitoes: cholesterol as a driver for nectar-to-blood feeding transition

Amir Sapir, Sagiv Cohen, Benjamin Trabelcy, Yoram Gerchman, Alon Silberbush

Biology and the Environment, University of Haifa-Oranim

Sterol metabolism presents a major evolutionary paradox in animals. Many invertebrates require cholesterol for development, yet have lost the ability to synthesize it. Studying C. elegans, we showed that cholesterol auxotrophy evolved through reconfiguration of the remnant cholesterol-synthesis enzyme DHCR-24 to convert environmental plant and fungal sterols into cholesterol. This work provides a framework for understanding how essential metabolic pathways are repurposed rather than eliminated during evolution. Here, we extend this framework to mosquitoes, which undergo a major dietary transition from larval feeding on aquatic detritus to nectar and blood feeding in adults. Focusing on the Asian tiger mosquito, Aedes albopictus, we found that eggs receive a maternal contribution of cholesterol that declines during larval development, leading to developmental arrest when environmental sterols are absent. Strikingly, this decline coincides with upregulation of the sterol-conversion enzyme DHCR-24, consistent with activation of an environmental sterol–to–cholesterol conversion program required for completion of development. In adults, we discover that cholesterol acquired from the blood supports efficient egg production, completing a sterol metabolic cycle across generations. Comparative analyses indicate that DHCR-24 is widespread among insects but absent from some mosquito lineages, such as Anopheles, suggesting the evolution of alternative sterol-conversion routes. Our results show that cholesterol is one of the major metabolic drivers of the evolutionary transition from nectar to blood feeding, a transition that has made mosquitoes the deadliest animals on Earth through their role as disease vectors.

Talk 30

Can pathogen ecology and evolution within vertebrate hosts explain wildlife epidemiology? A case study of Bartonella bacteria in rodents

Hadas Hawlena, Ruth Rodríguez-Pastor, Nadav Knossow, Naama Shahar, Rami Amasha, Hagai Ktriel, Jeffrey E. Barrick

Mitrani Department for Desert Ecology, Ben-Gurion University

Pathogens circulating in wildlife communities pose major threats to global biodiversity and human health. To predict and control disease risk, it is therefore essential to identify the mechanisms driving pathogen epidemiology in natural reservoir hosts. Achieving this requires linking processes across biological scales—for example, how within-host dynamics influence pathogen transmission and persistence at the population level. However, logistical constraints on sampling and experimental manipulation in natural systems often limit our ability to uncover these mechanisms and to bridge scales. Here, I present a case study illustrating the power of integrating mathematical modeling, long-term field tracking, laboratory experiments, evolutionary assays, and immunological and genetic analyses to overcome these challenges. The study focuses on Bartonella bacteria infecting rodent communities in the northwestern Negev dunes, where infection prevalence consistently exceeds 75%, despite strong host immune responses that prevent reinfection. Using an agent-based model, we show that under assumptions of post-infection immunity, the observed prevalence cannot be explained unless infections persist far longer and immune waning occurs faster than suggested by laboratory experiments. Long-term tracking of wild rodents confirmed natural variation in infection duration, ranging from transient infections to persistent infections lasting several years, even in the absence of external transmission via vectors or direct host-to-host contact. Genetic analyses further suggest that long-lasting infections arise from immune-mediated interactions among co-infecting Bartonella strains within hosts. Complementary evolution experiments reveal that, beyond interstrain interactions, rapid Bartonella evolution enables strains to repeatedly escape host immune responses. Together, these results indicate that pathogen persistence in wildlife populations can be maintained by within-host eco-evolutionary dynamics alone, even without continuous external transmission. More broadly, this work underscores the need to incorporate within-host ecological and evolutionary processes into epidemiological theory and suggests that effective disease control may require disrupting internal host–pathogen feedbacks rather than relying solely on vector management.

Talk 31

Genes that are Used Together are More Likely to be Fused Together in Evolution by Mutational Mechanisms: A Bioinformatic Test of the Used-Fused Hypothesis

Evgeni Bolotin, Daniel Melamed, Adi Livnat

Institute of Evolution, University of Haifa

Cases of parallel or recurrent gene fusions in evolution as well as in genetic disease and cancer are difficult to explain, because unlike point mutations, they can require the repetition of a similar configuration of multiple breakpoints rather than the repetition of a single point mutation. The used-together-fused-together hypothesis holds that genes that are used together repeatedly and persistently in a specific context are more likely to undergo fusion mutation in the course of evolution for mechanistic reasons. This hypothesis offers to explain gene fusion in both evolution and disease under one umbrella. Using bioinformatic data, we tested this hypothesis against alternatives, including that all gene pairs can fuse by random mutation, but among pairs thus fused, those that had interacted previously are more likely to be favored by selection. Results show that across multiple measures of gene interaction, human genes whose orthologs are fused in one or more species are more likely to interact with each other than random pairs of genes of the same genomic distance between pair members; that an overlap exists between genes that fused in the course of evolution in non-human species and genes that undergo fusion in human cancers; and that across six primate species studied, fusions predominate over fissions and exhibit substantial evolutionary parallelism. Together, these results support the used-together-fused-together hypothesis over its alternatives. Multiple implications are discussed, including the relevance of mutational mechanisms to the evolution of genome organization, to the distribution of fitness effects of mutation, to evolutionary parallelism and more.

Talk 32

The legacy of past heatwaves on 'off-host' parasite stages: Reduced infection risk and costs in the Daphnia-Pasteuria system

Justine Boutry, Noa Lavi Shasha, Frida Ben-Ami

School of zoology, Tel Aviv University

Heatwaves challenge our understanding of how environmental stressors reshape host-parasite interactions, particularly during the critical "off-host" stages of endoparasites. These stages, often dismissed as inert and unaffected by environmental changes, remain a black box in ecological research despite their key role in parasites' life cycle. Here, we examined how heatwaves affect the infectivity and progression of infection of Pasteuria ramosa, a bacterial parasite of the planktonic crustacean Daphnia magna. In order to measure the respective influences of the bacterial genotype and the heatwaves, we exposed the off-host stages (=spores) from four genetically distinct parasite clones to three temperature regimes (20°C, 30°C, 40°C), and tested their subsequent effects on host and parasite traits. Heatwaves reduced parasite infectivity, regardless of parasite genotype. Intriguingly, heat-stressed spores induced genotype-specific shifts in their host: one host clone increased castration rates at higher temperatures, while others experienced moderate to dramatic declines. Furthermore, individuals exposed to heat-stressed spores that remained uninfected, exhibited enhanced survival, suggesting reduced costs of resistance against damaged parasite spores. This study provides insights into how heatwaves, endured only by the parasite, can modulate various aspects of host-parasite interactions, underlying the importance of the parasite's environmental history in evolutionary ecology and epidemiology.

Talk 33
Reconciling conflicting selection pressures in the plant self-incompatibility system

Tamar Friedlander, Amit Jangid, Ohad Not Feldheim

Hebrew University of Jerusalem

Complex biological systems should often reconcile conflicting selection pressures. In systems based on molecular recognition, molecules must specifically identify certain partners while excluding others. Here we study how such selection pressures shape the evolution of the self-incompatibility system in plants. This system inhibits self-fertilization using specific molecular recognition between proteins, expressed in the plant female and male reproductive organs. We study the impact of these opposing selection pressures on the amino acid frequencies in these proteins' recognition domain. We build on a theoretical framework enabling promiscuous recognition between proteins, as found empirically, and employ stochastic simulations to study their evolution. We find that selection exerts asymmetric responses of amino acid frequencies, affecting female proteins considerably, but hardly the male. Using large deviations theory, we well-approximate the simulated frequencies and find agreement with genomic data. Our work offers a general theoretical framework to study the impact of multiple selection pressures, applicable to additional biological systems.

Talk 34

GRANDMA: An Iterative Phylogenomic Framework for Inferring Nested and Multiple Allopolyploidization Events

Ronen Shtein, Tom Ulanovski, Dorothée Huchon, Tal Pupko, Itay Mayrose

School of Plant Sciences and Food Security, Tel Aviv University

Allopolyploidy, genome duplication resulting from hybridization, is a pervasive driver of diversification in flowering plants, yet reconstructing these reticulate evolutionary histories remains a significant methodological challenge. Current phylogenomic methods are either limited to identifying single hybridization events or fail to resolve complex, hierarchically structured scenarios where ancient polyploids act as parents in subsequent hybridizations ("nested hybridizations"). Furthermore, different inference methods often yield highly divergent network topologies when used on the same empirical data. One of the most commonly applied methods is GRAMPA, which utilizes gene-tree reconciliation on multi-labeled species trees (MUL-trees) under Maximum Parsimony, but is restricted to inferring a single allopolyploid event. To address these challenges, we present GRANDMA, an iterative framework that extends gene-tree reconciliation to infer multiple and nested allopolyploidization events. Unlike previous approaches, our method sequentially updates species and gene tree topologies to uncover layered reticulations. We introduce a completely re-implemented version of the tool that achieves up to a 10-fold reduction in execution time compared to the original GRAMPA implementation. To further enhance scalability, we implemented a "split mode" that partitions the dataset into subtrees following each inference step, improving efficiency on larger phylogenies. We validate these methods using simulated datasets and an empirical analysis of the genus Kalanchoe (Crassulaceae), a group characterized by extensive cytonuclear discordance. Our results demonstrate that this accelerated framework can accurately disentangle complex evolutionary webs, offering a step towards a scalable solution for reconstructing the reticulate history of diverse plant lineages.

Talk 35
Genomic signatures of increasing disease burden in recent prehistory

Keith D. Harris, Yuval Talmor, Merav B. Yefe Nof, Nimrod Marom, Yitzchak Jaffe, Viviane Slon, Gili Greenbaum

Ecology, Evolution and Behavior, Hebrew University of Jerusalem

One of the strongest selection pressures experienced by human populations is that driven by diseases on immune-related genomic regions. While it has been hypothesized for some time that disease burdens increased with the shift to agricultural and urbanized lifestyles, direct evidence for this hypothesis is lacking. Here, we capitalize on the accumulation of ancient genomic data to study changes in disease burden in human populations over the past 12,000 years. We investigated changes in genetic diversity and balancing selection in two distinct geographical and cultural centers in Southwest Eurasia and Eastern Asia, and found that not only is the major histocompatibility complex (MHC) the genomic region with the most substantial increases in diversity in terms of enrichment of genes and rates of increase, but that the rates of changes for individual genes are highly correlated between the two cultural centers, indicating similar selection pressures. We identify periods of time with substantial peaks in MHC diversity increase that primarily correspond to periods with settlement intensification, increased connectivity, and the expansion of animal domestication, which suggest that the most intensive disease burden occurred following the transition to sedentary lifestyle but prior to urbanization. These findings demonstrate the potential of our approach in uncovering the interplay between cultural shifts and selection, and provide strong support to the hypothesis that the levels of disease burden have substantially increased in recent prehistory following changes in lifestyle, connectivity and the introduction of domesticated animals.

Talk 36

Genome size variation is attributed to adaptive transposable elements silencing efficiency

Evgenii Potapenko, Bar Shermeister, Tali Mandel, Sariel Hübner

Galilee Research Institute (Migal), Tel-Hai College

Genome size varies in orders of magnitude across kingdoms, yet notable differences are also evident within species. Theory predicts that large genomes may be advantageous in small populations, yet empirical support has been contradictory, particularly regarding the link between genome size and environmental variation. Here, we investigate the role of genome size variation in adaptation using two sister species, Hordeum bulbosum and H. spontaneum, sampled across diverse environments and comprehensively assessed at genomic and phenotypic levels. We detected a consistent variation of circa 10% in genome size among populations of both species despite differences in mating system (selfing vs. outcrossing) which effected the variation within populations. Water shortage was identified as the major driver of genome expansion, mediated by the accumulation of transposable elements (TEs). Genome-wide association studies further identified TE silencing as the primary mechanism regulating genome size. Importantly, selection favored smaller genomes under benign conditions, whereas stressful environments reduced TE regulation, promoting TE accumulation and genome expansion. This expansion, in turn, increased genetic variability available for selection. Our results demonstrate that genome size is not a highlight the exaptive role of genome size variation in enhancing evolvability under changing climates.

Talk 37
Ape genomes reveal natural protection mechanisms against human diseases

Nachshon Egyes, Simon Fishilevich, Katharina Lange, Nitzan Haim, Mimi Shwartz, Ron Moran, Georgii Bazykin, Martin Kuhlwilm, Tomas Marques-Bonet, David Gokhman

Molecular Genetics, Weizmann Institute of Science

Human evolution has led to extraordinary adaptations, including the three-fold increase in our brain size, the transition to upright walking, and our particularly extended maturation and learning phase. However, these changes have also propelled the emergence of severe disorders, including Alzheimer's disease, bronchial asthma, and carcinoma. Here, we studied the evolutionary dynamics of disease emergence and disappearance by comparing the pathogenicity of variants in humans and other apes. Specifically, we intersected human disease-causing variants from the ClinVar archive with high-coverage genomes of 332 great ape individuals from diverse genetic backgrounds. Strikingly, we found 382 human disease-causing variants that are neutral in great apes, suggesting the existence of protection mechanisms that either evolved in apes or disappeared in humans. Our study revealed that the mechanisms protecting many of these variants are not restricted to a specific pathogenic variant, but are rather the result of the entire gene becoming protected in apes against pathogenic mutations. Interestingly, genes underlying diseases that affect fertility or hearing are particularly likely to evolve protection mechanisms in evolution. We further illustrated this by uncovering the compensatory mechanism in chimpanzees against a pathogenic allele in BMP15, which causes complete ovarian dysgenesis in humans, but is the wildtype allele in chimpanzees. Overall, our targeted approach not only sheds light on the evolutionary dynamics of disease resistance but also provides a framework for leveraging these natural protection mechanisms to inform therapeutic development.

Talk 38

A chromosome-level assembly of the endemic species Trifolium israeliticum reveals recent transposon expansion

Guy Horev, Evgenii Potapenko, Ari Meerson, Sivan Golan, Dikla Lifshitz, Einav Mayzlish-Gati, Sariel Hübner

Bioinformatics, Tel Hai College

Global biodiversity is under intense pressure, particularly in transition zones like the Flora Palaestina region, a critically important biodiversity hotspot and center of origin for numerous Crop Wild Relatives. Genomic approaches are essential for effective conservation, enabling population management strategies such as genetic rescue and the definition of critical ecological corridors. To safeguard endemic species in this heavily impacted region, the Israeli Biodiversity Conservation Consortium was established. Our inaugural effort is the genetic characterization of the endangered, endemic Israel clover, Trifolium israeliticum. Utilizing PacBio Hi-Fi and Hi-C sequencing, we generated a high-quality, chromosome-level de novo genome assembly. The assembly spans 870 Mbp and is resolved into 6 superscaffolds (N50: 144Mbp), consistent with 6 chromosomes established in cytogenetic data. Protein prediction confirmed the high quality with 46,068 yielded proteins and a 98% BUSCO completeness score. Comparative syntenic analysis with related Trifolium species further reveals a massive genomic rearrangement in T. israeliticum, suggesting significant genome instability and a potential reduction in fitness. Transposome analysis revealed a major peak of LTR expansion approximately 8 million years ago, suggesting its predicted divergence from T. subterraneum. Critically, a second, recent LTR expansion was identified in T. israeliticum that likely contributes to its current population instability. This high-quality genomic infrastructure illuminates the genetic drivers of extinction in T. israeliticum and provides an essential proof-of-concept and scalable roadmap for guiding conservation efforts for this species and additional endemic plant species.

Talk 39
Uncovering the regulatory changes that shaped human skeletal evolution

Nadav Mishol, Yizhi Yan, Itamar Nini, Adi Rozenblatt, Aya Kigel, Gal Bodek, Noam Priel, Lucas Estaban Wange, Simon Fishilevich, Zicong Zhang, Tomas Marques-Bonet, Fumitaka Inoue, David Gokhman

Molecular Genetics, Weizmann Institute of Science

Phenotypic divergence between species is thought to be driven primarily by gene regulatory changes. However, how these changes shaped human evolution remains largely obscure. Skeletal alterations have been particularly central in human evolution, facilitating upright locomotion and large brains, and influencing childbirth and our distinctive faces. Here, we employed massively parallel reporter assays (MPRAs) in key skeletal cells - chondroctyes - to uncover the functional role of the 540,000 enhancer and promoter substitutions that distinguish humans from their ape relatives. Using this atlas, we identified 15,077 sequences whose activity has diverged since our split from chimpanzees. We identified the FOS family of transcription factors as key players in shaping human-specific gene regulation. We also found that extra-cellular matrix (ECM) genes have diverged particularly extensively, indicating their key role in human evolution.

Talk 40
Applying biomedical tools in ecological research; Immunity and stem cell transplantation for corals

Shani Talice, Shany K. Barkan, Grace A. Snyder, Itamar Kozlovsky, Uzi Hadad, Yehu Moran, Orly Gershoni-Yahalom, Nikki Traylor-Knowles, Benyamin Rosental

Microbiology and Immunology, Ben Gurion University

We present the adaptation of human-oriented immunological methodologies to comparative studies in marine invertebrates, highlighting two projects that leverage flow cytometry–based techniques for the isolation and analysis of coral cells. Together, these studies demonstrate how advanced cellular and molecular immunology techniques can be translated from human systems to marine organisms, providing new insights into cnidarian immunity, regeneration, and resilience. Project 1 focuses on the cellular and functional characterization of immune cells in corals and sea anemones, with an emphasis on phagocytic populations. Our results demonstrate the presence of specialized immune phagocytes distinct from digestive or pinocytic cells. Furthermore, we observed that phagocytic activity increases under thermal stress, indicating that immune activation is coupled to elevated temperatures and may play a fundamental role in the early stages of coral bleaching. Project 2 explores the development of stem cell transplantation approaches in Hexacorallia. Our goal is to establish a framework for enhancing coral resilience through stem cell–based therapies. Using the model sea anemone Nematostella vectensis, which enables tracking of transgenic cell lines in vivo, we successfully followed mCherry-positive transplanted cells for up to two months. Confocal microscopy and flow cytometry confirmed the integration and proliferation of transplanted cells within host tissues, while RNA-deep sequencing validated their incorporation and differentiation. Serial transplantation experiments further demonstrated the long-term viability of candidate stem cell populations. We are currently translating this work to stony corals.
The specific projects funded by: ERC, NSF-BSF, Revive & Restore.

Talk 41
Metamorphosis: A natural and human history

Oren Harman

How many creatures walking on this earth / Have their first being in another form?" the Roman poet Ovid asked two thousand years ago. He could not have known the full extent of the truth: today, biologists estimate a stunning three-quarters of all animal species undergo some form of metamorphosis. But why must creatures go through massive destruction and remodeling to become who they are? Tracing the interweaving paths from Aristotle through Darwin, and from Rumi to Kafka to the paintings of Dali and the music of Richard Strauss, I show how the age-old preoccupation with metamorphosis, both in science and in culture, takes us to the very heart of questions of human identity and selfhood.

Talk 42
Morphologically complex flowers from a pollinator's perspective

Tamar Keasar

Department of Biology and the Environment, University of Haifa – Oranim

Plant-pollinator interactions have molded the stunning diversity of flower forms in nature. The flowers' morphology determines their accessibility for foraging pollinators. In some plant species, flower parts fuse to form elaborate structures. Consequently, insects require intricate motor routines to access their nectar and pollen. Learning to handle such 'complex' flowers efficiently requires much practice in the short term, but successful foragers often reap high long-term rewards. How may the short-term barriers to exploiting complex flowers be overcome, allowing the evolution and radiation of such flowers? A long-term research program in my lab addresses this question by combining field observations, behavioral experiments, evolutionary modeling, and exploration of large published datasets. Using the latter approach, we recently found that complex flower morphologies correlate with higher nectar (but not pollen) production across numerous plant species. In line with predictions from a game-theoretic model, we also demonstrated community-level matching between flower and bee morphologies. Communities of mostly shallow and radial flowers interacted with more bee species, had fewer interactions with eusocial bees, and were visited by smaller and shorter-tongued bees, than communities dominated by deep and bilateral flowers. Furthermore, the matching between bee and flower traits increased with latitude. Our research suggests pathways to the evolution of morphologically complex flowers by considering the behavior, life-history, and community composition of their pollination partners.

Talk 43
Uncovering the Role of Regulatory Variants in Neanderthal and Denisovan Evolution

Ryder Easterlin[1], Simon Fishilevich[2], Chengyu Deng[1], Nadav Mishol[2], Nadav Ahituv[1], David Gokhman[2]

[1] Institute for Human Genetics, University of California San Francisco, San Francisco, CA, USA
[2] Department of Molecular Genetics, Weizmann Institute of Science, Israel

Changes in gene regulation are key drivers of human evolution. However, which regulatory changes shaped human adaptations, and especially how, remains largely unknown. Here, we employed massively parallel reporter assays in skeletal and neural cells to uncover the functional role of all 57,406 variants that distinguish Neanderthals and Denisovans from other lineages. This comprehensive catalog revealed 792 single-nucleotide variants that altered archaic human gene expression. Interestingly, we detected examples of both divergent and convergent evolution between modern and archaic humans. For example, both lineages silenced the activity of an enhancer of *KDM8*, a gene involved in tumor progression, but Neanderthals and Denisovans achieved this through motif disruption, whereas modern humans accomplished this through hypermethylation. We also identified several skeletal and neural pathways that were particularly influenced by differentially active variants, including facial morphology, speech, and the motor system. Finally, we identified a substitution within the *PPM1E* gene that markedly increased gene activity. Introducing this allele into modern human embryonic stem cells using a CRISPR/Cas9 system, and differentiating them into neural progenitors confirmed that the archaic substitution significantly increases *PPM1E* expression. We then explored the phenotypic effect of *PPM1E* upregulation in archaic humans, and found that it likely decreased neuronal mushroom spine number, root number, and neurite length. Together, our findings provide the first comprehensive functional map of regulatory variants distinguishing archaic and modern humans, illuminating how changes in gene regulation may have shaped neural and skeletal traits that define these lineages.

Poster 1
Parthenogenic crayfish invasion in Israel, adaptivity aspects, and a possible biocontrol approach

Sharon Moscovitz, Shai A. Shaked, Noa Aschulai, Eliahu D. Aflalo, Hanoch Glassner, Dana Milstein, Tamar Guy-Haim, Yael Olek, Zohar Yanai, Ofer Ovadia, Amir Sagi

Life Sciences, Ben Gurion University of the Negev

The marbled crayfish Procambarus virginalis is a parthenogenetic invasive species created accidentally and spread worldwide by humans, thus lacking evolutionary history. A single individual can establish an entire population. Two introduction sites were recorded in Israel: in Ein Meshotetim, Siach stream, Haifa, and in Tzenan, Beit Guvrin. P. virginalis threatens amphibians, tolerates a wide range of conditions, and lacks natural enemies and predators in Israel, which does not inhabit local or endemic crayfish. P. virginalis further spread might negatively alter Israel's freshwater biodiversity. Since the 1980s, the giant river prawn Macrobrachium rosenbergii has been cultured in Israel. Non-GMO methods exploiting its sexual plasticity enable the production of monosex populations, which cannot reproduce. These populations have been applied since 2017 as biocontrol agents against snails in aquaculture. Given their predatory capacity and reproductive barriers, we assessed the feasibility of using monosex M. rosenbergii against P. virginalis. In a POC lab experiment, female prawns successfully preyed on small crayfish. In a field observation at the invaded Siach site, prawns were placed in August 2023, and the crayfish population was monitored until February 2024. However, the limited survey duration and high human disturbance restricted our conclusions. In the Tzenan site, digging efforts yielded few individuals, and they recovered completely even after two dry seasons, displaying astonishing adaptability to long dry periods. Further size-specific predation trials revealed that prawns predated on crayfish only when larger than them, while no reverse predation, of P. virginalis over M. rosenbergii, was observed. These experiments demonstrate the potential of monosex M. rosenbergii as sustainable biocontrol agents against P. virginalis, and a preliminary model based on the detailed experiments will be examined for biocontrol feasibility in small, isolated habitats.

Poster 2

Variation in Coloration and Ecological Adaptation of Amphibians Across Israel's Climatic Gradient

Gad Degani

Biotechnology, MIGAL – Galilee Research Institute, Kiryat Shmona, Israel

Amphibians in Israel show exceptional adaptive diversity across the country's climatic gradient, from Mediterranean habitats in the north to desert ecosystems in the south. This study examines variations in coloration, morphology, and ecological traits among representative species, emphasizing their adaptive and conservation significance.Hyla savignyi exhibits rapid skin color modulation linked to temperature and substrate, while Bufotes viridis (syn. Pseudepidalea viridis) shows polymorphic dorsal patterns reflecting local environmental pressures. The Eastern spadefoot toad Pelobates syriacus displays subtle dorsal patterning that enhances camouflage at the southern edge of its distribution. The Levant water frog Pelophylax bedriagae expresses diverse morphs—from cryptic brown to vivid green-yellow—indicating adaptation to varied aquatic habitats and possible roles in sexual signaling.The endemic Hula painted frog Latonia nigriventer combines cryptic dorsal coloration with stable ventral markings used for individual identification. Among urodeles, the fire salamander Salamandra infraimmaculata shows variability in spot patterns and mucus metabolites shaped by environmental stressors, while the banded newt Ommatotriton vittatus demonstrates pronounced seasonal dimorphism between terrestrial and aquatic phases.These examples underline the importance of coloration and morphological plasticity for survival across heterogeneous landscapes. Understanding such adaptive strategies is crucial for conserving amphibian diversity amid habitat loss and climate change. Keywords: Amphibians, coloration, adaptation, morphology, Israel, Hyla savignyi, Bufotes viridis, Pelophylax bedriagae, Latonia nigriventer, Ommatotriton vittatus, conservation.

Poster 3

Epitranscriptomic variation in banded newts (Ommatotriton Vittatus) across life stages and sexes in the semi-arid habitat in Northern Israel

Monika Almozlino, Ari Meerson, Gad Degani, Dani Bercovich

Biotechnology, Tel Hai College

The banded newt, Ommatotriton vittatus, is considered endangered in Israel, which is the southern border of its distribution and requires adaptation to highly unstable habitats. Banded newts have both aquatic and terrestrial forms, going through metamorphosis and various phenotypic changes during their life. Our group has previously reported on the extensive transcriptomic remodeling based on sex and especially the life stage of the newt. These dramatic changes in gene expression are likely accompanied by extensive epitranscriptomic regulation, which remains poorly understood. In this study, direct RNA sequencing was used to characterize m6A RNA modifications in 12 newts from the Nehalit population. We focused on 127 genes with multiple differentially modified regions (DMRs) in their transcripts, involved in structural, translational, and extracellular matrix processes. Among them, 18 genes showed clustering of methylation patterns according to life stage, particularly keratins and translation-related proteins, suggesting that m6A plays a regulatory role in structural remodelling and developmental transitions. In contrast, the majority of DMR genes were associated with housekeeping and stress-response functions and did not show life-stage-specific clustering. Cross-analysis with differential expression data further indicated that muscle, immune, and connective tissue pathways are co-regulated at both the transcriptional and epitranscriptomic levels. These findings provide the first evidence of m6A methylation patterns in O. vittatus and highlight their role in developmental transitions. The results advance understanding of transcriptomic–epitranscriptomic regulation in amphibian plasticity, and more generally, in vertebrate development.

Poster 4
Hypomethylation in Oikopleura dioica genome

Yael Klirs, Prof. Dorothée Huchon

School of Zoology, Tel-Aviv University

Cytosine DNA methylation is a conserved eukaryotic epigenetic modification that regulates gene expression, cellular differentiation, and development. It is broadly present across animal phyla, with only a few documented cases of secondary loss. Methylation patterns vary among animals; vertebrates typically exhibit high global CpG methylation, whereas many invertebrates display sparse or mosaic methylation. Because methylated regions tend to undergo CpG depletion, most invertebrates display bimodal CpG observed/expected (O/E) distributions. We investigated DNA methylation in tunicates and found that the tunicate Oikopleura dioica shows a unimodal CpG O/E distribution centered around 1, consistent with a loss of cytosine methylation. To evaluate this possibility, we (1) searched for key enzymes involved in cytosine methylation across tunicates, and (2) analyzed Oxford Nanopore reads we obtained from O. dioica for modified nucleotides. HMMER searches revealed the absence of all canonical enzymes required for cytosine methylation and demethylation in O. dioica. Nanopore-based methylation calls detected a small number of CpG sites with high coverage and apparent methylation frequencies of 1.0; however, given the lack of methylation machinery, these signals may represent basecalling artefacts rather than genuine methylated loci. Overall, our results support the loss of genome-wide cytosine methylation in O. dioica. The few CpG sites flagged as methylated warrant cautious interpretation, as they may reflect technical artefacts rather than residual biological methylation. If confirmed, this finding would place O. dioica among the exceptionally small group of animal lineages that have secondarily lost DNA cytosine methylation, offering new insights into the evolutionary plasticity of this regulatory system.

Poster 5

Programmed mtDNA ribosome frameshifting is selectively constrained across 17,530 metazoan species

Noam Shtolz, Michele Brischigliaro, Dan Mishmar, Antoni Barrientos

Life Sciences, Ben-Gurion University of the Negev

Throughout evolution, mitochondrial DNA (mtDNA) encodes essential genes for oxidative phosphorylation. Human mtDNA is compact (93% coding) and transcribed into polycistronic RNAs cleaved into individual mRNAs, except the ATP8-ATP6 gene pair. These essential ATP synthase subunits remain bi-cistronic with overlapping open reading frames conserved across metazoan evolution. Recently, we discovered that translation of this gene pair in humans relies on programmed ribosome frameshifting (PRF), where ribosomes slip on a heptanucleotide sequence, encounter an RNA hairpin structure and a -1 frame ATP8 stop codon, creating a molecular switch between complete ATP8 or truncated ATP8 plus ATP6, thus enabling coordinated stoichiometric regulation of both genes. We hypothesized that PRF served as selective constraint enabling the ATP8-ATP6 overlap. Analyzing 17,530 metazoan mtDNA sequences, we found the overlap averages ~11 nucleotides in non-mammalian species versus 46 nucleotides in mammals. In-silico screening revealed that the three PRF components—slip sequences, -1-frame stop codons, and hairpin structures—co-occur in species with extended overlaps but vary across taxa. Using DMS-MaPseq, we experimentally validated RNA structures in representative species: mouse (43 nt), chicken (11 nt), Drosophila (7 nt), and cephalopods, demonstrating that hairpin structures change with overlap length. Through systematic mutational analysis of the human hairpin, we identified critical nucleotides whose disruption abolishes hairpin formation, confirmed in vitro. Our findings suggest that while some PRF components are conserved across metazoans, mammals evolved an extended ATP8-ATP6 overlap with increased PRF machinery dependence. This offers an evolutionary explanation for selective constraints maintaining co-translated mtDNA gene pairs across metazoan evolution.

Poster 6
tSNP: A dimensionality reduction algorithm for genetic data

Ori Sharon, Prof. Liran Carmel

Department of Genetics, The Hebrew University of Jerusalem

Population structure reflects non-random genetic relationships shaped by geography, culture, and history. Dimensionality reduction methods, most notably principal component analysis (PCA), are widely used to visualize genome-wide single-nucleotide polymorphism (SNP) data in two or three dimensions while trying to preserve patterns of population structure. However, these generic methods do not explicitly exploit the ternary nature of SNP genotypes, which encode the count of reference alleles per locus (either 0, 1, or 2), and may therefore fail to capture subtle structure. Here, we introduce tSNP, a dimensionality reduction algorithm specifically tailored to ternary genetic data. It represents SNPs as lines, and genotypes as dots, and finds a two-dimensional embedding that optimizes geometric relationships between them in a way that captures allele-sharing patterns that are informative about population structure. We benchmark its performance against PCA, UMAP, and t-SNE on multiple simulated and empirical datasets, and examine cases where tSNP outperforms other methods in revealing large-scale patterns of population structure. These results indicate that directly exploiting the ternary representation of SNP data is a promising direction for dimensionality reduction in population genetics.

Poster 7

Changes in relatedness between mating pairs in the Asiatic wild ass (Equus hemionus) population following a water source management in the Negev Highlands

Noa Yaffa Kan-Lingwood, Alan R. Templeton, Naama Shahar, Dan I. Rubenstein, Amos Bouskila, Shirli Bar-David.

Mitrani Department of Desert Ecology, Ben-Gurion University

Inbreeding avoidance is a mating pattern explained in evolutionary terms by enhancing offspring fitness through maintenance of heterozygosity, a measure of genetic diversity. Among equids, two main mating systems occur: female-defense polygyny, where males maintain stable harems, and resource-defense polygyny, where solitary males defend territories near resources such as water. In the latter, social structure is fission–fusion, with flexible female group membership. While inbreeding avoidance occurs in harem systems, evidence from fission–fusion systems remain limited. We examined inbreeding avoidance in the fission–fusion Asiatic wild ass (Equus hemionus) population of the Negev Highlands and tested how a water source management intervention conducted in 2020 affected mating pair relatedness (MPR). The intervention increased water sources and consequently the number of territorial mating males. We evaluated changes in MPR through time and space (old versus new water sources). From 2020–2024, fecal samples were collected via direct observations and non-invasive genetic sampling. DNA was genotyped at 625 SNPs to assign parentage and estimate relatedness among mating pairs. Throughout all years of the study, we identified 558 unique genotypes from 2,509 samples, including 73 offspring with both parents sampled. Based on Kolmogorov-Smirnov (KS) tests, the overall MPR was significantly higher than expected under random mating ($r = 0.071$; KS $p = 0.0002$). Annual MPR significantly decreased after management (2020–2022 vs. 2019; KS $p = 0.004$), but by 2023 it no longer differed from pre-management (KS $p = 0.155$). MPR was higher at the old versus the new water sources (KS $p = 0.006$). Spatial analyses indicated that most males that reproduced before the management did not relocate to new water sources, implying that newly established territorial males at new water sources achieved matings with non-related females. These results suggest that water distribution can influence mating patterns and support genetic diversity, but the re-increase of MPR to pre-management levels by 2023 suggests that inbreeding avoidance is not consistently maintained and may require continued management.

Poster 8
A-to-I editing generates unparalleled complexity in the neural proteome of cephalopods

Kobi Shapira, Ruti Balter, David Gorelik, Joshua J C Rosenthal, Erez Y. Levanon, Eli Eisenberg

Bar-Ilan University

Post-transcriptional and post-translational modifications lead to the generation of diverse protein products from a single gene and make a crucial contribution to cells' complexity. Among these modifications, adenosine-to-inosine RNA editing (A-to-I editing) is a post-transcriptional mechanism capable of reprogramming protein-coding sequences ("recoding"). While prevalent across various metazoan taxa, it attains unparalleled proportions in coleoid cephalopods, where tens of thousands of sites undergo recoding. Numerous messages contain multiple editing sites, each presenting a binary option, resulting in an exponentially large number of potential protein isoforms. However, the extent to which this complexity is realized in the cephalopod nervous system remains unknown. Here, we employ deep-sequencing complemented by a graph-theoretic computational analysis to unravel the extent of this phenomenon in the Longfin Inshore Squid (Doryteuthis pealeii) and the common octopus (Octopus vulgaris). Targeted sequencing, utilizing both short- and long-read approaches, reveals an unprecedented abundance of encoded isoforms in highly edited squid transcripts, up to 67,000 from a single gene. These numbers even surpass the number of splice variants encoded by Drosophila melanogaster's dscam gene (Down Syndrome Cell Adhesion Molecule), a renowned example of extreme diversity due to post-transcriptional RNA processing. Analysis of whole-transcriptome sequencing data from the common octopus further underscores the widespread diversification across genes in coleoid cephalopods. Remarkably, at least 21% of well-covered genes manifest at least 50 distinct editing-isoforms. The distribution of expression levels per isoform exhibits a broad spectrum with no discernible dominance of a small subset of isoforms, suggesting a functional role for numerous distinct isoforms.

Poster 9
Sympatric speciation in killer whales may be driven by mother's curse and mito-nuclear compatibility

Yoav Livne, Yoav Ram

School of Zoology, Tel Aviv University

Killer whales (Orcinus orca) are diversifying into ecotypes, some sympatric and some allopatric, that differ in habitat, morphology, culture, and diet. Most explanations invoke ecological specialization or culturally mediated barriers to gene flow. We propose an alternative mechanism in which divergence is driven by the matrilineal social system of killer whales, characterized by bisexual philopatry and outbreeding, together with selection against incompatibilities between nuclear and mitochondrial genes. Maternal mitochondrial inheritance and female philopatry can promote pod-specific, male-harming mitochondrial alleles via "mother's curse" dynamics: selection against male-harming mitochondrial mutations is absent, and mitochondrial gene flow among pods is limited. Compensatory nuclear alleles that restore male function can then evolve within pods, generating mito-nuclear coadaptation. Consequently, mito-nuclear incompatibilities that reduce fitness in offspring produced by parents from different mito-nuclear coadapted backgrounds can act as a post-zygotic genetic barrier even when pods overlap spatially. This post-zygotic barrier can, in turn, select for assortative mating via culturally transmitted cues linked to matrilineal identity (e.g., vocal dialects), reinforcing differentiation. We test this hypothesis using individual-based simulations of evolution in a subdivided matrilineal population. The model includes three bi-allelic loci, a haploid mitochondrial locus and a diploid nuclear locus, that jointly determine mito-nuclear compatibility and male fitness, and a nuclear assortment modifier locus that biases female mate choice toward males from the same mitochondrial lineage (often clan-linked). We find that this mechanism can generate stable genetic divergence among pods even in the absence of ecological selection, due to a combination of genetic, social, and cultural processes.

Poster 10

Bacterial Secretion Systems as Drivers of Ecological Adaptation: A Pan-Genomic Analysis Reveals Niche-Specific Evolutionary Patterns

Erez Weisberg

Microbiology and Plant Health, Hebrew University Of Jerusalem Faculty of Agriculture

Bacteria profoundly shape their environments through secretion systems—large, often multi-gene protein complexes that deliver effectors across cell membranes to modulate host physiology, mediate interbacterial competition, and facilitate ecological adaptation. While most research has focused on micro-scale interactions linking individual secretion systems to specific virulence phenotypes in model pathogens, a macro-scale understanding of how these systems distribute across bacterial phylogeny and ecological niches remains largely unexplored. Here, we leverage comparative genomics of over 84,000 unique bacterial genomes to reveal the phylogenetic constraints and ecological drivers shaping secretion system evolution across the bacterial kingdom. We analyzed 84,000 non-redundant bacterial genomes from 10 phyla, each systematically profiled for 14 major secretion systems (T1SS-T11SS, Sec, Tat, eCIS) using signature gene detection. Genomes were enriched with ecological metadata including host associations, tissue sites, and environmental parameters. To distinguish genuine ecological adaptations from phylogenetic artifacts, we employed genome-wide association studies with multiple phylogenetically-corrected statistical methods (Scoary2, EvoLink), ensuring detected correlations reflect adaptive evolution rather than shared ancestry. Our preliminary analysis has already revealed striking niche-specific secretion system patterns. For example, T3SS is prevalent in mollusca-associated Vibrio (79%) but nearly absent from marine Vibrio strains (18%). Phyllosphere-adapted Sphingomonas show near-universal T1SS presence (98%) compared to non-phyllosphere relatives (74%). Skin-associated Acinetobacter exhibit pronounced T2SS enrichment (84%) versus other human-associated strains (36%). Additional patterns include dramatic secretion system depletion in intracellular bacteria and opposing tissue-specific distributions of T5SS subtypes within human hosts. These examples represent a subset of the numerous ecological associations we are uncovering across all 14 secretion systems. These patterns demonstrate that secretion systems function as key drivers of ecological specialization beyond their traditional roles in pathogenesis. Future directions include pipeline optimization and systematic analysis of genomic contexts flanking secretion systems to discover previously uncharacterized effectors, chaperones, and transcriptional regulators mediating ecological adaptation.

Poster 11
Changes in heritability of autoimmune diseases in the last 12,000 years

Ester Notarius

Evolution, Ecology and Behavior, Hebrew University of Jerusalem

Human populations have experienced dramatic cultural upheavals over the last millennia, including the major transitions to agricultural and urbanized societies. These changes have generated selection pressures that have affected genomic variation and shifted the genetic diversity across our genomes. One of the major changes we have recently identified, through analyses of ancient DNA (aDNA), is an increase in genetic diversity in immune-related genes due to the increase in disease burden associated with major cultural transitions. Such correlated shifts may affect the genetic architecture of traits and their heritability, particularly for autoimmune diseases which are strongly affected by variation in immune-related genes. To investigate how genetic-diversity shifts over the last 12,000 years have influenced the heritability of autoimmune diseases, we used aDNA to track heterozygosity changes across loci associated with both autoimmune and other complex phenotypes. We first integrated GWAS data from the UK biobank and polygenic scores (PGS) from the PGS catalog to compute the effect sizes of genes associated with autoimmune diseases, and then utilized a mathematical scaling relationship between heritability and heterozygosity to quantify heritability changes of different phenotypes. Using this approach, we found that autoimmune diseases exhibit greater increases in heritability compared to other complex phenotypes. For example, we observe that the heritability of multiple sclerosis has increased by about 50% over the last 12,000 years (Fold Change = 1.52; 95% CI: 1.2–1.9); a conservative permutation simulation procedure indicated that this result falls within the 91st percentile compared to a randomized simulation. These results imply that major events in human history, specifically those increasing pathogen exposure, have shaped the genetic architecture of autoimmune disease and have led to higher heritability of these disorders today compared with past populations.

Poster 12

What a Functional Morphologist Can Learn About Bat Evolution from a Rodent and a Tongue

Aleksandra Panyutina

The Bat Lab for Neuro-Ecology, Tel Aviv University

Echolocation is a crucial tool for spatial orientation in at least two major groups of mammals. The role of echolocation in the diversification of these groups can be debated, but its extraordinary importance is beyond doubt. This makes the question of how echolocation originated particularly intriguing. Until recently, discussions about the origin of echolocation in bats were largely speculative. To date, there is still no clear answer as to which morphological traits unequivocally indicate the presence of echolocation. Consequently, identifying the point of its emergence in the fossil record remains impossible. However, we do have keys to this problem. One such key is a non-bat echolocating mammal, Typhlomys. Typhlomys is an echolocating rodent that emits signals at around 90 kHz. These signals are very similar in structure to the FM calls of bats. Moreover, they are organized into bouts, as in bats. Typhlomys is currently the only known mammal that uses ultrasonic echolocation for navigation in an aerial environment outside Chiroptera. It therefore represents the only extant model that can be used to reconstruct a scenario for the emergence of echolocation in bats. Another key is the independent origin of echolocation in some pteropodids. Until recently, their echolocation was considered primitive; however, studies have shown that Rousettus can use its echolocation apparatus very smartly. But did their ancestors possess the laryngeal echolocation typical of most bats? And if they did, why might it have been lost? Most importantly, how does Rousettus manage to produce echolocation clicks at frequencies above 40 kHz using a structure such as the tongue? By combining the morpho-ecological model of Typhlomys with our current understanding of echolocation in fruit bats, we can propose a possible scenario for the origin and evolution of echolocation in bat ancestors and outline a pathway for testing the resulting hypotheses.

Poster 13

Volatile but persistent co-existence of self-compatibility and self-incompatibility in plants

Amit Jangid, Ohad Noy Feldheim, Tamar Friedlander

Department of Plant Sciences and Genetics, Hebrew University of Jerusalem Rehovot, Israel

Plants employ diverse mating strategies, including self- and cross-fertilization or their mixture. Despite the ubiquity of mixed-mating – the use of both self- and cross-fertilization in the same population – its evolutionary sources and dynamic stability remain elusive. Here we study self-incompatibility, where self-fertilization is disabled by molecular recognition, and enabled if mutations disrupt this recognition. Using population-level stochastic simulations, we model the effects of two main parameters on the prevailing mating mode: promiscuity of molecular recognition and inbreeding depression – penalizing self-compatibility. We reveal a phase diagram with three regimes: complete self-incompatibility (SI), complete self-compatibility (SC), and a mixture combining both. The latter mixed mode, described here for the first time, exhibits vigorous, non-decaying fluctuations in the proportions of individuals occupying either mating mode. Finally, we find that transitions between mating modes are often reversible. This study offers new insight into the evolutionary dynamics of plant reproductive systems.

Poster 14
Heat Stress Activates Hexacorallia Immune Cells and Inhibits Endo-Symbiosis

Alona Azarov, Shany Barkan, Shani Talice, Oren Levy, Nikki Traylor-Knowles, Orly Gershini-Yahalom, Benyamin Rosental

The Shraga Segal Department of Microbiology, Immunology and Genetics, Ben Gurion University

Coral reefs are vital ecosystems, supporting nearly a quarter of all marine life and contributing significantly to ocean biodiversity. Corals, which are marine animals in the subclass Hexacorallia, live in a symbiotic relationship with intracellular algae that supply most of their nutrients. When exposed to heat stress, coral cells expel these algae, resulting in coral bleaching. If the elevated temperatures continue, the algae will not return to the coral cells, which can lead to the coral's death. Some theories propose that during heat stress, algae release reactive oxygen species (ROS) that damage host tissues until expelled. However, our findings indicate that during heat stress-induced bleaching, immune activation markers such as ROS and Nitric Oxide (NO) are increased in the phagocytic cells of the Hexacorallian model, the symbiotic sea anemone Exaptasia diaphana (E. diaphana). These results imply that immune cells are responsible for the induction of ROS and NO, potentially triggering bleaching. Additionally, through our development of a cellular algae intake assay using apo-symbiotic E. diaphana cells, we demonstrate that heat stress, as well as immunogenic carboxylated beads, inhibit the endosymbiosis process while increasing phagocytic activity.

Poster 15
Increased survival of low-frequency lineages during fluctuations in resource abundance

Shira Zion, Sophia Katz, Ruth Hershberg

Medicine, Technion

Bacterial populations can endure prolonged resource exhaustion by entering long-term stationary phase (LTSP). We previously showed that LTSP Escherichia coli populations are dominated by high-frequency lineages that continually accumulate adaptive mutations. Here, we combined whole-genome sequencing with barcode-based lineage tracing to examine LTSP lineage dynamics at high resolution. We find that, contrary to random expectations, LTSP lineages disproportionately originate from barcodes that were rare during exponential growth, suggesting that slow growth enhances death phase survival and entry into LTSP. Conversely, after four months in LTSP, when populations were made to re-adapt to growth in fresh media, most surviving lineages were ones that were extremely rare during LTSP, while the most successful among them were those already relatively frequent at the final LTSP time point. Our results highlight the disproportionate role of rare lineages - often overlooked in standard analyses - in driving microbial adaptation to shifting conditions.

Poster 16
The effect of variants in cis-regulatory elements on divergent gene expression

G. Bodek, Y. Weiss, S. Fishilevich, Y. Bazykin, L. Kuderna, M. Kuhlwilm, T. Marques-Bonet, D. Gokhman

Molecular Biology, Weizmann Institute of Science

Human adaptations are thought to be driven primarily by changes to gene regulatory elements, and specifically to cis-regulatory elements such as promoters and enhancers. However, we are still far from understanding the relationship between sequence and expression changes, and the evolutionary forces that shape this relationship. Here, we study sequence divergence in genes whose expression has changed between humans and chimpanzees through cis-regulation. To this end, we utilized human-chimp hybrid cells. In these hybrid cells, the alleles of both species experience the same cellular environment, and thus any expression change can only be attributed to cis-regulatory changes between the species. We combined this data with the first comprehensive catalog of the single-nucleotide variants that separate humans from other apes, using whole genome sequencing of 139 great apes. We then compared sequence divergence in genes whose expression changed in human and chimp evolution to those with conserved expression. We found that the promoters of differentially expressed genes have accumulated significantly more variants and estimate that > 10% of the variants that separate these species altered gene expression. This estimate doubles to >20% when focusing on active chromatin and transcription factor binding sites. We found genes with more extreme expression changes show a greater number of derived variants, suggesting that extreme expression changes are the result of a gradual accumulation of sequences changes, rather than single events. Examining the evolutionary forces underlying this divergence, we found that sequence composition differences bias some genes toward more rapid expression evolution, alongside contributions from relaxed negative selection and positive selection. Together, our results shed light on how cis-regulatory sequence divergence contributes to gene expression differences between humans and chimpanzees, providing insight into the molecular mechanisms underlying regulatory evolution.

Poster 17
Discovery and functional characterization of cytotoxic cells in planarians

Eliya Sultan, Chew Chai, Orly Gershoni-Yahalom, Benyamin Rosental, Bo Wang

BGU

We rigorously map differential splicing events between human and mouse in several immune cell types using publicly available RNA sequencing datasets. We then tested if the change is in all cell types of the same species or just in immune cells.

Poster 18
A Transposable elements vantage on wheat domestication

Guy Ben Zvi, Sariel Hübner

Biology, Technion - Israel Institute of Technology

Domestication marks a major turning point in human history, which has also modified the genomes of the domesticated plants. Tetraploid wheat was one of the Neolithic founder crops and remains a major cultivated species today. We investigated how domestication altered the abundance and distribution of transposable elements (TEs) and structural variation (SV) in wheat, revealing genomic changes associated with domestication syndrome traits. Our results demonstrate that extensive TE proliferation before and during the Pleistocene–Holocene transition expanded standing genetic variation and phenotypic diversity. This expansion has provided raw material for selection by early farmers including of a 4Kbp Gypsy insertion in the BTR1-3B gene causing a loss of function and contributing to the establishment of the non-shattering phenotype. We further show that purifying selection was more efficient in purging TEs among wild populations, whereas domesticated wheat maintained TE clusters around genes that are under selection. We propose a model in which climatic instability triggered genome-wide TE bursts, expanding genetic variation including at domestication traits. As climate stabilized, purifying selection gradually removed deleterious TEs insertions, while early farmers selectively preserved advantageous phenotypes, thus maintaining TE-rich regions around key domestication genes. This model provides an integrative framework linking climate driven genomic changes, selection, divergence and domestication.

Poster 19
Exploring Heteropteran genomes: New insights from Oncopeltus homeoboxes

Itai Fein

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

One of the fundamental pillars of studying the evolution of insect embryonic development is the examination of segmentation and the molecular networks responsible for it. Like all other arthropods, the insect body is divided into multiple segments, with each segment developing different internal or external structures. Each segment, therefore, needs to receive an identity to ensure proper development. One of the most important and well-studied gene families in insect development is the homeobox gene family, which has been studied mostly in holometabolous (full metamorphosis) insects. To better understand the evolutionary history of insect segmentation, one should look at the presence of homeoboxes in the less “derived” hemimetabolous (partial metamorphosis) insects. In this work, we describe the homeobox genes in the genomes of bugs from the clades Heteroptera and Auchenorrhyncha. Our work shows that these clades have a novel homeobox gene in the “Hox-Like” class, which is expressed in the developing gemband of the large milkweed bug Oncopeltus fasciatus. In Heteroptera, this “Hemipteran Additional Hox-Like gene” also has conserved synteny, further hinting that this gene has a conserved role in embryonic development. Aside from this novelty, the homeobox gene repertoire in Heteroptera and Auchenorrhyncha is quite conserved, which makes them good candidates for understanding ancestral gene content and the segmentation mode of ancestral insect embryonic development.

Poster 20
Role of RdRps in the cnidarian model Nematostella vectensis

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

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

In invertebrates, the production of small interfering RNAs (siRNAs) is central to RNA interference (RNAi), a key antiviral defense mechanism that silences viral RNAs. Beyond this cytoplasmic role, studies in plants and fungi have shown that RNAi also contributes to genome stability by repressing repetitive and transposable elements. RNA-dependent RNA polymerases (RdRPs) are essential components of these pathways: they amplify antiviral responses through secondary siRNA production and, in some systems, participate in transcriptional regulation. However, the functions of RdRPs in animals outside of nematodes remain poorly understood. Basally branching animal lineages, such as cnidarians, provide a valuable framework for investigating the evolutionary origins of RNAi. We identified four RdRP homologs in the genome of the cnidarian Nematostella vectensis, which have been conserved for approximately 500 million years. Following injection of a synthetic viral mimic, poly(I:C), three N. vectensis RdRPs were upregulated and enriched in putative immune cell populations. RdRP knockout mutants exhibited elevated levels of the core virome present in most laboratory populations; however, the data indicate an absence of secondary siRNA production in N. vectensis. Subcellular localization analyses revealed distinct nuclear localization patterns of RdRPs and other RNAi components in embryos, suggesting a potential link between RNAi and transcriptional regulation. Upon poly(I:C) challenge, RdRP knockout embryos displayed nuclear stress phenotypes accompanied by cytoplasmic accumulation of double-stranded RNA. We propose that RdRPs in N. vectensis contribute to defense against viruses and repetitive elements, but likely through mechanisms distinct from canonical RNAi amplification. Future studies in cnidarians will help clarify the evolutionary origins and nuclear functions of RdRPs in epigenetic regulation.

Poster 21

A mixed clonal-plasmid outbreak of KPC-carrying Enterobacterales, simultaneously driven by an E. coli ST6448 clone and an IncN plasmid carrying an NTEKPC-Y element

Mor N. Lurie-Weinberger, Meirav Mor, Ella Kaplan, Darya Bychenko-Banyas, Ophir Kastel, Elizabeth Temkin, Nadya Rakovitsky, David Schwartz, Chaim Ben-Zvi, Alona Keren-Paz, Yehuda Carmeli

National Institute for Antibiotic Resistance & Infection Control - Ministry of Health, Tel Aviv Souasky Medical Center

Background: Carbapenemase-producing Enterobacterales (CPE) are a growing cause of outbreaks in healthcare institutions. Unlike clonal outbreaks, plasmid-driven outbreaks may involve multiple species, making it less obvious that an outbreak is occurring. Here we describe a large multi-species outbreak of KPC-producing Enterobacterales in an Israeli children's hospital. Methods: One hundred KPC-positive isolates collected during the outbreak in 2021-2022 were characterized using Fourier transform infrared spectroscopy (FTIR) and molecular and plasmid typing. Whole genome sequencing (WGS) was performed on 35 representative isolates. Conjugation experiments were used to check plasmid transferability Results: The isolates comprised 8 Enterobacterales species, most commonly Escherichia coli (n=40) and Klebsiella pneumoniae (n=38). Most E. coli isolates (40/49) formed a single FTIR phenotypic cluster, indicating a clonal outbreak, which WGS identified as ST6448. The K. pneumoniae isolates belonged to 5 different STs, which is inconsistent withclonal spread. Thirty-two of the 35 sequenced isolates carried blaKPC-2 and an IncN[pMLST15] type rep gene. ONT sequencing of E. coli and K. pneumoniae isolates identified an 89,315bp IncN[pMLST15] type plasmid carrying blaKPC-2 on a non-Tn4401-element NTEKPC-Y. PCR confirmed the presence of the IncN replicon in 82/100 isolates. Conjugation experiments revealed a high frequency of transfer of this plasmid from E. coli to K. pneumoniae, and a lower frequency from K. pneumoniae to E. coli. Conclusions: Our results suggest an outbreak with a mixed mode of transmission: clonal spread of E. coli and a parallel plasmid-driven outbreak of various species, which was likely the consequence of multiple in vivo conjugation events from E. coli to various Enterobacterales, and subsequent spread of two K. pneumoniae clones. Our findings highlight the complex and rapidly evolving epidemiology of carbapenemases. This outbreak demonstrates that the distinction between clonal and plasmid-mediated outbreak may be erroneous, and that containment of outbreaks with a mixed mode of transmission can be achieved via strict infection control efforts.

Poster 22
Density dependence introduces new types of gene drive dynamics

Sviatoslav R. Rybnikov, Gili Greenbaum, Adam Lampert

The Hebrew University of Jerusalem

Gene drives – artificial genetic constructs capable of rapidly spreading a fitness-reducing trait through a target population – are widely regarded as a promising pest and disease-vector control method. However, their field implementation requires an understanding of how the eco-evolutionary interactions in gene drives affect population dynamics. While most theoretical models assume that the fitness cost of a gene-drive allele is constant, many phenotypes are characterized by a density-dependent fitness cost. We developed a mathematical model in which gene-drive fitness costs depend on population density. We focus on two practically important classes of gene drives: additive drives, intended for unconditional spread, and dominant drives, expected to display threshold-dependent behavior. We show that density-dependent fitness costs alter the dynamics of both classes. Specifically, additive drives may exhibit, in addition to fixation or loss, bistability, oscillatory dynamics converging to a stable polymorphic equilibrium, or even sustained undamped oscillations. For dominant drives, density-dependent fitness costs can generate not only the standard fixation–loss bistability, but also fixation–polymorphism and fixation–cycling bistability. Even when density dependence does not change the qualitative outcome predicted under constant fitness costs, it can considerably modify quantitative predictions, leading to partial population suppression rather than complete eradication, or shifting the threshold between gene-drive spread and loss. The emergence of novel deployment outcomes and quantitative deviations underscores the need for heightened caution when deploying gene drives.

Poster 23
Eco-Evolutionary Cross Talk in Multiple-Species Biofilm

Adrian Lehvy

Life Sciences, Ben Gurion University

Microbial interactions are routinely characterized via phenotypic assays, and the by quantification of species abundances, in planktonic cultures. Inter-species trends alone provide a purely ecological perspective regarding community properties. Evolutionary trends are assayed on a single-species level, and on a different time-scale. In a community, ecological and evolutionary processes overlap in time, forming a feedback loop, and must therefore be studied together. Our work interrogates eco-evolutionary dynamics, using multiple-species biofilm, a model that approximates natural microbial habitats. Three bacteria—Klebsiella pneumoniae (KP), Pseudomonas aeruginosa (PA), and Pseudomonas fluorescens (PF)—were tagged with high-resolution chromosomal barcodes at a rate of ~10^5 lineages/species, significantly higher than previously published. The barcode design enables the simultaneous tracking of species abundance and intra-species lineage frequencies. Biofilm consortia, grown on a single carbon source, reached ecological equilibrium by ~80 generations. In dual- and triple-species consortia, early competition led to the extinction or, in some cases, near-extinction of the less competitive species, followed by stabilization. The relative impact of abiotic factors and biotic interactions shaped evolutionary adaptations, as evidenced by the emergence of distinct phenotypic trends in productivity and metabolic signatures. In fact, community interactions universally shaped evolutionary dynamics, which occurred on the background of standing genetic variation and de novo mutations. In some contexts, where initial lineage diversity influenced ecological equilibration outcomes, eco-evolutionary cross-talk is bi-directional. Collectively, lineage trajectory patterns shift in response to community-interactions. In KPPF, where PF was the primary source of selection pressure, certain barcodes in KP were consistently enriched, relative to single-species KP, which rules out abiotic effectors. The enriched lineages are potential drivers of the ecological equilibration that followed the near-extinction of KP. Modifying the experimental design with the proposed CRISPR-Cas lineage isolation mechanism will identify mutations that are instrumental in eco-evolutionary crosstalk, potentiating mechanistic research based on (GxG) gene-gene interactions.

Poster 24

CORAL: large-scale read-based inference of lineage-specific mutation rates, spectra, and signatures across eukaryotes

Asaf Pinhasi, Yosef Maruvka

The Department of Cell Biology and Cancer Science, Technion – Israel Institute of Technology

The rapid expansion of reference genomes across the tree of life creates unprecedented opportunities to study how mutational processes shape genome evolution. However, systematic cross-phyla analyses of mutation rates, mutation spectra, and mutational signatures have been limited by the computational cost and rigidity of multiple-species alignments (MSA). To overcome this barrier, we developed CORAL (Comparative Orthologous Read-based Analysis of Lineage Substitutions), a scalable framework for inferring lineage-specific substitutions without constructing large MSAs. CORAL fragments each sister genome into short synthetic pseudo-reads, aligns them independently to an outgroup reference, and assigns substitutions by simple parsimony. This approach enables efficient estimation of branch-specific mutation rates and high-resolution 96-context trinucleotide mutation spectra. Extensive benchmarking demonstrated that CORAL provides accurate and robust estimates across a wide range of species. Applying CORAL to thousands of eukaryotic species with calibrated divergence times, we generated the largest atlas of species-level mutation rates and spectra assembled to date, spanning over 5,000 animals, plants, fungi, and protists. Annual mutation rates varied by more than three orders of magnitude and showed strong negative associations with life-history traits, including lifespan and body mass. These relationships remained significant in multivariable analyses, indicating that mutation-rate evolution is tightly linked to species biology. Beyond absolute rates, context-normalized mutation spectra exhibited strong phylogenetic structure across eukaryotes, broadly recapitulating known evolutionary relationships. Distinct clades displayed characteristic spectral features, including prominent CpG-associated mutations in methylated vertebrates. Clade-specific spectra strongly predicted genomic trinucleotide composition, demonstrating that long-term mutational biases shape genome content. Finally, decomposition of species spectra revealed seven recurrent evolutionary mutational signatures, including conserved clock-like processes, cancer-associated signatures, and two novel signatures. Signature activities varied widely across taxa and were, in several cases, significantly associated with life-history traits and environmental context. Together, these results establish mutation rates, spectra, and signatures as conserved yet evolvable molecular traits and introduce a scalable framework for studying genome evolution across the tree of life.

Poster 25

Bayesian inference of demographic history from the distribution of distances between heterozygous sites

Michael Sheinman, Tommaso Stentella, Peter F. Arndt, Florian Massip

Complex systems, Weizmann Institute of Science

Segregating sites and their statistical distribution along chromosomes contain rich information about the degree of divergence or relatedness of homologous sequences in a population. The pattern of these sites is dictated by mutational processes and population dynamics together with recombination. Specifically, recombination partitions genomes into segments which are Identical by Descent (IBD), i.e. share the same coalescent tree. The Sequential Markov Coalescent approximation is commonly used together with Hidden Markov Models to jointly infer IBD segments and the population history. Here we introduce a novel methodology which does not infer recombination events, but exclusively the demographic history by considering only the distribution of distances between segregating sites. This quantity is directly observable and inherently a marginal distribution over both the ancestral recombination and coalescence events. Using our theoretical framework, we derive an analytical formula for the distribution of distances between segregating sites conditional on an arbitrary panmictic demography. Our method allows the likelihood function to be computed and takes advantage of Bayesian analysis to draw conclusions on model complexity, i.e. only consider histories with sufficient evidence. We validate our method with extensive simulations, showing that it is possible to precisely retrieve the true demographic model. Further, we can show that our analysis is well powered to precisely recover information about the recent past as well as the ancient past of a population. The simplicity of our approach makes it possible to analyze demographic histories to unprecedented accuracy for many diploid species, not limited to humans, but also including endangered species for which only one genome is available.

Poster 26

Evolutionary graph pangenome of the order Poales from chloroplast genome assemblies highlight phylogenetic inconsistencies

Rakan Haib, Sariel Hubner

Computer Science, Migal - Telhai

With the increased accessibility and democratization of genomic sequencing, the number of fully sequenced genomes across all taxonomies is exploding. To exploit the availability of complete genomes in evolutionary studies a comprehensive platforms such as pangenomes are urged to measure diversity in a population or species, from point mutations to large chromosomal rearrangements. By incorporating concepts from graph theory, a graph-pangenome can be studied directly to identify genomic regions and genes that underlie important evolutionary processes and traits. Here, I describe the development and application of graph-genomes method for the analysis of diversity across species. The developed platform, MineGraph, enables to construct graph-genomes from genome assembles following an optimization protocol, perform diversity and phylogenetic analyses and generate visualizations for inspection and inference.Graph-based phylogenetic frameworks represent genomes as variation graphs that retain alternative paths, shared segments, and structural differences across taxa, allowing evolutionary signal to be read from graph topology and path structure rather than from a single alignment. In contrast to traditional gene-based trees, which infer a strictly bifurcating history from selected orthologous loci and emphasize substitutional similarity, graph phylogenetics integrates genome-wide presence/absence and structural variation, making it better suited to capture reticulate evolution and complex evolutionary histories. MineGraph was packaged as a Docker container to ensure ease of use, accessibility, and reproducibility, empowering researchers to analyse genomic datasets efficiently. By combining advanced graph construction with user-friendly automation, this project provides a tool for studying genetic diversity and evolution, with applications in breeding, conservation, and evolutionary biology.

Poster 27

Genomic characterization of bulbous barley (Hordeum bulbosum) an untapped source of adaptive alleles

Noga Ben Sira, Guy Horev, Evgenii Potapenko, Sariel Hübner

Department of Bioinformatics, Tel Hai University

Global biodiversity is threatened by climate change and accelerating habitat loss, with particularly strong impacts in transitional regions that combine steep environmental gradients with high species richness and endemism. The Eastern Mediterranean spans sharp climatic gradients from Mediterranean to desert environments and is undergoing rapid desertification, making it a priority region for systematic genomic documentation of native flora. Here we studied bulbous barley (Hordeum bulbosum), a perennial, outcrossing wild relative of cultivated barley and an untapped donor of agronomically valuable alleles. H. bulbosum is the only perennial Hordeum species known to yield fertile offspring in crosses with cultivated barley, and it diverged from wild barley roughly 4–5 million years ago. It occurs as diploid and autotetraploid cytotypes, where in Israel only the tetraploid (4n=14) cytotype exist. We assembled a country-wide diversity panel of 224 tetraploid individuals sampled from 23 locations across Israel and generated genome-wide markers using genotyping-by-sequencing (GBS). We use the recently published haplotype-resolved H. bulbosum reference genome to call XX variants across all accessions. We report the resulting SNP resource and initial population-genomic analyses quantifying genetic diversity, population structure, and geographic differentiation along a steep environmental gradients across Israel. Together, these resources provide a national-scale genomic baseline for a widespread Israeli wild cereal and a foundation for future studies of population history and local adaptation, and for leveraging H. bulbosum diversity in barley research and improvement.

Poster 28
Segmental copy number amplifications are stable in the absence of selection

Nadav Ben Nun, Titir De, Pieter Spealman, Ina Suresh, Grace Avecilla, Farah Abdul-Rahman, Yoav Ram, David Gresham

Zoology, Tel Aviv University

Copy Number Variants (CNVs) are a primary engine of rapid adaptive evolution in yeast and fungi, particularly under strong selection. While selection for gene amplification in nutrient-limited environments is well-documented, the evolutionary dynamics of these variants upon the removal of selection remain difficult to quantify. Disentangling the mutational supply of revertants from selection against the CNV poses a challenge for standard methods. Here, we integrate yeast experimental evolution with neural-network simulation-based inference (nnSBI) to tackle this challenge. We evolved yeast lineages with adaptive segmental amplifications vs. whole-chromosome aneuploidies in chemostats with non-selective media. Using Neural Posterior Estimation (NPE), an nnSBI method, and a collective posterior approach to aggregate evidence across independent replicates, we inferred the joint distribution of reversion rates and fitness effects. Our results reveal distinct evolutionary fates dictated by genomic architecture. Segmental amplifications proved to be remarkably stable. Our model attributes this to negligible fitness costs, allowing these variants to persist. In contrast, aneuploid lineages rapidly reverted to euploidy. Our inference attributes this rapid loss not only to negative selection but to high aneuploidy reversion rates, significantly exceeding previous SBI estimates for segmental CNV rates. These findings demonstrate that while costly aneuploidies are transient and readily reversible, segmental CNVs are prone to persist as standing genetic variation. We highlight the utility of the collective posterior method in resolving cryptic parameters in evolutionary trajectories, and provide a quantitative basis for the reversibility of adaptation.

Poster 29

Isolation and transplantation of candidate stem cells in Hexacorallia: a model for coral cell therapy

Shani Talice, Itamar Kozlovski, Shany K. Barkan, Grace A. Snyder, Ton Sharoni, Tom Levy, Shelly Oisher, Uzi Hadad, Claytus Davis, Nikki Traylor-Knowles, Orly Gershoni-Yahalom, Yehu Moran, Benyamin Rosental

The Shraga Segal Department of Microbiology and Immunology, Ben Gurion University of the Negev

Cell transplantation represents an innovative strategy to strengthen coral resilience to global stressors such as ocean warming. Using a tractable transplantation system, we first investigated stem cell properties within Hexacorallia—the cnidarian subclass that includes reef-building corals—through the model organism Nematostella vectensis. We identified a population of candidate stem cells with defining features of stemness, including self-renewal, functional plasticity, and long-term survival. These cells successfully integrated into recipients and promoted recovery in chemotherapy challenge assays. Enrichment was achieved using aldehyde dehydrogenase (ALDH) activity as a functional marker. The ALDH-high fraction consistently exhibited strong engraftment and regenerative potential. Transplantation outcomes revealed morphological plasticity, quantified through flow cytometry and machine learning-based imaging. Bulk RNA sequencing further supported these results, identifying the mesenteries of N. vectensis as a potential stem cell niche. This work establishes the first experimental framework for stem cell biology in Hexacorallia, opening a previously unexplored dimension of cnidarian regeneration. Beyond validating stem cell transplantation in a cnidarian model, our ongoing research is now extending these principles directly to corals, where allorecognition and chimerism provide natural contexts for studying integration and tissue compatibility. Together, these studies establish a foundation for cellular approaches in Hexacorallia, opening new directions in stem cell biology, regeneration, and immunology, while also providing a basis for strategies to enhance coral resilience under climate change.

Poster 30

Saccharomyces Boulardii Rapidly Evolves to Improve Histidine Degradation and Production of Beneficial Metabolites

Ziv Ben-Moshe, Avihu H Yona, Haim Zeigerman

Biochemistry and Food Sciences, The Hebrew University of Jerusalem

The gut microbiome is pivotal in metabolic regulation, yet its therapeutic potential for amino acid accumulation disorders like histidinemia remains underexploited. Histidinemia, caused by histidase deficiency, results in toxic histidine buildup, potentially leading to neurological deficits. This study establishes a pioneering niche for Saccharomyces boulardii, a probiotic yeast, as an engineered therapeutic platform to catabolize histidine and produce bioactive metabolites beneficial to host physiology. Using adaptive laboratory evolution (ALE), we cultivated S. boulardii in nitrogen-limited media with histidine as the sole nitrogen source for over 1500 generations across four parallel lines, transitioning from ammonium sulfate-supplemented to histidine-only media after ~700 generations. Growth kinetics were monitored via optical density, plate-reader assays, and gas chromatography-mass spectrometry (GCMS), while metabolomics revealed histidine catabolism derivatives and unique metabolites in evolved strains, such as 4- imidazoleacrylic acid and imidazoleacetate, linked to reconfigured nitrogen metabolism. Genomic analyses elucidated adaptive mutations underpinning enhanced histidine utilization in selected colonies, deepening insights into metabolic adaptation mechanisms. In an ex vivo gut model, evolved strains eliminated histidine significantly faster than controls. Two of the populations displayed superior growth dynamics, with distinct lag, log, and stationary phases, reflecting optimized histidine catabolism. This dual-purpose strategy—reducing systemic histidine, while generating beneficial metabolites, positions S. boulardii as a transient, safe therapeutic for rare metabolic disorders. By illuminating genomic changes driving metabolic adaptation, this work advances microbiome engineering, offering a scalable framework for precision therapeutics and a deeper understanding of microbial evolution in metabolic disease management.

Poster 31
Impact of Horizontal Gene Transfer on population dynamics and outcomes of adaptation of Acinetobacter baylyi ADP1

Elizaveta Miticheva, Shimon Bershtein

Ben Gurion University of the Negev

Horizontal gene transfer (HGT) enables bacteria to exchange genetic material not only within a generation but also across species boundaries. This process is a key driver of the remarkable adaptability observed in prokaryotes. While most of our current understanding of HGT comes from analyses of past events inferred through genome sequencing and phylogenetics, understanding how to harness or counteract bacterial adaptability requires insights into the dynamics of ongoing HGT processes. In this study, we developed a model system based on the naturally transformable bacterium Acinetobacter baylyi ADP1. We constructed large chromosomally barcoded population and used a novel "suicidal barcoding" technique to generate an HGT-deficient control population. These strains share an identical genetic background and comparable fitness, differing only in their ability to undergo transformation. We subjected both HGT-capable and HGT-deficient populations to long-term laboratory evolution (LTLE) under various environmental conditions and monitored changes in fitness, clonal composition, and genetic structure. We saw improved in fitness in all the evolved populations, regardless their HGT capacity. For the HGT-capable populations, we observed changes in its transformation capacity during the course of evolution, which was different in different evolution conditions. We also started to explore the genetic changes which occurred during the adaptation.

Poster 32

Cross-Species Atlas of Bacterial RNA 3′ Ends Reveals Termination Mechanistic Signatures and Evolutionary Patterns

Amir Bar, Yael Altuvia, Michal Eldar and Hanah Margalit

The Hebrew University of Jerusalem

Deciphering the generation mechanisms and regulatory roles of bacterial transcript 3’ termini requires large-scale 3′ terminus data. We repurpose Pathogenx, an available RNAtag-seq dataset, leveraging RNAtag-seq-specific read patterns associated with 3’ termini, to generate the “Bacterminome” atlas, a rich resource of species-and condition-dependent transcript 3’ termini of 32 bacterial human pathogens grown under 10-12 conditions. Analysis of sequence elements near 3' termini revealed, along with the classical intrinsic terminator, other known and newly-detected signatures, highlighting the wealth of termination-associated sequence elements. Intriguingly, orthologous genes with corresponding 3’ termini show different termination mechanisms in different bacteria, often matching the dominant mechanism of the respective bacterial species. Analysis of condition-dependent 3' termini revealed some conservation across species, supporting the conjecture that alternative 3' termini can play a role in gene expression regulation. Our resource, available through a user-friendly web-server, provides a platform for studying transcription termination at an unprecedented scope.

Poster 33

Evolutionary Tradeoff Between Co-translational folding/assembly and Chaperone Dependency in Bacterial S-adenosyltransferases (MATs)

Tanya Rachel Shanthakumar, Dr. Shimon Bershtein

Life Sciences, Ben Gurion University

Bacterial S-adenosyltransferases (MATs) are a ubiquitous and conserved enzymes responsible for catalyzing the synthesis of S-adenosylmethionine (SAM), an essential cellular cofactor. Structurally, MATs exist as dimers of dimers, stabilized by a large, conserved dimeric interface and a smaller, recently evolved, highly divergent inter-dimeric interface. The molecular and structural determinants that drive and constrain the evolution of MATs remain poorly understood. To elucidate the evolutionary dynamics, we utilized Ancestral Sequence Reconstruction (ASR) and comparative analyses of extant and ancestrally reconstructed bacterial MAT homologs. We identified two independent evolutionary events leading to emergence and subsequent loss of obligate chaperonin dependence: within the Mollicutes and Proteobacteria. We assessed the chaperone dependency of MATs using cell-free in-vitro coupled transcription-translation system (PURExpress2.1). Notably, E.coli MAT exhibited obligatory chaperonin dependence despite optimizing the translation initiation rate. In contrast, N. gonorrhoea MAT demonstrated greater propensity for co-translational folding/assembly even when replaced with the ribosomal binding site of EcMAT resulting in reduced chaperonin assistance. Our analysis revealed a correlation between increased hydrophobicity at the inter-dimeric interface and enhanced chaperonin dependency, concomitant with greater kinetic stability. Chaperone dependency emerged later in MAT phylogeny alongside the acquisition of salt bridges. Furthermore, we identified a key mutation playing a crucial role in this evolutionary transition. Our findings prompted us to hypothesize that by acting on the inter-dimeric interface, evolution can tailor activity regulation, degradation propensity, chaperone dependency, extent of co-translational folding/assembly and other crucial properties of the MAT complex to meet the environmental and metabolic demands, while preserving its core function.

Poster 34

Antibiotic Exposure Dynamics Shape Evolutionary Trajectories and Fitness Costs of Ampicillin Resistance in E. coli

Yonatan Cohen, Priel Siman-Tov , Haim Zeigerman , Avihu Yona

faculty of agriculture, hebrew university of jerusalem

Antimicrobial resistance (AMR) is a growing challenge to global health. An important yet relatively understudied factor of how resistant lineages spread is the fitness cost of resistance: resistant strains with lower costs are more likely to persist and spread in the absence of antibiotics, increasing epidemiological risk. Here, we evolved Escherichia coli under two ampicillin (Amp) exposure regimens. In the “Const” regimen, populations experienced continuous exposure to gradually increasing concentrations. In the “Pulse” regimen, populations underwent brief, high-dose challenges followed by drug-free recovery. Despite achieving comparable endpoint resistance in both treatments (MIC ≈ 4,000 μg/mL), the associated fitness costs differed substantially. Const-evolved populations exhibited a ≈26% reduction in growth rate, whereas Pulse-evolved populations reached the same MIC with roughly half the cost (≈13% reduction in growth rate). Whole-genome sequencing revealed that these contrasting regimens are accompanied by distinct evolutionary routes to resistance. Const populations primarily acquired canonical Amp-resistance mutations (e.g., ampC, rpoD, envZ, marR). In contrast, Pulse populations exhibited unique changes characterized by disruption of non-canonical loci associated with IS-element activity, consistent with genomic rearrangements that ultimately increase efflux capacity (including upregulation of mdtE and the acrB–tolC system). Together, these results show that antibiotic exposure dynamics can strongly shape both the genetic mechanisms of resistance and the fitness burden they impose. Continuous exposure preferentially selects for resistance strategies linked to antibiotic deactivation (e.g., AmpC), whereas pulsed high-dose challenges favor reduced intracellular drug accumulation, consistent with decreased permeability and/or enhanced efflux. These regime-dependent trajectories have direct implications for predicting the spread potential of resistant strains under clinically relevant dosing patterns.

Poster 35
Candidate stem cell isolation and transplantation in Hexacorallia

Meydan Cohen

Life Sciences, Ben-Gurion University of the Negev

Stem cells enable cell therapy through their ability to self-renew, differentiate, and persist throughout an organism's life. In humans, this principle is exemplified by bone marrow transplantation, where stem cells from a healthy donor transfer a functional genotype to a diseased recipient. A similar strategy could, in principle, be applied to reef-building corals, which exhibit strong genotypic variation in heat tolerance and survival under climate-driven warming. However, such an approach requires the ability to isolate and transplant stem cells in Hexacorallia, the group that includes corals and sea anemones. Here, we establish a functional stem-cell transplantation system using the sea anemone Nematostella vectensis, the only hexacorallian with fluorescent transgenic lines. Using in vivo tracking and flow-cytometry-based cell sorting, we identify a cell subpopulation that can be transplanted from donor to recipient, where it persists long-term, self-renews, proliferates, differentiates into multiple lineages, and rescues animals from otherwise lethal chemotherapy. Importantly, this stem-cell-like population can be enriched using species-non-specific cell surface markers, and analogous populations are present in other hexacorallians, including stony corals. These results provide the first functional framework for stem-cell-based cell therapy in corals and represent a critical step toward the future transfer of heat-resilient traits between coral genotypes.

Poster 36

Investigating C/EBPB as a novel candidate regulator of mitochondrial and nuclear gene expression

Gavriel Minor, Gilad Barshad, Sara Dadon and Dan Mishmar

life sciences, Ben Gurion University

Radiation of eukaryotes ~2BYA is accompanied by the emergence of mitochondria as a central player in cellular metabolism. As most mitochondrial genes were transferred to the host cell genome, a bi-genomic system was created. It is currently believed that mito-nuclear coregulation is governed solely by signaling and that mitochondrial DNA (mtDNA) transcription is separately regulated by mitochondrial-dedicated factors encoded by the nuclear DNA (nDNA). In contrast, we have identified mitochondrial localization and mtDNA binding by known transcriptional regulators of nDNA genes, pointing to the involvement of the general cellular regulatory system in mtDNA regulation. Here, we study the impact of one such transcriptional regulator, C/CAAT enhancer binding protein B (C/EBPB), on the mito-nuclear co-regulation of OXPHOS genes expression. First, bioinformatics analysis suggests that LIP is the only C/EBPβ isoform (LIP, LAP1, and LAP2) with potential mitochondrial localization. This prediction was supported by subcellular fractionation in U87 cells, whereas the nuclear fraction was enriched by LAP1 and LAP2. Second, C/EBPβ silencing in U87 cells led to elevation of mtDNA transcription. These findings suggest that C/EBPβ may act as a repressor of mtDNA transcription, and hence serves as an candidate to co-regulate OXPHOS gene expression in both genomes.

Poster 37
Predicting complex phenotypes from ancient genomes

Sefi Weinstein

Department of Ecology, Evolution & Behavior, Hebrew University

Reconstructing the change of phenotypes over time is a major goal in evolutionary biology. While in most cases this requires indirect inference from contemporary data, the sequencing of ancient DNA (aDNA) now allows us to directly access the temporal axis of evolution. However, inferring phenotypes from aDNA, which is usually low-coverage and fragmented genomes, is difficult. This is particularly difficult for complex polygenic phenotypes, in which prediction of phenotype even in high coverage modern genomes is not always accurate. One of the main methods for inference of polygenic traits is the polygenic score (PGS) approach, in which effect sizes inferred from large biobanks are summed along the entire genomes. However, this is problematic in aDNA where only a small fraction of the genome is sequenced. Here, we investigate the potential of imputation, a statistical procedure where sequencing gaps are filled using large reference panels, to predict phenotypes in aDNA. We developed a method in which we simulate low-coverage samples from a real high-coverage aDNA sample to evaluate imputation accuracy. We impute the simulated samples and compare the PGS values of the simulated samples to the original one, that acts as a ground truth. Using this method, we can evaluate the minimum coverage threshold that allows us to reconstruct the genome sufficiently to infer phenotypes accurately. Using these phenotypic prediction method, we investigate the genetic structure of different complex traits by analyzing and comparing their prediction accuracy following imputation.

Poster 38
Ancient DNA analysis of early Levantine farmers from Motza, Israel

Giulia Di Crosta, Marie Anton, Jacob Vardi, Hamoudi Khalaily, Israel Hershkovitz, Rachel Sarig, Hila May, Viviane Slon

Tel Aviv universiy

The Neolithic Revolution represents one of the most profound socio-economic transformations in human history, marking the transition from mobile hunter-gatherer societies to sedentary agricultural communities. The southern Levant, encompassing modern-day Israel, Jordan, Lebanon, Palestine, and Syria, plays a central role in this process, as it preserves some of the earliest evidence for agriculture and animal domestication. During the Pre-Pottery Neolithic (PPN; ca. 11,800–7,800 BCE), major shifts in subsistence strategies were accompanied by population growth, migration events, and increasing social and cultural complexity, including the development of elaborate burial practices. Ancient DNA (aDNA) analysis has emerged as a powerful tool for investigating these processes, providing direct insights into genetic diversity, population structure, and kinship relationships among prehistoric communities. However, in the southern Levant, the reconstruction of Neolithic population history has been hampered by poor DNA preservation due to warm climatic conditions and the limited availability of well-preserved human remains. The site of Motza, located in central Israel, offers a unique opportunity to overcome these limitations. Occupied continuously from the Pre-Pottery Neolithic through the Middle Iron Age (ca. 8600–500 BCE), Motza has yielded exceptionally well-preserved archaeological deposits, including settlements, ritual structures, and burial contexts containing skeletal remains of at least 200 individuals. This makes the site an ideal case study for exploring the genetic makeup of early agricultural populations in the region. Here, we present the results of a large-scale aDNA investigation of individuals from Motza. Petrous bones were micro-CT scanned and sampled using minimally invasive drilling procedures. DNA was extracted, converted into double-indexed single-stranded libraries, and screened using shallow shotgun sequencing and targeted mitochondrial DNA enrichment. Of the 72 individuals analyzed, 50 yielded authentic aDNA, displaying characteristic post-mortem damage patterns and low levels of modern contamination. Genome-wide SNP capture (1240k panel) was subsequently applied to all positive libraries, enabling high-resolution analyses of genetic ancestry, biological sex determination, and population affinities. This extensive dataset provides unprecedented insights into the population dynamics of PPN societies in the southern Levant.