Group B - Poster theme overview

Poster area	Board numbers	Theme	Set-up and take-down
Blomster salen	001-040	S09 New frontiers in sex evolution: evolutionary patterns and innovations	**Set-up:**
Blomster salen	041-074	S03 Genome Plasticity and Evolutionary Innovation	Tueday, 12:50-17:30
Blomster salen	075	S18 Microbial evolution meets AI: genome architecture, immunity and microbial community dynamics.	(During lunch break, before
Blomster salen	076	S08 Epigenomics, structural variation, and genomic offset: Predicting climate adaptation in crops and wild relatives	poster session)
Main hall	077-127	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	
Main hall	128-130	L06 From Ancient Pathogen Genomics to Palaeoepidemiology	**Poster session:**
Harlekin	131	S13 Perspectives on paleo-omics: defining functional evolution of ancient viruses in the era of big data	Tuesday 18:00-20:00
Harlekin	132	L01 Insights into the past through the lens of palaeoproteomics	
Harlekin	133-164	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	**Take-Down:**
Harlekin	165-184	S14 Evolution of Host-Pathogen Interactions in the Genomic Age	Wednesday, 17:00-18:00
Harlekin	185-206	S11 The evolution of recombination landscapes	
2nd floor: Arkaden 8	207-234	S25 Deep time human genomics	
2nd floor: Arkaden 8	235-239	S17 Unicellular organisms in major evolutionary transitions	
2nd floor: Arkaden 8	240-251	S12 Reconstructing the deep Tree of Life: challenges and new approaches	
2nd floor: Arkaden 8	252-261	S07 From Trees to Graphs: Methodological Advances and Innovative Applications of Graphs in Evolutionary Analysis	
2nd floor: Arkaden 8	262-274	L03 Beyond limits: unlocking the potential of ancient animal genomics	
2nd floor: Arkaden 7	275-285	S20 Mapping fitness landscapes with mechanistic models, machine learning and experiments	
2nd floor: Arkaden 7	286-302	S21 From genomic graphs to evolutionary insights: standardising pangenomes for population inference	
2nd floor: Arkaden 6	303-307	L02 Ancient plant DNA in the genomic era	
2nd floor: Arkaden 6	308-342	S15 Detecting selection and local adaptation on (im)possible systems	
2nd floor: Arkaden 4+5	343-348	L04 Understanding adaptive evolution through the lens of hologenomics	
2nd floor: Arkaden 4+5	349-356	S02 Powers and pitfalls of artificial intelligence for molecular evolution and phylogenetics	
2nd floor: Arkaden 4+5	357-364	S10 Learning from Evolution: AI Models for Genomic Function	
2nd floor: Arkaden 2+3	365-368	S16 The genetic basis of evolutionary rescue	
2nd floor: Arkaden 2+3	369-380	S24 Molecular mechanisms of selfish elements and strategies	

Group B - Detailed poster overview

Board number	Poster area	Paper number	Paper Title	Theme	Presenter name	Presenter organisation	Presenter country
001	Blomster salen	407	From Self-Incompatibility to Mixed Mating: Evolutionary transitions between mating modes in plants	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Amit Jangid	Hebrew University Of Jerusalem	Israel
002	Blomster salen	321	Inferring the demographic history of Caenorhabditis elegans while accounting for its self-fertilising reproductive mode	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Chenxi Wang	University Of Edinburgh	United Kingdom
003	Blomster salen	1575	Evolutionary Origins of Vertebrate Gonad Differentiation in an Agnathan Lineage	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Sara Good	The University Of Winnipeg	Canada
004	Blomster salen	1698	Homologous Chromosome Reuse in Sex Chromosome Turnover	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Yukako Katsura	SOKENDAI	Japan
005	Blomster salen	295	The contribution of small RNAs to the evolution of separate sexes and sex chromosomes in the plant Silene latifolia	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Aline Muyle	CNRS	France
006	Blomster salen	320	Sex without crossovers mimics clonal reproduction in a multicellular eukaryote	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Stefan Steckenborn	Max Planck Institute For Plant Breeding Research	Germany
007	Blomster salen	290	Leaving X: how scale insects repeatedly evolved alternatives to chromosomal sex determination	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Andrew Mongue	University of Florida	United States
008	Blomster salen	791	Non-canonical genomic consequences of early sex chromosome degeneration under extreme heterochiasmy in Caribbean robber frogs	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Antoine Houtain	VUB	Belgium
009	Blomster salen	938	Diversity and Distributions in Egg-Laying vs. Live-Bearing Onychophora	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Arianna Lord	Eawag	Switzerland
010	Blomster salen	1640	Chromosome-level assembly of multiple abalone genomes reveals extensive gene duplication and domain expansion within gamete recognition proteins	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Damien Wilburn	The Ohio State University	United States
011	Blomster salen	415	Determining the timing of sex-biased transmission distortion in human trios and its role in mitigating sexually antagonistic conflicts	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Elise Lucotte	CNRS	France
012	Blomster salen	757	Integration of p53 genes into sex determination mechanisms	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Elzemiek Geuverink	University of Groningen	Netherlands
013	Blomster salen	834	Elucidating molecular mechanisms of sex determination in stick insects	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Emelyne Gaudichau	Unil	Switzerland
014	Blomster salen	1594	Exploring the Biophysical Consequences of Abalone Lysin Evolution with NMR Spectroscopy and Molecular Dynamics	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Eric Todd	The Ohio State University	United States

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Board number	Poster area	Paper number	Paper Title	Theme	Presenter name	Presenter organisation	Presenter country
015	Blomster salen	1617	Genetic trade offs between reproductive success and disease reveal sex specific pleiotropic pathways	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Eva Brigos	Institut de Biologia Evolutiva (CSIC-UPF)	Spain
016	Blomster salen	1098	Incipient sex chromosomes in the dioecious alpine plant Silene exscapa.	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Fabien Duez	Isem	France
017	Blomster salen	925	The enduring mystery of faster-X and faster-haploid adaptation: reconciling theories with data	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Filip Ruzicka	Institute Of Science And Technology Austria	Austria
018	Blomster salen	878	Repeat landscapes and neo-sex chromosome evolution in the Owl Monkey Aotus (Mammalia, Platyrrhini).	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Gustavo Toma	Universidade Federal de Sao Carlos	Brazil
019	Blomster salen	1530	Sex-Biased Germline Genome Architecture in the Sea Lamprey (Petromyzon marinus)	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Ilya Kisselev	University of Winnipeg	Canada
020	Blomster salen	702	Differential Amplification of Satellite DNAs in the Sex Chromosomes of the Engystomops freibergi–E. petersi frog Species Complex	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Jennifer Pompeo	University Of Campinas	Brazil
021	Blomster salen	1214	Disentangling the autosomal and X-linked response to female-limited selection of X chromosomes in Drosophila melanogaster	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Jessica Abbott	Lund University	Sweden
022	Blomster salen	1601	Phylogenomic insights into the genetic basis of repeated parthenogenesis in Timema stick insects	S09 New frontiers in sex evolution: evolutionary patterns and innovations	João Souto	University Of Lausanne	Switzerland
023	Blomster salen	1263	A shared genomic region underlying disparate ecologically and sexually selected traits in two Lake Malawi cichlids	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Joel Elkin	University Of Cambridge	United Kingdom
024	Blomster salen	440	Spatial transcriptomics of the sex-changing fish brain	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Kaj Kamstra	University Of Otago	New Zealand
025	Blomster salen	1572	When Auto- and Allopolyploidy Meet: Premeiotic Genome Duplication Stabilizes Meiosis in Asexual Hybrids	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Karel Janko	University of Ostrava	Czech Republic
026	Blomster salen	148	Selfish male reproduction in stick insects	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Luca Soldini	University Of Lausanne	Switzerland
027	Blomster salen	1110	Rapid chromosome evolution in an anuran population resulting from secondary contact between lineages with different sex chromosomes	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Lucas Henrique Bonfim Souza	University Of Campinas	Brazil
028	Blomster salen	1239	Human Sex Chromosome Diversity in the Turkana	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Margaret (Maggie) Hassler	Arizona State University	United States
029	Blomster salen	1704	Male Xist Expression and Atypical X-Chromosome Regulation in the White-Footed Deer Mouse (Peromyscus leucopus)	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Maria Andrade Ludena	UC Irvine	United States
030	Blomster salen	329	Rare sex, recessive deleterious mutations, and the maintenance of genetic diversity	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Mélodie Bastian	Universite Paris Saclay, LISN	France
031	Blomster salen	249	Reversible Y chromosome evolution under extreme heterochiasmy in the common frog	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Paris Veltsos	Vrije Universiteit Brussel	Belgium
032	Blomster salen	1418	Breathing without lungs: integrative omics analyses into the functional complexity of lungless salamander mucus	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Paul Nicolosi	The Ohio State University	United States
033	Blomster salen	1399	Defining the interaction landscape within the mammalian sperm acrosome through evolutionary and structural analysis	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Regina Edgington	The Ohio State University	United States
034	Blomster salen	1332	Genomic footprints and genetic drivers of rapid sex chromosome turnover in European true frogs	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Ricard Fontserè	Vrije Universiteit Brussel	Belgium
035	Blomster salen	1474	Evolution of protein interactions underlying fertilization in an early diverging fungus	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Sujal Phadke	California State University San Marcos, CA	United States
036	Blomster salen	743	The effects of chromosome number and recombination landscapes on the fitness consequences of different reproductive modes.	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Sylvain Glémin	CNRS, Université Rennes	France
037	Blomster salen	1441	Mating system shifts and polyploidy shape evolutionary dynamics in Rorippa	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Uliana Kolesnikova	MPI For Plant Breeding Research	Germany
038	Blomster salen	833	Sperm competition intensifies purifying selection on testis-specific genes in primates	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Vasili Pankratov	Aarhus University	Denmark
039	Blomster salen	1241	Genetic basis of complex traits in closely related black widow spiders	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Vladislav Ivanov	University Of Rostock	Germany
040	Blomster salen	740	The role of genomic imprinting in the evolution of separate sexes	S09 New frontiers in sex evolution: evolutionary patterns and innovations	Yangfan Feng	Centre National De La Recherche Scientifique (cnrs)	France
041	Blomster salen	1333	Structurally complex loci as engines of adaptation: insights from amylase evolution	S03 Genome Plasticity and Evolutionary Innovation	Omer Gokcumen	University At Buffalo	United States
042	Blomster salen	1151	A toxic gene duplication ignites a sulfide-powered metabolic engine in horses	S03 Genome Plasticity and Evolutionary Innovation	Kaitlin Taylor	Vanderbilt University	United States
043	Blomster salen	1481	Host plant sharing correlates with increased Horizontal Gene Transfer in Lepidoptera	S03 Genome Plasticity and Evolutionary Innovation	Audrey Portal	Université Claude Bernard Lyon 1	France
044	Blomster salen	559	Pangenomic analysis reveals extent and mutagenic impact of rare transposable elements in Arabidopsis	S03 Genome Plasticity and Evolutionary Innovation	Aurélien Petit	Institut de Biologie de l'École Normale Supérieure, Université Paris Sciences et Lettres (PSL)	France

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Board number	Poster area	Paper number	Paper Title	Theme	Presenter name	Presenter organisation	Presenter country
045	Blomster salen	39	Ancestral architecture and evolutionary specialization of the vertebrate brain revealed by 3D single-cell transcriptomics in lamprey	S03 Genome Plasticity and Evolutionary Innovation	Bing Su	Kunming Institute Of Zoology, Chinese Academy Of Sciences	China
046	Blomster salen	1375	Genomic context mediate non-neutrality of synonymous mutations in Pseudomonas fluorescens under carbon limitation	S03 Genome Plasticity and Evolutionary Innovation	Caio Gomes Tavares Rosa	Mcgill University	Canada
047	Blomster salen	1146	Genome plasticity driven by transposable elements in ant-farmed fungi	S03 Genome Plasticity and Evolutionary Innovation	Caio Leal-Dutra	Universidade Federal de Minas Gerais (UFMG)	Brazil
048	Blomster salen	1168	Searching for shared genomic routes to termitophily in rove beetles (Aleocharinae)	S03 Genome Plasticity and Evolutionary Innovation	Caroline Høegh-Guldberg	Institute Of Entomology, Biology Centre Cas	Czech Republic
049	Blomster salen	563	Riding the heat wave: transcriptomic insights from yeast	S03 Genome Plasticity and Evolutionary Innovation	Chloé Haberkorn	Stockholm University	Sweden
050	Blomster salen	1139	Transposons as telomeres: conflict and innovation in essential chromosome components	S03 Genome Plasticity and Evolutionary Innovation	Chris Ellison	Rutgers University	United States
051	Blomster salen	1486	Opsin phylogeny illuminates the origins of animal vision	S03 Genome Plasticity and Evolutionary Innovation	Christopher Kay	University Of Bristol	United Kingdom
052	Blomster salen	2	Pervasive translation of short open reading frames and de novo gene emergence in Arabidopsis	S03 Genome Plasticity and Evolutionary Innovation	Claire Patiou	University Of Muenster	Germany
053	Blomster salen	1042	Mechanisms of evolution in the open ocean: clues from two populations of North Atlantic Ocean Physalia physalis	S03 Genome Plasticity and Evolutionary Innovation	Dalila Destanović	Yale University	United States
054	Blomster salen	1340	How much is enough for genomic surveillance of Escherichia and Klebsiella bloodstream infection-associated lineages, plasmids and AMR genes?	S03 Genome Plasticity and Evolutionary Innovation	Dorottya Nagy	University of Oxford	United Kingdom
055	Blomster salen	73	MTALTCO1 is a novel mitochondrial alternative protein that challenges conventional understandings of mitochondrial genomics	S03 Genome Plasticity and Evolutionary Innovation	Francis Robitaille	University Of Montreal	Canada
056	Blomster salen	546	The Trehalose Trail- Evolutionary insights into trehalose metabolic pathways and tradeoffs	S03 Genome Plasticity and Evolutionary Innovation	Ganesh Muthu Gangadharan	Institute For Stem Cell Science And Regenerative Medicine (bric-instem), Bangalore, India	India
057	Blomster salen	1075	Comparative Genomics of Domestication Across Laboratory and Semi-Wild Zebrafish Strains	S03 Genome Plasticity and Evolutionary Innovation	Irene Adrian-Kalchhauser	University Of Bern	Switzerland
058	Blomster salen	296	Evolutionary strategies of bacteria adaptation to leaf surface	S03 Genome Plasticity and Evolutionary Innovation	Jean-Baptiste Leducq	Université Laval	Canada
059	Blomster salen	587	Interplay between the role of DNA methylation in regulating gene expression and TE-silencing in a reptilian methylome	S03 Genome Plasticity and Evolutionary Innovation	Joshua Hufton	Uppsala universitet	Sweden
060	Blomster salen	1583	Towards an evolutionary understanding of the allotetraploid shamrock (lesser trefoil; Trifolium dubium)	S03 Genome Plasticity and Evolutionary Innovation	Katie E. Herron	University College Dublin	Ireland
061	Blomster salen	1173	Agricultural Transition in Europe Is Associated with PGA Copy-Number decrease and a Functionally Distinct Haplotype	S03 Genome Plasticity and Evolutionary Innovation	Kendra Scheer	University At Buffalo	United States
062	Blomster salen	203	Comparative Transcriptomic Analysis of Chemosensory Recognition in Frankliniella occidentalis and Thrips palmi Karny	S03 Genome Plasticity and Evolutionary Innovation	Kunhyang Park	Korea Research Institute Of Bioscience And Biotechnology (kribb)	South Korea
063	Blomster salen	1207	The molecular origins and implications of segmental duplications across vertebrate genomes	S03 Genome Plasticity and Evolutionary Innovation	Landen Gozashti	University Of California Berkeley	United States
064	Blomster salen	574	Getting Something from Nothing in Archaea: De Novo Gene Birth Across the Tree of Life	S03 Genome Plasticity and Evolutionary Innovation	Lars Eicholt	University of Oxford	Germany
065	Blomster salen	129	Ecological r-Selection Promotes a Proliferation-Plasticity Synergy Underpinning Cancer Drug Tolerance	S03 Genome Plasticity and Evolutionary Innovation	Lu Yang	Kunming Institute Of Zoology, Chinese Academy Of Sciences	China
066	Blomster salen	85	The cost of altered translation accuracy shapes adaptation to antibiotics in E. coli	S03 Genome Plasticity and Evolutionary Innovation	Laasya Samhita	Ashoka University	India
067	Blomster salen	189	Hybridization-derived gene copy number variation shapes genome stabilization and evolutionary novelty in a hybrid sparrow species	S03 Genome Plasticity and Evolutionary Innovation	Qiujie Zhou	Lund University	Sweden
068	Blomster salen	864	Going Retro: Mapping Invasive Retrotransposon Impacts on the Worm Genome	S03 Genome Plasticity and Evolutionary Innovation	Sara Wighard	IMBA (Institute Of Molecular Biotechnology)	Austria
069	Blomster salen	447	Dynamic evolution of retroviral envelope-derived sequences in primates	S03 Genome Plasticity and Evolutionary Innovation	So Nakagawa	Tokai University School Of Medicine	Japan
070	Blomster salen	423	Predicting co-option of transposable elements from multi-omics signatures	S03 Genome Plasticity and Evolutionary Innovation	Sofia Irene Garcia Bautista	University of Edinburgh	United Kingdom
071	Blomster salen	538	Population-scale variation and coordinated dynamics of transposable elements in Mediterranean fig (Ficus carica L.)	S03 Genome Plasticity and Evolutionary Innovation	Tommaso Giordani	Department of Agriculture, Food and Environment	Italy
072	Blomster salen	803	Turnover and introgression shape the dynamic evolution of a sexual mimicry polymorphism shared across the genus Xiphophorus	S03 Genome Plasticity and Evolutionary Innovation	Tristram Dodge	Stanford University	United States
073	Blomster salen	1485	Impact of Helitrons on evolution of multigene families	S03 Genome Plasticity and Evolutionary Innovation	Vladimir Kapitonov	Marine Biological Laboratory	United States
074	Blomster salen	632	Interlocus gene conversion causes mosaic divergence in tandem paralogues - modeling HMA4 evolution in Arabidopsis halleri	S03 Genome Plasticity and Evolutionary Innovation	Yannick Schäfer	University Of Cologne	Germany
075	Blomster salen	1518	Evolutionary Dynamics of Adherence-Mediating Fimbriae in Pathogenic Bacteria	S18 Microbial evolution meets AI: genome architecture, immunity and microbial community dynamics.	Gleb Ebert	University Of Gothenburg	Sweden
076	Blomster salen	1412	Structural variants and chromatin state: how does genetic architecture shape adaptation to climate?	S08 Epigenomics, structural variation, and genomic offset: Predicting climate adaptation in crops and wild relatives	Claire Mérot	CNRS - Université de Rennes	France
077	Main hall	715	Evolutionary Stasis Traps the Emperor Penguin in a Blue-Shifted Anthropocene Ocean	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Nadir Dbouk	Vanderbilt University	United States
078	Main hall	1032	When do genomic proxies reflect fitness? A mutation-based, fitness-explicit view of genetic load and adaptive potential	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Alberto Garcia Jimenez	Technical University of Denmark (DTU)	Denmark

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Board number	Poster area	Paper number	Paper Title	Theme	Presenter name	Presenter organisation	Presenter country
079	Main hall	38	Genome Evolution in Coast Redwood (Sequoia sempervirens): First Insights from a New Haplotype-Resolved Assembly	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Alexandra Sasha Nikolaeva	UC Berkeley	United States
080	Main hall	1162	Genetic diversity and genomic inbreeding signatures correlate with IUCN status across vertebrates	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Amanda Gardiner	University Of Cambridge	United Kingdom
081	Main hall	1356	Evaluating Genetic Diversity Indicators Across Wild and Domesticated Cotton Populations	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Ana Wegier	Biology Institute, UNAM and Royal Botanic Gardens, KEW	Mexico
082	Main hall	199	A translocation associated with fertility problem and colour phenotype in cattle have been maintained at high frequency by balancing selection	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Anna M Johansson	Swedish University Of Agricultural Sciences	Sweden
083	Main hall	1618	From bottlenecks to monitoring: SLiM5 simulations of genomic signals in managed Mauritian bird populations	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Anna Stuart	University Of Kent	United Kingdom
084	Main hall	503	Harnessing hybridization genomics to guide assisted gene flow in Central European white oak populations	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Clara Groot-Crego	Austrian Research Centre For Forests (bfw)	Austria
085	Main hall	1102	Genomic signatures of load accumulation during parallel colonization of the Baltic Sea	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Daniel Hancock	Dtu	Denmark
086	Main hall	1304	A cross-species population genomic analysis of solitary bees	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Dean Hodapp	iomE, Johannes Gutenberg University Mainz	Germany
087	Main hall	1071	Epigenomic potential as an evolutionary buffer under extreme genomic erosion in the Apennine brown bear	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Diana Lobo	Department of Biotechnology and Life Sciences, University of Insubria	Italy
088	Main hall	65	Population Dynamics in North Asia since the Last Glacial Maximum	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Elena Gusareva	Nanyang Technological University	Singapore
089	Main hall	1067	Dramatic changes in European Ash forests as result of a large-scale replacement of a native endophyte with its Asian relative	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Erik Dahl Kjaer	Københavns Universitet	Denmark
090	Main hall	1357	Delineating drivers of genetic diversity and population structure in data-deficient deep-diving marine mammals	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Fang Fei Tham	University Of Auckland	New Zealand
091	Main hall	710	Whole-genome sequencing from mammalian snowprints	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Harry Gordon	University of East Anglia	United Kingdom
092	Main hall	1028	Fine-scale population structure and genetic diversity of the sugar kelp, Saccharina latissima, in Ireland	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Jack Burton	Queen's University Belfast	United Kingdom
093	Main hall	1175	Plasticity across generations: DNA methylation correlates with intergenerational response to parasite infection in an endangered species	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	James Bazely	Queen Mary University Of London	United Kingdom
094	Main hall	704	Using genomics to inform the conservation of Lake Tanganyika's top predator fishes (Lates spp)	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Jessica Rick	University Of Arizona	United States
095	Main hall	302	Integrating Genetics and Ecology to Assess the Extinction Risk of European Birds	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Jiaqi Xu	Zhejiang University	China
096	Main hall	98	Effect of landscape heterogeneity on the conservation of genetic diversity of Zea mays ssp. mexicana	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	José Carlos Moreno Juárez	Universidad Nacional Autónoma De México	Mexico
097	Main hall	893	Using historical butterfly specimens to track genomic erosion in clouded apollo populations in Sweden	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Lars Littmann	Stockholm University	Sweden
098	Main hall	40	Genome-wide signatures of drift in African wild dogs overcome within 10 generations following reintroduction	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Laura Tensen	University Of Greifswald	Germany
099	Main hall	1665	Immunogenetic Signatures Underlying Pathogen Tolerance Following a Severe Population Bottleneck	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Leiting Yang	University Of Copenhagen	Denmark
100	Main hall	643	Genomic erosion and purging in populations of the Swedish sand lizards	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Lucia Caroli	Lund University	Sweden
101	Main hall	823	Genomic connectivity, adaptation and conservation management of Australian little penguins	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Lucy Ockert	University of New South Wales	Australia
102	Main hall	755	The genetic basis behind highly admixed ecotypes: the case of boreal and eastern migratory caribou	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	M. Lisette Delgado	Trent University	Canada
103	Main hall	1554	From deserts to forests: sequencing of the giant forest hog completes the genomic history of the African Suids	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Marta Maria Ciucani	University Of Copenhagen	Denmark
104	Main hall	238	Genetic diversity, census size, conservation status and the efficacy of purifying selection across plant species	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Martin Lascoux	Uppsala University	Sweden
105	Main hall	484	Immune Signatures of Gastrointestinal Helminth Infection in Transcriptomes of European Bison	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Mateusz Konczal	Adam Mickiewicz University in Poznan	Poland
106	Main hall	946	Large scale, low coverage population genomics assessing genetic variation and population structure across vulnerable Swedish sand lizard populations	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Mette Lillie	Uppsala University	Sweden
107	Main hall	338	Joint inference of demography and selection from genomic time series	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Paul Bunel	Inrae	France

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Board number	Poster area	Paper number	Paper Title	Theme	Presenter name	Presenter organisation	Presenter country
108	Main hall	108	Comparative population genomics of oil-collecting bees in the highly fragmented Brazilian Cerrado biodiversity hotspot	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Paulo Sousa	Martin-Luther-University Halle-Wittenberg	Germany
109	Main hall	1052	Harbour porpoise whole genomes document a rapid radiation across the North Atlantic and guides management units	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Morgan McCarthy	Globe Institute, University of CPH & Swedish Museum Of Natural History	Sweden
110	Main hall	554	Genomic analysis of field-collected feathers: An optimized ddRAD protocol for noninvasive monitoring of dispersal in the endangered capercaillie	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Román Sapino	Institute Of Evolutionary Biology (CSIC-UPF)	Spain
111	Main hall	382	Applying genomics to the management of Wallacean flagship taxa: evaluating the evolutionary potential of insurance populations	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Rosie Drinkwater	Ludwig-maximilians-universität München	Germany
112	Main hall	84	Demographic changes in a declining narwhal population in East Greenland using a 15-year time series	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Sam Fenton	University Of Copenhagen	Denmark
113	Main hall	1460	Tracking the Recovery of Bowhead Whales in Qeqertarsuup tunua, West Greenland, through a 25-Year Genomic Time Series	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Santiago Jose Avila Quintero	Globe Institute, University Of Copenhagen	Denmark
114	Main hall	648	Genomic consequences of admixture in a Swedish sand lizard population	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Seraina Emilia Bracamonte	Uppsala University	Sweden
115	Main hall	29	Museum samples track declining genetic diversity of the Eastern honey bee (Apis cerana)	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Shanlin Liu	Institute Of Zoology	China
116	Main hall	1087	Ecotypic diversity as a pathway to persistence under environmental change in a Californian butterfly	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Veronika Mrazek	Uppsala University	Sweden
117	Main hall	590	Molecular-aided management of genetic resources: a case study in traditional horse populations from France	S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world	Yumi Shakya	INRAE	France
118	Main hall	1331	Beyond Misfolding: Mapping How Cellular Context Converts Mutations into Fitness Costs	S06 Synthetic and Systems Biology Approaches to Dissecting the Molecular Mechanisms of Evolution	Ashley Brown	Arizona State University	United States
119	Main hall	1367	Understanding RNase P regulation: How E. coli evolves to compensate for defects in an essential and universally conserved enzyme	S06 Synthetic and Systems Biology Approaches to Dissecting the Molecular Mechanisms of Evolution	Emily Tonge	University Of Glasgow	United Kingdom
120	Main hall	1	Core elements play distinct roles in promoter birth and transcriptional regulation	S06 Synthetic and Systems Biology Approaches to Dissecting the Molecular Mechanisms of Evolution	Hsin-Hung Chou	National Taiwan University	Taiwan
121	Main hall	193	Clonal interference and the fate of synonymous mutations in P. fluorescens	S06 Synthetic and Systems Biology Approaches to Dissecting the Molecular Mechanisms of Evolution	Jacob Van Oorschot	Mcgill University	Canada
122	Main hall	479	Genome editing reveals: distinct and independent effects on life-history traits of three SNPs in one intron in Drosophila melanogaster	S06 Synthetic and Systems Biology Approaches to Dissecting the Molecular Mechanisms of Evolution	Julia Beets	Vrije Universiteit Amsterdam	Netherlands
123	Main hall	410	Vertebrate Evolutionary History of Oncosupression under Selection Pressure	S06 Synthetic and Systems Biology Approaches to Dissecting the Molecular Mechanisms of Evolution	Mikhail Potievskiy	National Medical Radiological Research Center	Russian Federation
124	Main hall	631	Using saturation mutagenesis to map the evolutionary forces that shaped human regulatory elements	S06 Synthetic and Systems Biology Approaches to Dissecting the Molecular Mechanisms of Evolution	Omer Ronen	Weizmann Institute Of Science	Israel
125	Main hall	673	Ribosomal frameshifting drives natural selection against codon repeats	S06 Synthetic and Systems Biology Approaches to Dissecting the Molecular Mechanisms of Evolution	Ruoxi Wang	University Of Michigan	United States
126	Main hall	363	Ancestral reconstruction of the emergence of catalytic activity through multimerisation of a SH3 binding domain	S06 Synthetic and Systems Biology Approaches to Dissecting the Molecular Mechanisms of Evolution	Stella Cellier-Goetghebeur	Université De Montréal	Canada
127	Main hall	496	Co-evolution of Olfactory and Taste Receptors in Birds	S06 Synthetic and Systems Biology Approaches to Dissecting the Molecular Mechanisms of Evolution	Xulan Shen	Zhejiang University	China
128	Main hall	816	A Clostridium tetani genome recovered from 3000-year-old human remains in Papua New Guinea	L06 From Ancient Pathogen Genomics to Palaeoepidemiology	Sojung Han	University Of Vienna	Austria
129	Main hall	940	Pangenome graph-guided assembly of ancient pathogen genomes	L06 From Ancient Pathogen Genomics to Palaeoepidemiology	Daria Evseeva	Eberhard Karl University Of Tübingen	Germany
130	Main hall	207	Characterization of the ancient human oral microbiota recovered from teeth	L06 From Ancient Pathogen Genomics to Palaeoepidemiology	Vincent Thygesen	University Of Copenhagen	Denmark
131	Harlekin	352	Investigating the evolutionary dynamics underlying DNA virus immune response	S13 Perspectives on paleo-omics: defining function-al evolution of ancient viruses in the era of big data	Rutvi Rajpara	University of Tartu	Estonia
132	Harlekin	1134	Advancing hominin taxonomic identification through an extended enamel palaeoproteomics database	L01 Insights into the past through the lens of palaeoproteomics	Viridiana Villa Islas	University Of Copenhagen	Denmark
133	Harlekin	646	The Genomic Adaptation of Peromyscus Maniculatus (North American Deer Mouse) in High-Altitude Environments	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Larissa Rockenbach	University Of Kansas	United States
134	Harlekin	202	Diverse Patterns of Transposable Element Expression in Macaca mulatta and Tissue-Specific Regulation of Adjacent Genes	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Nakyoung Kim	KRIBB	South Korea
135	Harlekin						
136	Harlekin	125	Diaporthe species present an one-compartment genome architecture	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Alicia Sofia Tempesta Brasil Silka	Federal University Of Parana (ufpr)	Brazil

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Board number	Poster area	Paper number	Paper Title	Theme	Presenter name	Presenter organisation	Presenter country
137	Harlekin	851	Massive genomic flux in a young autogamous diploid revealed through new approach to legacy sequence data	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Alistair Hockey	The University Of Western Australia	Australia
138	Harlekin	660	Convergent evolution of immune regulation as a foundation of mammalian high-altitude adaptation	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Allie Graham	University Of Kansas	United States
139	Harlekin	1002	Genetic trade-offs in the pleiotropic architecture of human cardiometabolic health	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Anna Basquet-Muniente	Institut de Biologia Evolutiva (CSIC-UPF)	Spain
140	Harlekin	1369	Comparative genomic insights into rediploidisation after whole genome duplication	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Anthony Redmond	University College Dublin	Ireland
141	Harlekin	1285	Asynchronous evolution of mammalian antimicrobial peptides balances constraint and diversification	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Athulya Girish Kizhakke	Ashoka University	India
142	Harlekin	265	SwarmGenomics: Unlocking the Potential of Public Genomic Data	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Aure Kylmänen	Tu Dortmund University	Germany
143	Harlekin	1003	Slow lorises with active viruses: The use of publicly available genomes in the searching for novel endogenous retroviruses	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Charles Michie	Oxford Brookes University	United Kingdom
144	Harlekin	159	Horizontal gene transfers underpin ribose heterotrophy and central carbon metabolism remodeling in Gloeobacteraceae (Cyanobacteria)	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Edi Sudianto	University of Liège	Belgium
145	Harlekin	674	Investigating the predictability of indels across insect	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Frances Swift	The University of Edinburgh	United Kingdom
146	Harlekin	196	Correcting for Global Synonymous Selection Improves the Accuracy of Episodic Positive Selection Inference	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Hannah Verdonk	Institute for Genomics and Evolutionary Medicine, Temple University	United States
147	Harlekin	1225	No Longer Frog-otten: publicly available anuran genomes reveal a diversity of vertebrate endogenous retroviruses	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Hayley Free	Oxford Brookes University	United Kingdom
148	Harlekin	234	A timetree resource for common mammals in zoological parks	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Jack Craig	Temple University	United States
149	Harlekin	1476	Denisovan variants in CNTNAP2 likely contributed to human adaptation in the Americas	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Kelsey Witt	Clemson University	United States
150	Harlekin	346	Non-canonical DNA studied in bird telomere-to-telomere genomes can explain sequencing drop-out on dot chromosomes	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Linnéa Smeds	Penn State University	United States
151	Harlekin	19	Beyond consensus genomes: a raw-read four-gamete framework uncovers intra-host recombination	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Luis Daniel González Vázquez	Universidade de Vigo	Spain
152	Harlekin	1286	Toxins among the branches: Evolution of xenobiotic processing gene families in bats	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	M. Elise Lauterbur	University Of Vermont	United States
153	Harlekin	310	Comparative evolution of genes across 581 vertebrate genomes reveals lineage-specific adaptive dynamics	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Marco Sollitto	Università di Firenze	Italy
154	Harlekin	266	Comparative transcriptomics suggests that breast secretory epithelium reuses ancestral molecular modules that predate mammalian evolution.	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Marie Saitou	Norwegian University Of Life Sciences	Norway
155	Harlekin	124	EVOLUTION AND ADAPTATION OF Dothideomycetes: INFLUENCE OF THE DYNAMICS BETWEEN PROLIFERATION AND CONTROL OF TRANSPOSABLE ELEMENTS	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Matheus Sampaio Araujo	Federal University Of Parana (ufpr)	Brazil
156	Harlekin	844	Transition of tetracycline resistance plasmid pT181 from independent multicopy replicon to predominantly integrated chromosomal element over 65 years	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Megan Phillips	Emory University	United States
157	Harlekin	630	Comparative ape and human genomics reveals natural protection mechanisms against human diseases	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Nachshon Egyes	Weizmann Institute of Science	Israel
158	Harlekin	552	Comparative genomics provides insights into genome evolution in Orthoptera	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Pinli Hu	University Of St Andrews	United Kingdom
159	Harlekin	1386	Evolutionary patterns and processes become better defined as the timetree of life grows larger	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	S. Blair Hedges	Temple University	United States
160	Harlekin	1305	Diversification of highly repetitive silk protein heavy-chain fibroin across butterflies and moths	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Samantha Standring	Brigham Young University	United States
161	Harlekin	1338	Recycling published data from wild Drosophila populations to investigate de novo gene retention.	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Sarah Lucas	University Of Muenster	Germany
162	Harlekin	1104	Genetic Pathway-Level Convergence Underlies the Diversity of Mammalian Life-Histories	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Theodoros Danis	Vanderbilt University	United States
163	Harlekin	596	Structural genetic diversity across the Tree of Life: macro-evolutionary patterns of intra-specific structural variation	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Thomas Brazier	Ecobio, Cnrs/university Of Rennes	France
164	Harlekin	1477	Convergent mechanisms underlying polar adaptation in fishes	S04 Mining the Archive: Evolutionary Genomics from Public Repositories	Tina Cai	University of California, Santa Cruz	United States
165	Harlekin	1090	Lungworm infection triggers sex-specific effects in gene expression in their cane toad hosts	S14 Evolution of Host-Pathogen Interactions in the Genomic Age	Tsering Chan	University Of New South Wales	Australia

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166	Harlekin	1339	Evolution of early animal immunity	S14 Evolution of Host-Pathogen Interactions in the Genomic Age	Blaire Padayhag	University College Dublin	Ireland
167	Harlekin	950	Phylogenetic comparative analysis of APOBEC3 Z-domain gene family evolution: Implications for bat immunity	S14 Evolution of Host-Pathogen Interactions in the Genomic Age	Brenda Delamonica	Stony Brook University	United States
168	Harlekin	1161	Tracing the early evolution of bilaterian antiviral immunity through Xenacoelomorpha	S14 Evolution of Host-Pathogen Interactions in the Genomic Age	Carmen Fontanes Eguiguren	University College Dublin	Ireland
169	Harlekin	1133	Population discontinuity in the Paris Basin linked to evidence of the Neolithic Decline	S14 Evolution of Host-Pathogen Interactions in the Genomic Age	Frederik Seersholm	University of Copenhagen	Denmark
170	Harlekin	1506	Repeated evolution of viral resistance in Caenorhabditis through mutation of a glycosyltransferase gene	S14 Evolution of Host-Pathogen Interactions in the Genomic Age	Gaotian Zhang	Institut de Biologie de l'Ecole Normale Superieure, CNRS	France
171	Harlekin	324	Time series RNA-seq shows temporal expression of host resistance related genes	S14 Evolution of Host-Pathogen Interactions in the Genomic Age	Luca Pecalli	University Of Basel	Switzerland
172	Harlekin	1379	Rodent Lung Mycobiomes as a Lens for Pathogen Surveillance and Phylosymbiosis	S14 Evolution of Host-Pathogen Interactions in the Genomic Age	Luisa Zamora Chavez	Arizona State University	United States
173	Harlekin	272	Gill-associated microbiome as indicators of population stress and condition in Eastern Baltic Cod	S14 Evolution of Host-Pathogen Interactions in the Genomic Age	Maria Cortazar	Uppsala University	Sweden
174	Harlekin	1237	Divergent and convergent evolution in avian TLR4 receptor system	S14 Evolution of Host-Pathogen Interactions in the Genomic Age	Michal Vinkler	Charles University, Faculty of Science	Czech Republic
175	Harlekin	825	Population-scale discovery and analysis of non-reference endogenous retrovirus insertions in wild house mice	S14 Evolution of Host-Pathogen Interactions in the Genomic Age	Naoki Osada	Hokkaido University	Japan
176	Harlekin	1522	Mammal-microbe evolution from global to local scales	S14 Evolution of Host-Pathogen Interactions in the Genomic Age	Nathan Upham	Arizona State University	United States
177	Harlekin	652	Integrating RNA structure and protein interactions to uncover the mechanisms of viral and cellular ires function	S14 Evolution of Host-Pathogen Interactions in the Genomic Age	Riccardo Delli Ponti	Italian Institute Of Technology	Italy
178	Harlekin	848	Uncovering the Global HLA diversity	S14 Evolution of Host-Pathogen Interactions in the Genomic Age	Sim Chin Yee (Faith)	Nanyang Technological University	Singapore
179	Harlekin	1402	Phageome dynamics across infant development in a wild primate gut microbiome	S14 Evolution of Host-Pathogen Interactions in the Genomic Age	Sophia Kottke	Arizona State University	United States
180	Harlekin	1587	Coordinated evolution of the DTX3L–PARP antiviral complex	S14 Evolution of Host-Pathogen Interactions in the Genomic Age	Stéphanie Jacquet	UMR 5290 Mivegec, CNRS	France
181	Harlekin	1288	Context-specific immune gene regulation is highly pleiotropic and actively evolving in human populations	S14 Evolution of Host-Pathogen Interactions in the Genomic Age	Tauras VILGALYS	University Of Georgia	United States
182	Harlekin	162	Evolutionary responses of Pseudomonas entomophila to insect-associated thermal stress reveal enhanced fitness and virulence	S14 Evolution of Host-Pathogen Interactions in the Genomic Age	Triveni Shelke	Indian Institute Of Technology Delhi	India
183	Harlekin	454	Genome-wide coadaptation constrains loss of the cag pathogenicity island in Helicobacter pylori	S14 Evolution of Host-Pathogen Interactions in the Genomic Age	Xiaoqi Zang	Shanghai Institute Of Immunity And Infection Chinese Academy Of Science	China
184	Harlekin	14	Honey bee pathogen profiling: molecular insights into microbial and parasitic communities	S14 Evolution of Host-Pathogen Interactions in the Genomic Age	Yeahji Jeong	Queen Mary University Of London	United Kingdom
185	Harlekin	1427	Recombination rate landscape in Lepidoptera group with rapid karyotype evolution	S11 The evolution of recombination landscapes	Alice Groudko	Wellcome Sanger Institute	United Kingdom
186	Harlekin	1462	Divergence and meiotic chromosome behavior along the polyploid continuum	S11 The evolution of recombination landscapes	Alison Scott	Max Planck Institute For Plant Breeding Research	Germany
187	Harlekin	304	Recombination rate and efficiency of linked selection in small and large stickleback populations	S11 The evolution of recombination landscapes	Chaowei Charlene Zhang	The University Of Hong Kong	Hong Kong
188	Harlekin	780	The Pattern of Polymorphism in Arabidopsis thaliana Reflects Non-Random Genome Organization	S11 The evolution of recombination landscapes	Elizaveta Grigoreva	Gregor Mendel Institute	Austria
189	Harlekin	277	Comparing fine-scale mutation and recombination landscapes in two rhesus macaque populations as assessed from both short- and long-read sequencing	S11 The evolution of recombination landscapes	Gabriella Spatola	Arizona State University	United States
190	Harlekin	1111	Do similars attract? Extensive association of repetitive sequences characterizes the NORs in an anuran species complex	S11 The evolution of recombination landscapes	Helena Milanez	University of Campinas	Brazil
191	Harlekin	1204	The Evolutionary Dynamics of Extended Recombination Suppression at a Distyly Supergene	S11 The evolution of recombination landscapes	Huiqin Yi	Stockholm University	Sweden
192	Harlekin	626	Meiosis (re)invented? Prdm9-independent meiotic recombination in dogs	S11 The evolution of recombination landscapes	Jasmin Cichy	Max Planck Institute For Evolutionary Biology	Germany
193	Harlekin	523	PRDM9 in Cnidarians: Structure and evolution of a major driver of recombination maps	S11 The evolution of recombination landscapes	Julie Clement	IHPE, Univ. Perpignan Via Domitia, Univ. Montpellier, CNRS, Ifremer	France
194	Harlekin	611	Fitness consequences of recombination hotspot positioning in dogs and wolf-dog hybrids	S11 The evolution of recombination landscapes	Julien Joseph	University of Aarhus	Denmark
195	Harlekin	21	Directional selection on quantitative traits can drive evolution of recombination rate in natural populations	S11 The evolution of recombination landscapes	LeAnn Williams	Mississippi State University	United States
196	Harlekin	339	Multi-omics reveal drivers of divergent sex-specific recombination in two passerines	S11 The evolution of recombination landscapes	Lisa Ammer	University of Edinburgh	United Kingdom
197	Harlekin	354	Genetic differentiation is constrained to regions of suppressed recombination in locally adapted populations with higher gene flow	S11 The evolution of recombination landscapes	Maria Akopyan	University Of California, Riverside	United States
198	Harlekin	502	The effect of linkage on polygenic adaptation	S11 The evolution of recombination landscapes	Matthew Hartfield	University Of Edinburgh	United Kingdom
199	Harlekin	322	Genetic determinants of intraspecific variation in crossover frequencies in the honeybee, Apis mellifera	S11 The evolution of recombination landscapes	Matthew Webster	Uppsala University	Sweden
200	Harlekin	231	A null model for the evolution of the recombination landscape	S11 The evolution of recombination landscapes	Mete Yuksel	University Of Toronto	Canada

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Board number	Poster area	Paper number	Paper Title	Theme	Presenter name	Presenter organisation	Presenter country
201	Harlekin	687	The genetic architecture, variation, and evolution of X-chromosomal SpermiR clusters in Mus musculus subspecies affecting recombination rates and hybrid sterility	S11 The evolution of recombination landscapes	Rajalekshmi Narayana Sarma	Max Planck Institute For Evolutionary Biology	Germany
202	Harlekin	404	Consequences of low effective recombination on deleterious mutations near regions under balancing selection in wild populations of C. elegans	S11 The evolution of recombination landscapes	Roman Stetsenko	University Of Edinburgh	United Kingdom
203	Harlekin	1244	Intra- and interspecific population genomics uncover the emergence of a supergene underlying a morpho-social polymorphism in the ant genus Myrmecina	S11 The evolution of recombination landscapes	Romuald Laso-Jadart	ISYEB	France
204	Harlekin	61	Recombination dynamics and patterns of molecular evolution in a widespread species with holocentromeres	S11 The evolution of recombination landscapes	Ruiyi Qiu	Max Planck Institute For Plant Breeding Research	Germany
205	Harlekin	1684	The harmonic mean recombination rate: properties, measurement, and implications	S11 The evolution of recombination landscapes	Tyler Kent	University Of Chicago	United States
206	Harlekin	48	Mutation and recombination rates in free-ranging deer: implications for speciation and demographic inference	S11 The evolution of recombination landscapes	Aaron Shafer	Trent University	Canada
207	2nd floor: Arkaden 8	1010	South American genetic diversity and adaptive strategies shaped by climatic dynamics since the late Pleistocene	S25 Deep time human genomics	Amit Gourav Ghosh	Nanyang Technological University	Singapore
208	2nd floor: Arkaden 8	427	Detecting Human-Specific DNA Methylation Changes through Comparative Analysis of Great Apes and Ancient Hominins	S25 Deep time human genomics	Chen Leibson	Hebrew University of Jerusalem	Israel
209	2nd floor: Arkaden 8	1323	Ancient DNA reveals the northeastern Tibetan Plateau as a hub of regional populations during the Bronze Age	S25 Deep time human genomics	Chengcheng Zhang	Fudan University	China
210	2nd floor: Arkaden 8	699	The genomics of the first identified Irish Mesolithic community	S25 Deep time human genomics	Corey Alwell	Trinity College Dublin	Ireland
211	2nd floor: Arkaden 8	1127	Fault-tolerant pedigree reconstruction from pairwise kinship relations	S25 Deep time human genomics	Edward C. Huang	Max Planck Institute for Evolutionary Anthropology	United States
212	2nd floor: Arkaden 8	686	Establishing biological links on a small and large scale: palaeogenetic study of individuals from the Saint-Memmie hypogeum (Marne, 3000 BCE)	S25 Deep time human genomics	Félicie Beck	Museum Of Natural History (Paris)	France
213	2nd floor: Arkaden 8	218	Reconstructing the Bantu expansion through an individual-based simulation integrating genomic and linguistic evolution	S25 Deep time human genomics	Francesco Giannelli	Uppsala University	Sweden
214	2nd floor: Arkaden 8	964	Understanding sedaDNA taphonomy through time	S25 Deep time human genomics	Frederikke M. Sønderborg	University Of Copenhagen	Denmark
215	2nd floor: Arkaden 8	1378	Centromere-Spanning Haplotypes Provide Insight into Human Evolution	S25 Deep time human genomics	Hailey Loucks	University Of California, Santa Cruz	United States
216	2nd floor: Arkaden 8	809	Genomic mosaic structure in mainland Southeast Asia through haplotype-based analyses of ethnic minority groups	S25 Deep time human genomics	Koki Yoshida	The University of Tokyo	Japan
217	2nd floor: Arkaden 8	1527	Tracing the demographic shifts of a Roman city on the Danubian Frontier during the Migration Period through paleogenetics	S25 Deep time human genomics	Leonardo Vallini	University Of Mainz	Germany
218	2nd floor: Arkaden 8	684	Optimising imputation and IBD segments retrieval in ancient genomes	S25 Deep time human genomics	Linda Ongaro	Trinity College Dublin	Ireland
219	2nd floor: Arkaden 8	720	From population branch statistics to human traits: phenotypic insights into recent human adaptation	S25 Deep time human genomics	Manuel Ferrando-Bernal	Ucsf	United States
220	2nd floor: Arkaden 8	280	Archaic introgression in pre-European contact Americas	S25 Deep time human genomics	Martina Gulì	Smurfit Institute of Genetics, Trinity College Dublin	Ireland
221	2nd floor: Arkaden 8	462	Tracking the demography in the Ryukyu Archipelago using time-series ancient genomes	S25 Deep time human genomics	Masatoshi Matsunami	University of the Ryukyus	Japan
222	2nd floor: Arkaden 8	707	Unlocking secrets of the epigenome: towards high-resolution bisulfite sequencing of ancient DNA (aDNA)	S25 Deep time human genomics	Natassja Brien	Mcmaster University	Canada
223	2nd floor: Arkaden 8	1131	Genomic insights into population connectivity among Classic Maya centres	S25 Deep time human genomics	Niall Moore	Trinity College Dublin	Ireland
224	2nd floor: Arkaden 8	1473	Regulatory remodeling and phenotypic relevance of lineage-specific sites across human lineages	S25 Deep time human genomics	Qiong Zhu	Fudan University	China
225	2nd floor: Arkaden 8	522	Using ancient DNA methylation to Predict Exposure to Smoke in Ancient Societies	S25 Deep time human genomics	Raphael Sirat	Hebrew University Of Jerusalem	Israel
226	2nd floor: Arkaden 8	917	The Royal Warship Kronan: Revealing the Crew through Archaeogenomics	S25 Deep time human genomics	Reyhan Yaka	Centre for Palaeogenetics, Stockholm University	Sweden
227	2nd floor: Arkaden 8	1355	Reconstructing the genetic landscape and evolutionary history of Pakistan using ancient and modern genomes	S25 Deep time human genomics	Rodelmar Ocampo Luna	CCG	Mexico
228	2nd floor: Arkaden 8	1085	Genomic Analysis and Environmental Adaptation in the Prehistoric Western Mediterranean	S25 Deep time human genomics	Samantha Rossini	University Of Rome Tor Vergata	Italy
229	2nd floor: Arkaden 8	537	Genomic Echoes of the Past: The Evolutionary History of Sicily	S25 Deep time human genomics	Silvia Ghirotto	University of Ferrara	Italy
230	2nd floor: Arkaden 8	692	Reframing the Neolithic Y-chromosome bottleneck in Europeans under purifying selection and structure	S25 Deep time human genomics	Stefan Strütt	University Of Bern	Switzerland
231	2nd floor: Arkaden 8	624	A new method for inferring demographic history and structure from the distribution of heterozygous sites	S25 Deep time human genomics	Tommaso Stentella	Max Planck Institute For Molecular Genetics	Germany
232	2nd floor: Arkaden 8	1251	Archaeogenomic Evidence for Social Organization and Connectivity in Teotihuacan	S25 Deep time human genomics	Xavier Roca-Rada	Brown University	United States
233	2nd floor: Arkaden 8	1469	Understanding brain evolution and psychiatric disease risk through the lens of Neanderthal divergence	S25 Deep time human genomics	Yaen Chen	University of California, San Francisco	United States
234	2nd floor: Arkaden 8	161	Studying archaic human structural variation with high-coverage genomes	S25 Deep time human genomics	Yaniv Swiel	Max Planck Institute for Evolutionary Anthropology	Germany
235	2nd floor: Arkaden 8	1019	The genomics of synergistic coevolution in mutualistically interacting bacteria	S17 Unicellular organisms in major evolutionary transitions	Aparajita Bhattacharya	Max Planck Institute for Evolutionary Anthropology	Germany
236	2nd floor: Arkaden 8	773	Tracing the evolutionary history of Saccharimonadia (TM7) bacteria through paleogenomics	S17 Unicellular organisms in major evolutionary transitions	I-Ting Huang	Harvard University	United States
237	2nd floor: Arkaden 8	640	The evolution of gene regulatory networks during the transition from unicellular to multicellular life	S17 Unicellular organisms in major evolutionary transitions	Jan Kreider	Lund University	Sweden
238	2nd floor: Arkaden 8	1107	Unicellular and Multicellular Selection Impose Fundamentally Distinct Constraints on Cellular Phenotype Evolution	S17 Unicellular organisms in major evolutionary transitions	Mark Kim	Cornell University	United States
239	2nd floor: Arkaden 8	1409	Proteins that emerged after the Great Oxygenation Event used less now-scarce manganese and iron-sulfur clusters, but not less heme	S17 Unicellular organisms in major evolutionary transitions	Nandini Manepalli	University Of Arizona	United States
240	2nd floor: Arkaden 8	650	Are interphylum spiralian relationships resolvable?	S12 Reconstructing the deep Tree of Life: challenges and new approaches	Ana Serra Silva	University College London	United Kingdom

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241	2nd floor: Arkaden 8	412	Ancient metagenomics reveals subglacial microbiomes driven by oxygen availability	S12 Reconstructing the deep Tree of Life: challenges and new approaches	Bianca De Sanctis	University Of Cambridge	United Kingdom
242	2nd floor: Arkaden 8	488	Developing profile mixture models for large-scale structural phylogenetics	S12 Reconstructing the deep Tree of Life: challenges and new approaches	Charley G. P. McCarthy	Université Paris-Saclay	France
243	2nd floor: Arkaden 8	539	The emergence of metabolisms through Earth history and implications for biospheric evolution	S12 Reconstructing the deep Tree of Life: challenges and new approaches	Edmund Moody	University Of Barcelona	Spain
244	2nd floor: Arkaden 8	95	The Dayhoff Exchange Score - a new metric to understand entropic saturation in phylogenomic datasets	S12 Reconstructing the deep Tree of Life: challenges and new approaches	James Fleming	University Of Barcelona	Spain
245	2nd floor: Arkaden 8	31	GLADE: Accurate Reconstruction of Orthogroup Histories and Gene Gain, Loss, and Duplication	S12 Reconstructing the deep Tree of Life: challenges and new approaches	Laurence Belcher	University Of Oxford	United Kingdom
246	2nd floor: Arkaden 8	1226	A Comprehensive Phylogenomic Framework for Brachiopod Evolution among Lophotrochozoans	S12 Reconstructing the deep Tree of Life: challenges and new approaches	Mingzhu Yang	University of Bristol	United Kingdom
247	2nd floor: Arkaden 8	802	Database-centred curation of BUSCO derived phylogenomic datasets	S12 Reconstructing the deep Tree of Life: challenges and new approaches	Morgan Jones	University Of Bristol	United Kingdom
248	2nd floor: Arkaden 8	672	Revisiting deep archaeal relationships with an expanded phylogenomic dataset	S12 Reconstructing the deep Tree of Life: challenges and new approaches	Pedro Romero-Tena	CNRS	France
249	2nd floor: Arkaden 8	865	IQ2MC: A New Framework to Infer Phylogenetic Time Trees Using IQ-TREE 3 and MCMCtree with Mixture Models	S12 Reconstructing the deep Tree of Life: challenges and new approaches	Piyumal Demotte	Australian National University	Australia
250	2nd floor: Arkaden 8	1635	Parallel and scalable balanced minimum evolution algorithm for large-scale phylogenetic inference	S12 Reconstructing the deep Tree of Life: challenges and new approaches	Qiyun Zhu	Arizona State University	United States
251	2nd floor: Arkaden 8	52	The effect of gene tree dependence on summary methods for species tree inference	S12 Reconstructing the deep Tree of Life: challenges and new approaches	Wanting He	The University Of Melbourne	Australia
252	2nd floor: Arkaden 8	541	Implementing a general SMC approximation to enable whole chromosome simulations beyond humans.	S07 From Trees to Graphs: Methodological Advances and Innovative Applications of Graphs in Evolutionary Analysis	Hossameldin Ali	University Of Oxford	United Kingdom
253	2nd floor: Arkaden 8	1472	The Interplay of Kinship and History: Why Close Relatives Improve Demographic Inference from IBD	S07 From Trees to Graphs: Methodological Advances and Innovative Applications of Graphs in Evolutionary Analysis	Sohini Ramachandran	Brown University	United States
254	2nd floor: Arkaden 8	947	Reconstructing hybrid speciation via the ancestral recombination graph	S07 From Trees to Graphs: Methodological Advances and Innovative Applications of Graphs in Evolutionary Analysis	Alexander Mackintosh	Swedish Museum of Natural History	Sweden
255	2nd floor: Arkaden 8	1320	Unraveling the dynamics of selection at HLA loci: the impact of balancing selection at different levels of biological organization	S07 From Trees to Graphs: Methodological Advances and Innovative Applications of Graphs in Evolutionary Analysis	André Maróstica	Universidade De São Paulo	Brazil
256	2nd floor: Arkaden 8	1261	The dawn of phylogenetic comparative graph neural networks (PCGNNs): Applications to quantitative trait imputation and ancestral state reconstruction	S07 From Trees to Graphs: Methodological Advances and Innovative Applications of Graphs in Evolutionary Analysis	Austin Patton	Arcadia Science	United States
257	2nd floor: Arkaden 8	1335	Towards scalable ARG-based inference of speciation	S07 From Trees to Graphs: Methodological Advances and Innovative Applications of Graphs in Evolutionary Analysis	Francisco De Borja Campuzano Jiménez	University of Antwerp	Belgium
258	2nd floor: Arkaden 8	425	Methods for inferring coalescent tree topologies from genomic data: a comparison based on the transmission of reproductive success	S07 From Trees to Graphs: Methodological Advances and Innovative Applications of Graphs in Evolutionary Analysis	Frederic Austerlitz	Cnrs	France
259	2nd floor: Arkaden 8	1542	Identifying modern human-specific adaptations using Ancestral Recombination Graphs	S07 From Trees to Graphs: Methodological Advances and Innovative Applications of Graphs in Evolutionary Analysis	Luiz Carlos Machado	Cold Spring Harbor Laboratory	United States
260	2nd floor: Arkaden 8	300	Folio: a stable encoding of phylogenies	S07 From Trees to Graphs: Methodological Advances and Innovative Applications of Graphs in Evolutionary Analysis	Mark Tanaka	University Of New South Wales	Australia
261	2nd floor: Arkaden 8	530	Multiple Merger Detection with Polymorphism Data	S07 From Trees to Graphs: Methodological Advances and Innovative Applications of Graphs in Evolutionary Analysis	Miles Anderson	Technical University of Munich	Germany
262	2nd floor: Arkaden 8	1086	Museomics of the Unwelcomed. A Genomic Pipeline to Explore Historical Samples	L03 Beyond limits: unlocking the potential of ancient animal genomics	Alice Piai	Museu de Ciències Naturals de Barcelona	Spain
263	2nd floor: Arkaden 8	1200	Disentangling ancient admixture and incomplete lineage sorting using DNA from museum specimens, a case study in Sphingidae (Lepidoptera)	L03 Beyond limits: unlocking the potential of ancient animal genomics	Anna K. Hundsdoerfer	Senckenberg Naturhistorische Sammlungen Dresden	Germany
264	2nd floor: Arkaden 8	1366	Climatic influences on the genetic connectivity of sky islands rodents	L03 Beyond limits: unlocking the potential of ancient animal genomics	Damien Rivera	Arizona State University	United States

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Board number	Poster area	Paper number	Paper Title	Theme	Presenter name	Presenter organisation	Presenter country
265	2nd floor: Arkaden 8	577	Beyond bones: Pleistocene to Holocene transition in Central Europe through sedimentary ancient DNA	L03 Beyond limits: unlocking the potential of ancient animal genomics	Dheeraj Chaudhary	Tel Aviv University	Israel
266	2nd floor: Arkaden 8	150	Ancient genomes illuminate the origins and dynamic history of East Asian cattle	L03 Beyond limits: unlocking the potential of ancient animal genomics	Donghee Kim	Seoul National University	South Korea
267	2nd floor: Arkaden 8	433	Genomic Continuity and Subtle Change in Central Asian Sheep from the Bronze to the Iron Age	L03 Beyond limits: unlocking the potential of ancient animal genomics	Germán Hernández Alonso	The University Of Edinburgh	United Kingdom
268	2nd floor: Arkaden 8	854	Extending the Shelf Life: Optimizing Ancient DNA Recovery from Highly Degraded Material in Museum Collections	L03 Beyond limits: unlocking the potential of ancient animal genomics	Hannah Moots	Centre For Palaeogenetics	Sweden
269	2nd floor: Arkaden 8	1422	Yak X: an archaic bovine from Denisova Cave	L03 Beyond limits: unlocking the potential of ancient animal genomics	Jonas Oppenheimer	Centre for Palaeogenetics	Sweden
270	2nd floor: Arkaden 8	229	A multi-species study of domestic animals in Neolithic Sweden	L03 Beyond limits: unlocking the potential of ancient animal genomics	Katia Bougiouri	Globe Institute, University of Copenhagen	Denmark
271	2nd floor: Arkaden 8	75	Dogs were widely distributed across Western Eurasia during the Palaeolithic	L03 Beyond limits: unlocking the potential of ancient animal genomics	Lachie Scarsbrook	LMU Munich	Germany
272	2nd floor: Arkaden 8	810	Metagenomics studies of Stone Age anthropogenic birch bark tar from Estonia	L03 Beyond limits: unlocking the potential of ancient animal genomics	Madeleine Thirolle	Institute of Genomics, University of Tartu	Estonia
273	2nd floor: Arkaden 8	565	Reducing read loss in competitive mapping of ancient DNA	L03 Beyond limits: unlocking the potential of ancient animal genomics	Mads V Hartmann	Technical University Of Denmark	Denmark
274	2nd floor: Arkaden 8	105	Describing early sheep domestic genetic diversity using ancient genomes from Asikli Höyuk, in Central Anatolia.	L03 Beyond limits: unlocking the potential of ancient animal genomics	Pedro Morell Miranda	Center For Paleogenetics - Stockholm University	Sweden
275	2nd floor: Arkaden 7	695	Predicting fitness effects of genetic variants by protein language models: experimental validation and calibration in plant species	S20 Mapping fitness landscapes with mechanistic models, machine learning and experiments	Guillaume Ramstein	Aarhus University	Denmark
276	2nd floor: Arkaden 7	902	Paying for expression: the adaptive landscape of gene regulation in the arabinose operon	S20 Mapping fitness landscapes with mechanistic models, machine learning and experiments	Anuradha Mukherjee	University Of Zurich	Switzerland
277	2nd floor: Arkaden 7	176	Phylogenetic variation in intrinsic antimicrobial drug susceptibility constrains resistance evolution	S20 Mapping fitness landscapes with mechanistic models, machine learning and experiments	Camille Bédard	Université Laval	Canada
278	2nd floor: Arkaden 7	332	Exploring Antifungal Resistance Through a Heterologous Expression System to Study Convergent Evolution and Fitness Landscapes	S20 Mapping fitness landscapes with mechanistic models, machine learning and experiments	David F. Jordan	Université Laval	Canada
279	2nd floor: Arkaden 7	1656	Fitness landscape estimation in the wild: genotypes and phenotypes underlying reproductive success in an Antirrhinum majus flower colour hybrid zone	S20 Mapping fitness landscapes with mechanistic models, machine learning and experiments	Hilde Schneemann	Institute Of Science And Technology Austria	Austria
280	2nd floor: Arkaden 7	1044	Landscape or seascape? Mapping an empirical fitness landscape in different genetic and environmental backgrounds	S20 Mapping fitness landscapes with mechanistic models, machine learning and experiments	Ilya Carey	University Of Zurich	Switzerland
281	2nd floor: Arkaden 7	450	Pleiotropic stabilizing selection shapes genetic architecture of complex traits	S20 Mapping fitness landscapes with mechanistic models, machine learning and experiments	Joshua Schraiber	University Of Southern California	United States
282	2nd floor: Arkaden 7	904	Molecular evolution on an adaptive seascape in fluctuating environments	S20 Mapping fitness landscapes with mechanistic models, machine learning and experiments	Laetitia Britschgi	University of Zurich	Switzerland
283	2nd floor: Arkaden 7	481	Probability and Distribution of Epistatic Interactions	S20 Mapping fitness landscapes with mechanistic models, machine learning and experiments	Luka Biočanin	University Of Jyväskylä	Finland
284	2nd floor: Arkaden 7	709	A Mutation–Selection Codon Model with Stochastic Tunneling for Multi-Nucleotide Substitutions	S20 Mapping fitness landscapes with mechanistic models, machine learning and experiments	Oliver Lyon	University Of Calgary	Canada
285	2nd floor: Arkaden 7	1560	Employing Pichia display to characterize rapidly evolving reproductive proteins in the marine mollusk abalone	S20 Mapping fitness landscapes with mechanistic models, machine learning and experiments	Trenton Winters	The Ohio State University	United States
286	2nd floor: Arkaden 7	67	A simple test demonstrates that many prokaryotic accessory genes are adaptive.	S21 From genomic graphs to evolutionary insights: standardising pangenomes for population inference	Adam Eyre-Walker	University Of Sussex	United Kingdom
287	2nd floor: Arkaden 7	658	Bringing clownfishes into the pangenome era: what more can we learn about their diversification ?	S21 From genomic graphs to evolutionary insights: standardising pangenomes for population inference	Anna Marcionetti	University Of Lausanne	Switzerland
288	2nd floor: Arkaden 7	187	Pangenome-based genotyping of structural variants in medical cohorts	S21 From genomic graphs to evolutionary insights: standardising pangenomes for population inference	Chiara Paleni	Human Technopole	Italy
289	2nd floor: Arkaden 7	1287	Reference-free pangenomes illuminate genomic diversity in African Anopheles malaria vectors	S21 From genomic graphs to evolutionary insights: standardising pangenomes for population inference	Clothilde Chenal	Wellcome Sanger Institute	United Kingdom
290	2nd floor: Arkaden 7	1515	Structural variants in Malawi cichlids radiation.	S21 From genomic graphs to evolutionary insights: standardising pangenomes for population inference	Ilia Artiushin	UAntwerpen	Belgium
291	2nd floor: Arkaden 7	1008	Constructing pangenome gene graphs with hundreds of thousands of bacterial genomes	S21 From genomic graphs to evolutionary insights: standardising pangenomes for population inference	Jackie Toussaint	Embl-ebi	United Kingdom
292	2nd floor: Arkaden 7	509	A pangenome approach for studying rapid adaptation in a species complex	S21 From genomic graphs to evolutionary insights: standardising pangenomes for population inference	Karim El Akoum	University Of Hamburg	Germany
293	2nd floor: Arkaden 7	418	Simulating population pangenomes with complex structural variants under the coalescent using MSpangenome.	S21 From genomic graphs to evolutionary insights: standardising pangenomes for population inference	Ludovic Duvaux	INRAE	France

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294	2nd floor: Arkaden 7	1524	Towards an unbiased characterization of genetic polymorphism	S21 From genomic graphs to evolutionary insights: standardising pangenomes for population inference	Magnus Nordborg	Gregor Mendel Institute	Austria
295	2nd floor: Arkaden 7	1212	Haplotype-resolved panNLRome in cultivated and wild bananas (Musa spp.) seen through the pangenomic lens	S21 From genomic graphs to evolutionary insights: standardising pangenomes for population inference	Marek Glombik	Earlham Institute	United Kingdom
296	2nd floor: Arkaden 7	1385	Independent hybridization events, followed by genomic rearrangements, shape genome evolution of polyploid A. kamchatica	S21 From genomic graphs to evolutionary insights: standardising pangenomes for population inference	Maria Vasilarou	Max Planck For Plant Breeding Research	Germany
297	2nd floor: Arkaden 7	1230	Graph Variant Explorer: Pangenomic analysis of ancient and modern DNA	S21 From genomic graphs to evolutionary insights: standardising pangenomes for population inference	Marianne Dehasque	Uppsala University	Sweden
298	2nd floor: Arkaden 7	1079	K-mer counts in pooled sequencing data rapidly estimate frequencies of known alleles in a pangenome graph	S21 From genomic graphs to evolutionary insights: standardising pangenomes for population inference	Miles Roberts	UC Berkeley	United States
299	2nd floor: Arkaden 7	668	Identifying unique variation and genetic load in Dutch cattle breeds through a pangenome	S21 From genomic graphs to evolutionary insights: standardising pangenomes for population inference	Rensco Hogers-Bijlaart	Wageningen University & Research	Netherlands
300	2nd floor: Arkaden 7	112	Pangenomics for De-Extinction: Towards the Great Passenger Pigeon Comeback	S21 From genomic graphs to evolutionary insights: standardising pangenomes for population inference	Simona Secomandi	The Rockefeller University	United States
301	2nd floor: Arkaden 7	1012	The diversity and evolutionary history of structural variation in European cattle genomes	S21 From genomic graphs to evolutionary insights: standardising pangenomes for population inference	Tobias van Elst	ETH Zurich	Switzerland
302	2nd floor: Arkaden 7	1026	From bacteria to humans, pangenome graphs provide unified coordinates for diversity, evolution, and somatic variation	S21 From genomic graphs to evolutionary insights: standardising pangenomes for population inference	Yuxin Ning	Quantitative Biology Center (QBiC), Eberhard Karls Universität Tübingen	Germany
303	2nd floor: Arkaden 6	536	Using ancient DNA to study historical plant communities surrounding lakes in Victoria, Australia through the Holocene	L02 Ancient plant DNA in the genomic era	Callum Swift	University Of Nottingham	United Kingdom
304	2nd floor: Arkaden 6	730	Tracing almond domestication through ancient DNA and metabolomics	L02 Ancient plant DNA in the genomic era	Raquel Sánchez-Pérez	CEBAS-CSIC	Spain
305	2nd floor: Arkaden 6	336	The lost tree of Rapa Nui: Genome assembly of the endemic, extinct-in-the-wild Sophora toromiro	L02 Ancient plant DNA in the genomic era	Signe Klemm	University Of Copenhagen	Denmark
306	2nd floor: Arkaden 6	931	Patterns of aDNA Damage Through Time and Environments – lessons from herbarium specimens	L02 Ancient plant DNA in the genomic era	Stefano Porrelli	Royal Botanic Gardens - Kew	United Kingdom
307	2nd floor: Arkaden 6	1114	ClonalRef: A novel palaeogenomic workflow for vegetatively propagated crops	L02 Ancient plant DNA in the genomic era	Surabhi Ranavat	University Of York	United Kingdom
308	2nd floor: Arkaden 6	1408	Polygenic Differentiation Reveals Selection on Autoimmune Disease Variants in the Finnish Population	S15 Detecting selection and local adaptation on (im)possible systems	Somnath Chindhe	Department of Biology, University Of Turku	Finland
309	2nd floor: Arkaden 6	379	Invasive African sacred ibis in Taiwan: insight from comparative genomics and population genetics	S15 Detecting selection and local adaptation on (im)possible systems	Chen Sia Ng	National Tsing Hua University	Taiwan
310	2nd floor: Arkaden 6	933	A likelihood-based method to infer the dispersal and the impact of natural selection using spatiotemporal data	S15 Detecting selection and local adaptation on (im)possible systems	Alessandro Lopez-Hernandez	Computational Population Genetics Group, LIIGH-UNAM	Mexico
311	2nd floor: Arkaden 6	765	Cryptic polygenic adaptation of body mass in a wild meerkat population	S15 Detecting selection and local adaptation on (im)possible systems	Alexander Downie	Max Planck Institute For Evolutionary Anthropology	Germany
312	2nd floor: Arkaden 6	951	Genomic determinants of reproductive success in a critically bottlenecked parrot	S15 Detecting selection and local adaptation on (im)possible systems	Audald Lloret-Villas	University of Copenhagen	Denmark
313	2nd floor: Arkaden 6	689	Improved inference on the architecture of complex traits in populations under strong polygenic selection by combining population and quantitative genetics	S15 Detecting selection and local adaptation on (im)possible systems	Bertrand Servin	INRAE - GenPhySE	France
314	2nd floor: Arkaden 6	914	Studying protective alleles of Sub-Saharan African Ancestry in Iberia: A genetic study of the Morenos from Huelva	S15 Detecting selection and local adaptation on (im)possible systems	Carlos Sarabia	Institute Of Evolutionary Biology (IBE-UPF CSIC), Barcelona	Spain
315	2nd floor: Arkaden 6	1258	A wavelet based multiscale alternative to sliding window analyses in population genetics	S15 Detecting selection and local adaptation on (im)possible systems	Eduardo Martin González Orozco	Max Planck Institute for Evolutionary Anthropology	Germany
316	2nd floor: Arkaden 6	727	Genomic Consequences of Extreme Isolation in the Raute	S15 Detecting selection and local adaptation on (im)possible systems	Elena Bosch	Universitat Pompeu Fabra	Spain
317	2nd floor: Arkaden 6	1005	How does inbreeding affect local adaptation in the mountain plant Arabis alpina?	S15 Detecting selection and local adaptation on (im)possible systems	Freya Way	Institute Of Ecology And Evolution, University Of Edinburgh	United Kingdom
318	2nd floor: Arkaden 6	1456	Looking for the ones that never made it out: purifying selection on de novo mutations during spermatogenesis	S15 Detecting selection and local adaptation on (im)possible systems	Genís Garcia-Erill	Aarhus University	Denmark
319	2nd floor: Arkaden 6	957	Local ancestry inference identifies adaptive admixture in Neolithic Europe	S15 Detecting selection and local adaptation on (im)possible systems	Georgia Mies	University of Pennsylvania	United States
320	2nd floor: Arkaden 6	491	Testing for local adaptation in rice landraces from Southeast Asia using gene expression	S15 Detecting selection and local adaptation on (im)possible systems	Isaura Rosas Reinhold	New York University	United States
321	2nd floor: Arkaden 6	263	Adaptive Divergence in a Sea of Gene Flow: Selection, Hybridization, and Structure in Baltic Herring	S15 Detecting selection and local adaptation on (im)possible systems	Jake Goodall	Uppsala University	Sweden
322	2nd floor: Arkaden 6	1440	Age reshapes selection on melanoma driver mutations	S15 Detecting selection and local adaptation on (im)possible systems	Jeffrey Townsend	Yale School of Public Health	United States
323	2nd floor: Arkaden 6	572	Signatures of differential local adaptation indicate climate matching with specific native-range habitats in invasive raccoons (Procyon lotor)	S15 Detecting selection and local adaptation on (im)possible systems	Joanna Kołodziejczyk	Institute Of Nature Conservation Polish Academy Of Sciences	Poland
324	2nd floor: Arkaden 6	749	Numerical challenges when inferring selection and population size history from the site frequency spectrum	S15 Detecting selection and local adaptation on (im)possible systems	Jonathan Wiese	University of Chicago	United States

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325	2nd floor: Arkaden 6	222	Can a natural Daphnia magna population (rapidly) adapt to a new predator?	S15 Detecting selection and local adaptation on (im)possible systems	Kathrin Otte	Hamburg University	Germany
326	2nd floor: Arkaden 6	313	Genomic conflicts between heat and cold tolerance during development in a desert bird	S15 Detecting selection and local adaptation on (im)possible systems	Lea Huber	Aarhus University	Denmark
327	2nd floor: Arkaden 6	386	A quantitative approach of polymorphism in bacteria beyond synonymous non-synonymous classification : impact of lifestyle in E. coli/Shigella	S15 Detecting selection and local adaptation on (im)possible systems	Manolo Mischler	Inserm	France
328	2nd floor: Arkaden 6	691	Identification of positive selection in the ancestral source populations of East Asians using ancient genomes	S15 Detecting selection and local adaptation on (im)possible systems	Masixuan Zhao	Institute of Vertebrate Paleontology and Paleoanthropology, CAS, Beijing	China
329	2nd floor: Arkaden 6	1057	Limited evidence for adaptive evolution of metabolic risk in Polynesian populations	S15 Detecting selection and local adaptation on (im)possible systems	Mathilde André	Institut Pasteur	France
330	2nd floor: Arkaden 6	378	FKBP5 Genetic Variants Under Selection Are Associated with Immune and Metabolic Phenotypes in the Taiwanese Han Population	S15 Detecting selection and local adaptation on (im)possible systems	Mei-Ling Kang	National Yang Ming Chiao Tung University	Taiwan
331	2nd floor: Arkaden 6	1167	Showcasing evolutionary patterns in marine phytoplankton with unresolved dispersal patterns through whole genome based molecular phylogenies of polar Chlamydomonas sp.	S15 Detecting selection and local adaptation on (im)possible systems	Michael Dills	UiT-The Arctic University Of Norway	Norway
332	2nd floor: Arkaden 6	722	Inferring the history of gene copy number evolution	S15 Detecting selection and local adaptation on (im)possible systems	Moritz Otto	University Of Cologne	Germany
333	2nd floor: Arkaden 6	309	Joint effects of balancing selection and population bottlenecks on the evolution of a regulatory region of human anti-viral APOBEC3	S15 Detecting selection and local adaptation on (im)possible systems	Naoko Fujito	Niigata University	Japan
334	2nd floor: Arkaden 6	767	Population Genomics Analysis of Rhynchophorus ferrugineus across its native and invasive range	S15 Detecting selection and local adaptation on (im)possible systems	Neelu Begum	Nyuad	United Arab Emirates
335	2nd floor: Arkaden 6	513	Linkage disequilibrium scaling improves robustness and power to detect genomic regions under selection in genetically structured species	S15 Detecting selection and local adaptation on (im)possible systems	Petri Kemppainen	University Of Helsinki	Finland
336	2nd floor: Arkaden 6	1231	Using phylogenetics to determine the fitness cost of resistance in viruses and bacteria	S15 Detecting selection and local adaptation on (im)possible systems	Pleuni Pennings	Université De Montpellier	France
337	2nd floor: Arkaden 6	1529	Tracing the impact of natural selection in admixed human populations from Mexico.	S15 Detecting selection and local adaptation on (im)possible systems	RAM GONZALEZ-BUENFIL	Center For Research And Advanced Studies of The National Polytechnic Institute	Mexico
338	2nd floor: Arkaden 6	1193	Fine-scale genetic structure and selection signatures underlying disease susceptibility in South Asia	S15 Detecting selection and local adaptation on (im)possible systems	Rubén Muñoz Miranda	Centro de Ciencias Genómicas	Mexico
339	2nd floor: Arkaden 6	519	Signatures of selection in admixed Indonesian cattle breeds	S15 Detecting selection and local adaptation on (im)possible systems	Sabhrina Gita Aninta	University of Copenhagen	Denmark
340	2nd floor: Arkaden 6	163	Evolutionary consequences of distyly loss in Linum: A shift toward higher selfing rates?	S15 Detecting selection and local adaptation on (im)possible systems	Zoe Postel	Slotte Lab, Stockholm University	Sweden
341	2nd floor: Arkaden 6						
342	2nd floor: Arkaden 6						
343	2nd floor: Arkaden 4+5	852	EXPLORING BULL KELP MICROBIAL DIVERSITY ACROSS AN ENVIRONMENTAL GRADIENT IDENTIFIES EUKARYOTE MICROBIOTA AND UNRAVELS ASSOCIATED METABOLIC PATHWAYS.	L04 Understanding adaptive evolution through the lens of hologenomics	Etienne Emonot	Cnrs	France
344	2nd floor: Arkaden 4+5	493	Integrated Host-Microbiome Contributions to Terrestrial Adaptations in Mangrove Sesarmid Crabs	L04 Understanding adaptive evolution through the lens of hologenomics	Ka Wing Karen Wong	The Chinese University Of Hong Kong	Hong Kong
345	2nd floor: Arkaden 4+5	770	Invisible engineers: distribution and diversity of nutrient-cycling prokaryotes associated with marine invertebrates	L04 Understanding adaptive evolution through the lens of hologenomics	Maggie Georgieva	Wellcome Sanger Institute	United Kingdom
346	2nd floor: Arkaden 4+5	892	The effect of host genetic bottlenecks on microbiome variance	L04 Understanding adaptive evolution through the lens of hologenomics	Niek Barmentlo	Vrije Universiteit Amsterdam	Netherlands
347	2nd floor: Arkaden 4+5	241	Coral holobionts evolve in response to a devastating disease	L04 Understanding adaptive evolution through the lens of hologenomics	Sarah Gignoux-Wolfsohn	University Of Massachusetts Lowell	United States
348	2nd floor: Arkaden 4+5	995	Contaminant Detection for the Study of Host-associated Microbial Signals in Historical Specimens	L04 Understanding adaptive evolution through the lens of hologenomics	Siu-kin Ng	Royal Botanic Gardens Kew	United Kingdom
349	2nd floor: Arkaden 4+5	1666	Measuring selection on rare disease using AI phenotype imputation in electronic health records (EHR)	S02 Powers and pitfalls of artificial intelligence for molecular evolution and phylogenetics	Daniel Jordan	Icahn School Of Medicine At Mount Sinai	United States
350	2nd floor: Arkaden 4+5	1689	Uncovering Non-Identifiable Demographic Histories using Generative AI	S02 Powers and pitfalls of artificial intelligence for molecular evolution and phylogenetics	Ekaterina Noskova	University of Edinburgh	United Kingdom
351	2nd floor: Arkaden 4+5	1292	Accurate and flexible reconciliation with neural networks	S02 Powers and pitfalls of artificial intelligence for molecular evolution and phylogenetics	Enzo Marsot	Lbbe	France
352	2nd floor: Arkaden 4+5	1420	Uncertainty and Interpretability in Neural Network Architectures for Population Genetic Inference	S02 Powers and pitfalls of artificial intelligence for molecular evolution and phylogenetics	Franz Baumdicker	University Of Giessen	Germany
353	2nd floor: Arkaden 4+5	225	Pixel2Phenotype: Hyperspherical Self-Supervised Latent Spaces for High-Throughput Drosophila Morphology	S02 Powers and pitfalls of artificial intelligence for molecular evolution and phylogenetics	Hyoungjun Park	EMBL	Germany

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354	2nd floor: Arkaden 4+5	568	Evolving Proteins Under Fitness Constraints: Does Complex Protein Modeling Help?	S02 Powers and pitfalls of artificial intelligence for molecular evolution and phylogenetics	Kaiyu Qiu	Max Planck Institute for Biology	Germany
355	2nd floor: Arkaden 4+5	1229	Toward a Prospective Framework for AI in Evolutionary Biology	S02 Powers and pitfalls of artificial intelligence for molecular evolution and phylogenetics	Ryan York	Arcadia Science	United States
356	2nd floor: Arkaden 4+5	562	A Computer Vision Framework for Quantifying Rapid Adaptation	S02 Powers and pitfalls of artificial intelligence for molecular evolution and phylogenetics	Stylianos Mavrianos	University Of Hamburg	Germany
357	2nd floor: Arkaden 4+5	1132	Revisiting estimation of bacterial mutation rates, fitness effect of mutations and resulting evolutionary dynamics through simulation-based methods	S10 Learning from Evolution: AI Models for Genomic Function	Aurélien Tauzin	Université Grenoble-alpes	France
358	2nd floor: Arkaden 4+5	184	Learning evolutionary constraints across the tree of life using a codon language model	S10 Learning from Evolution: AI Models for Genomic Function	Claudèle Lemay-St-Denis	University of Haifa	Israel
359	2nd floor: Arkaden 4+5	1376	Beyond classification accuracy: using model uncertainty to better understand lncRNA sequences	S10 Learning from Evolution: AI Models for Genomic Function	Daniel García-Ruano	University of Bordeaux	France
360	2nd floor: Arkaden 4+5	1126	Pan-Mammalian genomic insights into cancer resistance and therapeutic target discovery	S10 Learning from Evolution: AI Models for Genomic Function	Giada Padovani	University of Florida	United States
361	2nd floor: Arkaden 4+5	426	Training an AI model to predict population extinction based on genomic features	S10 Learning from Evolution: AI Models for Genomic Function	Jasmyn Gooding	University Of East Anglia	United Kingdom
362	2nd floor: Arkaden 4+5	94	Machine learning identifies the evolutionary genomic and statistical features that predict cross-population replication of GWAS signals	S10 Learning from Evolution: AI Models for Genomic Function	Joseph Lachance	Georgia Institute Of Technology	United States
363	2nd floor: Arkaden 4+5	472	Sequence-Based Detection of Programmed Ribosomal Frameshifts Using HMMs	S10 Learning from Evolution: AI Models for Genomic Function	Margaux Aubel	Oist	Japan
364	2nd floor: Arkaden 4+5	1576	AI-based prediction of variant fitness effects in Arabidopsis lyrata	S10 Learning from Evolution: AI Models for Genomic Function	Valentina Burskaia	Vlaams Instituut voor Biotechnologie (PSB UGent)	Belgium
365	2nd floor: Arkaden 2+3	90	Immune genes on the move: adaptive introgression in the European house mouse hybrid zone	S16 The genetic basis of evolutionary rescue	Jamie Winternitz	University Of Hamburg	Germany
366	2nd floor: Arkaden 2+3	873	Evolutionary repair of a broken mitotic entry switch	S16 The genetic basis of evolutionary rescue	Maria Rosa Domingo Sananes	Nottingham Trent University	United Kingdom
367	2nd floor: Arkaden 2+3	879	How can you survive accumulating loads of toxins? – The hidden roles of insect Na,K-ATPase β-subunits	S16 The genetic basis of evolutionary rescue	Marlena Herbertz	University of Hamburg	Germany
368	2nd floor: Arkaden 2+3	308	Evolution induced state shifts in a long-term microbial community experiment	S16 The genetic basis of evolutionary rescue	Mikko Kivikoski	University of Helsinki	Finland
369	2nd floor: Arkaden 2+3	1535	Transposon evolution under contrasting mating systems in Arabidopsis lyrata populations.	S24 Molecular mechanisms of selfish elements and strategies	Adrian Contreras Garrido	CNRS	France
370	2nd floor: Arkaden 2+3	1078	Do accessory chromosomes impact the phenotype of insect-pathogenic fungi?	S24 Molecular mechanisms of selfish elements and strategies	Aleksandra Gesiorska	Department Of Plant And Environmental Sciences, University of Copenhagen	Denmark
371	2nd floor: Arkaden 2+3	528	Ploidy variation and mating system shifts shape genome evolution in Arabidopsis lyrata	S24 Molecular mechanisms of selfish elements and strategies	Anna Glushkevich	The Max Planck Institute for Plant Breeding Research	Germany
372	2nd floor: Arkaden 2+3	102	How mobile elements structure the distribution of accessory genes	S24 Molecular mechanisms of selfish elements and strategies	Bram van Dijk	Utrecht University	Netherlands
373	2nd floor: Arkaden 2+3	291	Adaptive Divergence of Topoisomerase II Drives Satellite DNA-mediated Hybrid Incompatibility	S24 Molecular mechanisms of selfish elements and strategies	Cara Brand	Rutgers University	United States
374	2nd floor: Arkaden 2+3	996	The origin, spread, and demise of a recently active mammalian DNA transposon	S24 Molecular mechanisms of selfish elements and strategies	Harsha Sen	Princeton University	United States
375	2nd floor: Arkaden 2+3	1348	Investigating three-tiered interactions of ribosomal DNA, transposable elements, and satellite DNA as mechanisms of rapid genome evolution	S24 Molecular mechanisms of selfish elements and strategies	John Sproul	Brigham Young University	United States
376	2nd floor: Arkaden 2+3	1061	Teaching an old protein new tricks: the evolution of novelty through the lens of a selfish element	S24 Molecular mechanisms of selfish elements and strategies	Julian Ross	Institute of Molecular Biotechnology (IMBA)	Austria
377	2nd floor: Arkaden 2+3	629	Conjugation promotes the segregation of novel plasmid alleles under non-selective conditions	S24 Molecular mechanisms of selfish elements and strategies	Lisa Marie Hartmann	Kiel University	Germany
378	2nd floor: Arkaden 2+3	190	Recent expansion of LTR Retrotransposons in the genome of the Swedish Sand Lizard, Lacerta agilis	S24 Molecular mechanisms of selfish elements and strategies	Malavi Sengupta	Department Of Ecology And Genetics, Animal Ecology, Uppsala University	Sweden
379	2nd floor: Arkaden 2+3	1328	Transposable Elements Facilitate the Origin and Evolution of a Novel Antifreeze Protein Gene in Snailfishes	S24 Molecular mechanisms of selfish elements and strategies	Nathan Rives	University Of Arkansas	United States
380	2nd floor: Arkaden 2+3	247	Co-evolutionary dynamics of piRNA and KZFP defense systems against transposable elements	S24 Molecular mechanisms of selfish elements and strategies	Yusuke Nabeka	The Graduate University For Advanced Studies, Sokendai	Japan