Symposium	1: Crop evolu	ition: from Darwin's legacy	to genomics of admixture and climate resilience
Poster No.	-	Presenter Name	Abstract Title
S1-P01	955	Le Yu	Analysis of genetic variation and complex traits regulation of tobacco on subgenome level
S1-P02	1119	Yu-Chen Lin	Recent geographic dispersal of indica rice post domestication
S1-P03	427	Weixuan Ning	Population genomic studies of wild cotton (Gossypium hirsutum)
S1-P04	1286	Isabel Bojanini	Investigating genome-wide signatures of environmental adaptation in O. sativa ssp Indica
S1-P05	729	Sarai Reyes	MACHINE LEARNING FOR THE DETECTION OF NEXT-GENERATION GENETICALLY MODIFIED ORGANISMS THROUGH ANCESTRY INFERENCE
S1-P06	1232	Isaura Rosas Reinhold	Genome-environment association evidence edaphic adaptation in rice landraces (O. sativa subsp. indica) from SouthEast Asia
Symposium	2: Evolution a	nd regulation of sex chromo	osomes and sex determination
Poster No.	Abstract ID	Presenter Name	Abstract Title
S2-P01	143	Dandan Wang	Diversification of stickleback sex chromosomes driven by introgression
S2-P02	167	Zhihui Bao	Genetic Analysis of X Chromosome Suppression in the Male Germline of Drosophila melanogaster
S2-P03	216	Jiabi Chen	Human single-cell RNA-sequencing data supports the hypothesis of X chromosome insensitivity but is ineffective in testing the dosage compensation model
S2-P04	232	Xinning Dong	Evolutionary dynamics of the Drosophila Y chromosomes
S2-P05	306	Jie Wang	Sex chromosome evolution in Australian burrowing frogs Neobatrachus
S2-P06	408	Ruth Nanjala	HLA inference, diversity and selection analysis in Mexico
S2-P07	558	Yimeng Gao	Regulatory divergences in sex determination pathway cause hybrid male inviability in Caenorhabditis
S2-P08	704	Teng-Fei Xing	Extensive recombination suppression and genetic degeneration of a young ZW sex chromosome system in halfbeaks
S2-P09	805	Jiachen Li	Repeated evolution of transcript dosage compensation of independently formed nematode neo-X chromosome
S2-P10	893	Toni Gossmann	Implications of Sex-Specific Genomic Differentiation in the Great Tit (Parus major) Species Complex
S2-P11	1001	Weining Bai	Uncovering the Genetic Basis of Heterodichogamy in Pterocarya Using a Low-Input Pan-Genomic Approach
S2-P12	1083	Emma Diepeveen	The molecular evolution of ampliconic genes in primates
S2-P13	1352	Gaokang Liu	Evolutionary Genomics of Mamiellophyceae: Genomic insights into the lifecycle
S2-P14	1569	Yuying Lin	Y Chromosome Expansion in Poecilia wingei
S2-P15	1039	Aline Muyle	Epigenetic contribution to the evolution of separate sexes and sex chromosomes in the plant Silene latifolia
Symposium 4: Gene trees and beyond: genealogical methods and their applications in evolutionary genetics			
Poster No.	Abstract ID	Presenter Name	Abstract Title
S4-P01	241	Hongjin Wu	Powerful inference of bacterial evolution from genome-wide genealogies
S4-P02	419	Yufeng Wu	ScisTree2: An Improved Method for Large-scale Inference of Cell Lineage Trees and Genotype Calling from Noisy Single Cell Data

S4-P03	431	Chunhui Hao	Phylogenomic insights into the determinants of bacterial growth rate variation
S4-P04	534	Mingjie Liu	The molecular phylogeny of Nassariidae (Mollusca: Gastropoda)
S4-P05	560	Fengping Li	The molecular phylogeny of Caenogastropoda (Mollusca, Gastropoda)based on mitochondrial genomes and nuclear genes
S4-P06	574	Lina Uematsu	Dating LUCA and early evolutionary events using gene duplications
S4-P07	624	Robert Haobo Yuan	Incorporating punctuated evolution into Bayesian divergence time estimation
S4-P08	707	Siwen Gao	Fusang: a framework for phylogenetic tree inference via deep learning
S4-P09	751	Erik Widen	Evolutionary genomics approach to decipher genome stability in long-lived animals
S4-P10	838	Egor Lappo	Coalescent theory of the ψ directionality index
S4-P11	839	Jacky Kaiyuan Li	Demographic Inference with Inferred ARGs: An EM-Based Approach Incorporating Coalescent Time Uncertainty
S4-P12	878	Mingzhu Yang	Brachiopod phylogenomics and the Cambrian evolution of biomineralization
S4-P13	933	Chenxue Lin	Rooting the tree of eukaryotes using pre-LECA gene duplications
S4-P14	979	Sidney Davies	Tip-calibration approaches for deriving evolutionary timescales using genetic data
S4-P15	980	Junhyong Kim	Inferring cell lineage trees with the Neighbor-Joining method using transformer-based metric learning
S4-P16	990	Naoko Takezaki	Gene concordance factor and site concordance factor for the resolution of relationships of major groups of Neoaves
S4-P17	1022	Morgan Jones	A Phylogenomic Pipeline for Mining and Integrating Genomic Data: A Case Study Using Ecdysozoa
S4-P18	1197	Wenjie Zhu	Beyond Perfect Gene Trees: An Efficient Full-Likelihood Framework for Species Tree Inference
S4-P19	1269	Feifei Xia	Inferring population structure using genome-wide short tandem repeats
S4-P20	1282	Manel Ait El Hadj	Polymorphism-aware Framework to Analyse RNA-Seq Data for Trait Evolution Studies
S4-P21	1344	David Bonet Sole	Representation Learning on Ancestral Recombination Graphs with Transformers
Symposium	5: Human his	tory and past social organisatio	on in the light of palaeogenomes: new methods, new findings session A
Poster No.	Abstract ID	Presenter Name	Abstract Title
S5-P01	176	Yusuke Watanabe	Population history and cold adaptation in Upper Paleolithic hunter-gatherers of the Japanese archipelago
S5-P02	301	Jianxin Guo	Ancient genomes reveal coexistence of demic diffusion and cultural assimilation in the development of Bronze Age in southwest China
S5-P03	310	Miren Iraeta-Orbegozo	Mass violence, age and gender in the Early Iron Age of the Carpathian Basin
S5-P04	396	Sara Jang	Delineating multi-layered origins of human populations in Beringia using ancient and present-day genomes
S5-P05	627	Juhyeon Lee	Slab Grave expansion disrupted long co-existence of distinct Bronze Age herders in central Mongolia
S5-P06	700	Bahar Patlar	Selection on Semen Proteins: Human Genomic Clues to Neanderthal Mating Systems
S5-P07	1125	Zhe Xue	Mapping Fine-scale Genetic Connectivity in Large Ancient Biobanks
Symposium (1997)	6: Mutation r	ate rules: on the origin of germ	line mutations and their evolutionary fate
Poster No.	Abstract ID	Presenter Name	Abstract Title
S6-P01	85	Paco Majic	The evolution of mutation rates in the light of development and cell-lineage selection

S6-P02	68	Cai Li	A deep learning method for building INDEL mutation rate maps
S6-P03	205	Yawako Kawaguchi	Exploring variations in rates of genome structural evolution among vertebrates
S6-P04	227	Zhiqiang Wu	The mutation variation map for plant organellar genome
S6-P05	842	Yi Zou	The evolutionary dynamics of organellar pan-genomes in Arabidopsis thaliana
S6-P06	1453	Tian Tang	Evolutionary Dynamics and Maintenance of Epimutations Underpin Transcriptional Stability in Stress-Adapted Mangroves
Symposium '	7: The Origin,	Evolution, and Phenotypic Con	tributions of New Genes
Poster No.	Abstract ID	Presenter Name	Abstract Title
S7-P01	37	Ekaterina Guseva	Nsun7 is a conserved gene essential for spermatogenesis however is it classical methyltransferase?
S7-P02	44	Chuanzhu Fan	Neofunctionalization of tandem duplicate genes in Arabidopsis
S7-P03	140	Xinran Fan	Effect of codon use bias on horizontal gene transfer
S7-P04	237	Lei Shi	Cis-Regulatory Evolution of CCNB1IP1 Driving Gradual Increase of Cortical Size and Folding in Primates
S7-P05	286	Thomas Wolfe	The role of histone modifications and transposable elements in the epigenetic regulation of dosage after gene duplication
S7-P06	377	Haoran Cai	Expression variability following gene duplication facilitates gene retention
S7-P07	381	Chunyan Chen	The role of primate-specific genes in the phenotypic evolution of lorises
S7-P08	568	Frederic Bedard	The Impact of Protein Abundance Modifications on Fitness Following Gene Duplication
S7-P09	721	Amy Ó Brolcháin	Building a Placenta: Roles for Syncytin-Like Retroviral Envelopes of Livebearing Fish?
S7-P10	827	Olga Volovych	Laccase deficiency drives adaptive calcium metabolism in cockroaches
S7-P11	1063	Yongsung Lee	Horizontal gene transfers in the genomes of thermoacidophilic red algae
S7-P12	1076	Guan Jiayin	Evolution of Sex Pheromone Synthesis in Drosophila
S7-P13	1152	Ying Zhen	A versatile pipeline to identify convergently lost ancestral conserved fragments associated with convergent evolution of vocal learning
S7-P14	1358	Leo Camino	RNA-seq reveals genetic basis of structural coloration in the Neotropical butterfly Parides sesostris (Papilionidae)
S7-P15	524	Zheng Li	Genome-wide association study reveals the genetic basis for altered body conformation of game chickens
Symposium 9	9: Origin and	evolution of cell types	
Poster No.	Abstract ID	Presenter Name	Abstract Title
S9-P01	717	Xiaohan Lyu	Generation of bat iPSC cell lines across multiple species reveals high differentiation potential
S9-P02	215	Haixu Wu	3D single-cell transcriptome of lamprey identifies cellular and molecular innovations during the origin of the vertebrate brain
S9-P03	253	Tian Qin	Unveiling cell-type-specific mode of evolution in comparative single-cell expression data
S9-P04	646	Mark Kim	A Model for the Evolution and Deployment of Functional Gene Expression Programs Across Tissues
S9-P05	757	Shelbi Russell	Single cell sequencing reveals novel bacterial-induced pathways of eukaryotic differentiation
S9-P06	837	Liping Wang	Exploring Cell Types in Brown Algae Using Single-Cell RNA Sequencing

S9-P07	851	Xuefei Yuan	The molecular and cellular evolution of mammalian livers		
S9-P08	869	Wenxu Ren	Evolution of Transcription Factor Regulatory Networks in Vertebrate Immune Cells Using Single-Cell Multi- Omics		
S9-P09	1094	Zhenzhen Liu	Comparative Spatiotemporal Transcriptomics Unveils Conserved Lignification Trajectories and Evolutionary Signals During Nut Shell Development in Juglans		
S9-P10	1109	Lingyun Yang	Unicellular, Filamentous and Multicellular Cyanobacterial Genome Evolution Through Geological Time		
S9-P11	1279	Levin Alleweldt	Evolution of von Economo Neurons in the Anterior Cingulate Cortex Across Primates		
Symposium	10: Pangenom	e graphs and their applications	in biodiversity genomics		
Poster No.	Abstract ID	Presenter Name	Abstract Title		
S10-P01	618	Matteo Tommaso Ungaro	White lupin's genomic diversity and domestication history through pangenome graphs		
S10-P02	580	Yue Hao	Pangenome applications with de novo diploid genome assemblies in longitudinal cancer genome evolution		
S10-P03	354	Katharina Trost	A universal and constant rate of gene content change traces pangenome flux to LUCA		
S10-P04	97	Jia-Xing Yue	From pangenomes to pangenome graphs: resource curation, methods development, and biological discovery		
S10-P05	406	Zepu Miao	Accurate and scalable detection of structural variants from linear- and graph-based pangenomes		
Symposium 2	Symposium 29: Open symposium session A				
Poster No.	Abstract ID	Presenter Name	Abstract Title		
S29-P01	519	Yanileth Lopez Tacoaman	Exploring the drivers of gut microbiome diversification in Anolis lizards		
S29-P02	436	Shuting Wang	The evolution of Kallima butterflies		
S29-P03	537	Huy Chi Truong	Phylogenomics and Population Genetics of a Widespread Polytypic Bird Species Reveals Complex Evolutionary and Demographic History		
S29-P04	155	Ziyue Xu	Covariance and punctuation characterize the macroevolution of chemodiversity in gymnosperm volatile organic compound system		
S29-P05	180	Xiaoyu Meng	Single-cell multiome analyses of lungfish brain uncover cellular and molecular adaptation during water-to-land transition		
S29-P06	197	Igor Pantić	Novel random forest-based machine learning method for detecting subtle nuclear chromatin changes during programmed cell death		
S29-P07	361	Aleksandra Zeromska	Reconstruction the evolutionary history of the European snow vole based on ancient DNA and radiocarbon dating in the context of climate changes in the late Pleistocene and Holocene		
S29-P08	420	Jasmin Cichy	The mystery of Prdm9-independent meiotic recombination pathways in Canids		
S29-P09	449	Igor Pantić	Support vector machine model utilizing fractal features for detecting ethanol-induced alterations in cell nuclei		
S29-P10	450	Jovana Paunović Pantić	Detecting cell damage with AI: Gradient boosting tree algorithm combined with gray-level co-occurrence matrix		
S29-P11	528	Nicholas Chow	Compensatory mutations and the evolution of reduced costs of resistance in Pseudomonas aeruginosa		
S29-P12	656	Worapong Singchat	A Genetic and Histological Investigation of Testicular Abnormalities in North African Catfish		
S29-P13	1218	Xavier Martí-Pérez	Exploring Human Adaptation across Europe through a Polygenic Perspective		

S2P-P15 S4va Xaoling Deng Enfision yeas or holes of Collin, Mug174, forms Cajal body-like nuclear condensates and is essential for cellular quiescence S2P-P16 S4 Guan-Hong Wang Aligenes symbion enhance parsito it was passina it vipennis to leance of parsito it was passina it vipennis to leance of parsito it was passina it vipennis to leance of parsito it was passina it vipennis to leance of parsito it was passing with the parsito it was passing with passing parsito it was passing with the parsing with pa	S29-P14	349	Junhao Chen	Pervasive sex-dependent effects in the genetic architecture of starvation resistance in Drosophila melanogaster	
Symposium 31: Open symposium session CAbstract IUPresenter NameAbstract IIIPoster No.Abstract IDPresenter NameAbstract IIIS31-P011257Danijela PopovicThe natural and cultural history of brown bears in the Central Balkans as reconstructed through archaeological data and ancient DNAS31-P021259Aleksei SkudnovObligate aerobic bacteria show higher A>G mutation rate comparing to anaerobesS31-P031328Linjing LanEvolution of duplicated elements regulating myogenesis following the salmonid whole genome duplicationS31-P031481Gabriel Mochales-RiañoChromosome-level reference genome for the medically important Arabian horned viper (Cerastes gasperettii)S31-P061486Motahare Feizabadi FarahaniComparative Analysis of Single- vs. Double-Stranded Library Preparation Methods for Ancient DNA RecoveryS31-P07353Luca David ModjewskiEvidence for corrin biosynthesis in the last universal common ancestorS31-P08607Jiayou ShaoA Time-Scaled Phylogeny of Brachyna: Insights into Divergence, Radiation, and Drivers of Crab EvolutionS31-P10754Jianping XuPopulation genomic evidence for MATa-MATα and MATα-MATα sexual reproductions in Cryptococcus denoformansS31-P11822Chenhong LiA novel data filtering method resolves the controversy in the phylogeny of the ChondrichthyesS31-P131209Wentao TaoCAT-PMSF improves phylogenetic modeling and resolves Martialinae as the sister group to all remaining ants except LeptanilinaeS31-P141230Vivek SuranseScoripoins in disguise: Unra	S29-P15	547	Xiaoling Deng		
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S31-P011257Danijela PopovicThe natural and cultural history of brown bears in the Central Balkans as reconstructed through archaeological data and ancient DNAS31-P021259Aleksei SkudnovObligate aerobic bacteria show higher A>G mutation rate comparing to anaerobesS31-P031328Linjing LanEvolution of duplicated elements regulating myogenesis following the salmonid whole genome duplicationS31-P041359Damián ZepedaInferring the Evolutionary History of Lycalopex Foxes in South AmericaS31-P051481Gabriel Mochales-RiañoChromosome-level reference genome for the medically important Arabian horned viper (Cerastes gasperettii)S31-P061486Motahare Feizabadi FarahaniComparative Analysis of Single- vs. Double-Stranded Library Preparation Methods for Ancient DNA RecoveryS31-P07353Luca David ModjewskiEvidence for corrni biosynthesis in the last universal common ancestorS31-P08607Jiayou ShaoA Time-Scaled Phylogeny of Brachyura: Insights into Divergence, Radiation, and Drivers of Crab EvolutionS31-P10754Jianping XuPopulation genomic evidence for MATa-MATa and MATa-MATa sexual reproductions in Cryptococcus deneoformansS31-P11822Chenhong LiA novel data filtering method resolves the controversy in the phylogeny of the ChondrichthyesS31-P131209Wentao TaoCAT-PMSF improves phylogenetic modeling and resolves Martialinae as the sister group to all remaining ants except LeptanillinaeS31-P141230Vivek SuranseScorpions in disguise: Unraveling the cryptic Hottentotta diversity in IndiaS31-P151	Symposium	31: Open sym	posium session C		
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S31-P051481Gabriel Mochales-RiañoChromosome-level reference genome for the medically important Arabian horned viper (Cerastes gasperettii)S31-P061486Motahare Feizabadi FarahaniComparative Analysis of Single- vs. Double-Stranded Library Preparation Methods for Ancient DNA RecoveryS31-P07353Luca David ModjewskiEvidence for corrin biosynthesis in the last universal common ancestorS31-P08364Catherine CollinsThe evolutionary fate of laterally acquired genes depends on their utility and functional noveltyS31-P09607Jiayou ShaoA Time-Scaled Phylogeny of Brachyura: Insights into Divergence, Radiation, and Drivers of Crab EvolutionS31-P10754Jianping XuPopulation genomic evidence for MATa-MATα and MATα-MATα sexual reproductions in Cryptococcus deneoformansS31-P11822Chenhong LiA novel data filtering method resolves the controversy in the phylogeny of the ChondrichthyesS31-P131209Wentao TaoCAT-PMSF improves phylogenetic modeling and resolves Martialinae as the sister group to all remaining ants except LeptanillinaeS31-P141230Vivek SuranseScorpions in disguise: Unraveling the cryptic Hottentotta diversity in IndiaS31-P151389Pablo Esteban Uribe HerreraAncient mitogenomes reveals two divergent caballine horse lineages present at the Basin of Mexico towards the end of the Late PleistoceneSymposium 35: Open symposium session EPoster No.Abstract IIDPoster No.Abstract IIDPresenter NameAbstract Title	S31-P03	1328	Linjing Lan	Evolution of duplicated elements regulating myogenesis following the salmonid whole genome duplication	
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S31-P08364Catherine CollinsThe evolutionary fate of laterally acquired genes depends on their utility and functional noveltyS31-P09607Jiayou ShaoA Time-Scaled Phylogeny of Brachyura: Insights into Divergence, Radiation, and Drivers of Crab EvolutionS31-P10754Jianping XuPopulation genomic evidence for MATa-MATα and MATα-MATα sexual reproductions in Cryptococcus deneoformansS31-P11822Chenhong LiA novel data filtering method resolves the controversy in the phylogeny of the ChondrichthyesS31-P12886Saron TekieSpatiotemporal evolution of AMR in Streptococcus suis: Gene variants and transmission dynamics.S31-P131209Wentao TaoCAT-PMSF improves phylogenetic modeling and resolves Martialinae as the sister group to all remaining ants except LeptanillinaeS31-P151389Pablo Esteban Uribe HerreratAncient mitogenomes reveals two divergent caballine horse lineages present at the Basin of Mexico towards the end of the Late PleistoceneSymposium JS: Upper Simus ession EAbstract IDPresenter NamePoster No.Abstract IDPresenter NameAbstract Title	S31-P06	1486	Motahare Feizabadi Farahani	Comparative Analysis of Single- vs. Double-Stranded Library Preparation Methods for Ancient DNA Recovery	
S31-P09607Jiayou ShaoA Time-Scaled Phylogeny of Brachyura: Insights into Divergence, Radiation, and Drivers of Crab EvolutionS31-P10754Jianping XuPopulation genomic evidence for MATa-MATα and MATα-MATα sexual reproductions in Cryptococcus deneoformansS31-P11822Chenhong LiA novel data filtering method resolves the controversy in the phylogeny of the ChondrichthyesS31-P12886Saron TekieSpatiotemporal evolution of AMR in Streptococcus suis: Gene variants and transmission dynamics.S31-P131209Wentao TaoCAT-PMSF improves phylogenetic modeling and resolves Martialinae as the sister group to all remaining ants except LeptanillinaeS31-P141230Vivek SuranseScorpions in disguise: Unraveling the cryptic Hottentotta diversity in IndiaS31-P151389Pablo Esteban Uribe HerreraAncient mitogenomes reveals two divergent caballine horse lineages present at the Basin of Mexico towards the end of the Late PleistoceneSymposium 3:: Uprovid Strept No.Abstract IDPresenter NameAbstract Title	S31-P07	353	Luca David Modjewski	Evidence for corrin biosynthesis in the last universal common ancestor	
S31-P10754Jianping XuPopulation genomic evidence for MATa-MATα and MATα-MATα sexual reproductions in Cryptococcus deneoformansS31-P11822Chenhong LiA novel data filtering method resolves the controversy in the phylogeny of the ChondrichthyesS31-P12886Saron TekieSpatiotemporal evolution of AMR in Streptococcus suis: Gene variants and transmission dynamics.S31-P131209Wentao TaoCAT-PMSF improves phylogenetic modeling and resolves Martialinae as the sister group to all remaining ants except LeptanillinaeS31-P141230Vivek SuranseScorpions in disguise: Unraveling the cryptic Hottentotta diversity in IndiaS31-P151389Pablo Esteban Uribe HerreraAncient mitogenomes reveals two divergent caballine horse lineages present at the Basin of Mexico towards the end of the Late PleistoceneSymposium 35: Open symposium session EHerreraAbstract IDPoster No.Abstract IDPresenter NameAbstract Title	S31-P08	364	Catherine Collins	The evolutionary fate of laterally acquired genes depends on their utility and functional novelty	
S31-P10/54Jianping XudeneoformansS31-P11822Chenhong LiA novel data filtering method resolves the controversy in the phylogeny of the ChondrichthyesS31-P12886Saron TekieSpatiotemporal evolution of AMR in Streptococcus suis: Gene variants and transmission dynamics.S31-P131209Wentao TaoCAT-PMSF improves phylogenetic modeling and resolves Martialinae as the sister group to all remaining ants except LeptanillinaeS31-P141230Vivek SuranseScorpions in disguise: Unraveling the cryptic Hottentotta diversity in IndiaS31-P151389Pablo Esteban Uribe HerreraAncient mitogenomes reveals two divergent caballine horse lineages present at the Basin of Mexico towards the end of the Late PleistoceneSymposium 35: Open symposium session EPresenter NameAbstract IDPoster No.Abstract IDPresenter NameAbstract Title	S31-P09	607	Jiayou Shao	A Time-Scaled Phylogeny of Brachyura: Insights into Divergence, Radiation, and Drivers of Crab Evolution	
S31-P12886Saron TekieSpatiotemporal evolution of AMR in Streptococcus suis: Gene variants and transmission dynamics.S31-P131209Wentao TaoCAT-PMSF improves phylogenetic modeling and resolves Martialinae as the sister group to all remaining ants except LeptanillinaeS31-P141230Vivek SuranseScorpions in disguise: Unraveling the cryptic Hottentotta diversity in IndiaS31-P151389Pablo Esteban Uribe HerreraAncient mitogenomes reveals two divergent caballine horse lineages present at the Basin of Mexico towards the end of the Late PleistoceneSymposium 35: Open symposium session EMestract IDPresenter NameAbstract IDPresenter NameAbstract Title	S31-P10	754	Jianping Xu		
S31-P131209Wentao TaoCAT-PMSF improves phylogenetic modeling and resolves Martialinae as the sister group to all remaining ants except LeptanillinaeS31-P141230Vivek SuranseScorpions in disguise: Unraveling the cryptic Hottentotta diversity in IndiaS31-P151389Pablo Esteban Uribe HerreraAncient mitogenomes reveals two divergent caballine horse lineages present at the Basin of Mexico towards the end of the Late PleistoceneSymposium 35: Open symposium session EMexico TailPoster No.Abstract IDPresenter NameAbstract Title	S31-P11	822	Chenhong Li	A novel data filtering method resolves the controversy in the phylogeny of the Chondrichthyes	
S31-P131209Wentao Taoexcept LeptanillinaeS31-P141230Vivek SuranseScorpions in disguise: Unraveling the cryptic Hottentotta diversity in IndiaS31-P151389Pablo Esteban Uribe HerreraAncient mitogenomes reveals two divergent caballine horse lineages present at the Basin of Mexico towards the end of the Late PleistoceneSymposium 35: Open symposium session EHerreraAbstract IDPresenter NameAbstract Title	S31-P12	886	Saron Tekie	Spatiotemporal evolution of AMR in Streptococcus suis: Gene variants and transmission dynamics.	
S31-P15 1389 Pablo Esteban Uribe Herrera Ancient mitogenomes reveals two divergent caballine horse lineages present at the Basin of Mexico towards the end of the Late Pleistocene Symposium 35: Open symposium session E Poster No. Abstract ID Presenter Name Abstract Title	S31-P13	1209	Wentao Tao		
S31-P15 1389 Pablo Esteban Uribe Herrera end of the Late Pleistocene Symposium 35: Open symposium session E Poster No. Abstract ID Presenter Name Abstract Title	S31-P14	1230	Vivek Suranse	Scorpions in disguise: Unraveling the cryptic Hottentotta diversity in India	
Poster No. Abstract ID Presenter Name Abstract Title	S31-P15	1389	Pablo Esteban Uribe Herrera		
	Symposium	Symposium 35: Open symposium session E			
S35-P011573Sen HadifeHypoxia response is conserved between Cnidaria and Bilateria	Poster No.	Abstract ID	Presenter Name	Abstract Title	
	S35-P01	1573	Sen Hadife	Hypoxia response is conserved between Cnidaria and Bilateria	