Monday

Time	Audimax	Arcaded Courtyard	Big HS	HS33
0820 - 1000	**Opening remarks** **Bogdan Pasaniuc** Polygenic risk scores for precision medicine: promises and challenges. **Chiara Sabatti** Searching for causal variants in polygenic traits			
1000 - 1030		Coffee break		
1030 - 1200	**Thomas Hansen** The structure of evolutionary quantitative genetics **Jeff Endelman** Directional Dominance in Polyploids: Trait Analysis and Mate Selection			
1400 - 1600		Poster Session 1		
1600 - 1620	**Kerry Geiler-Samerotte** The Genotype-Phenotype-Phenotype-Phenotype Map		**Torsten Pook** Strategies to improve selection compared to selection based on estimated breeding values	**Frank Albert** Genetic variation in protein degradation
1620 - 1640	**Laura Luebbert** Efficient and accurate detection of viral sequences at single-cell resolution reveals novel viruses perturbing host gene expression		**Zhiwu Zhang** Emerging Marker Assisted Selection and Genomic Selection	**Jose Aquicira Hernandez** Scalable single-cell models for robust cell-state-dependent eQTL mapping
1640 - 1700	**Joshua Popp** Dynamic genetic regulation of gene expression in heterogeneous differentiating cultures		**Tobias Niehoff** Exploiting progeny variances for selection decisions improves genetic gain and variance in genomic breeding programs	**Daniel Kaptijn** Genetic regulation of single-cell personal gene correlations (co-eQTLs) is highly enriched for GWAS variants
1700 - 1720	**Natalia Ruzickova** Interpretable genomic predictions via effect propagation in gene regulatory networks		**Marcio Resende** Integrating single kernel Phenomic Selection with Genomic Selection: Applications in Corn Breeding	**Guillaume Ramstein** Prediction of variant effects by foundation AI models: in vivo validation at nucleotide and haplotype resolution in plant populations
1730 - 1900		Welcome reception		

Tuesday

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0820 - 1000	**Piter Bijma** Dark Genes: How transmission of infections boosts heritable variation and response to selection **Jason Wolf** Genetic analysis of intrafamilial interactions			
1000 - 1030		Coffee break		
1030 - 1200	**Susan Johnston** The causes and consequences of sex differences in recombination rates **Zach Lippman** Synergy among cryptic variants in a plant regulatory network drive non-linear phenotypic effects			
1400 - 1600		Poster Session 2		
1600 - 1620	**Peter Keightley** The impact of spontaneous mutation accumulation on quantitative variation in a mammalian species		**Jian Zeng** Genome-wide fine-mapping improves identification of causal variants	**Xiaoning Zhu** Deciphering the genetic mechanisms of complex traits in chicken AIL populations using multi-omics data
1620 - 1640	**Gregor Gorjanc** Quantitative genetic modelling of diverse populations using ancestral recombination graphs		**Xiangyu Jack Ge** GentroPy package for ancestry specific systematic fine-mapping of GWAS data, colocalization and drug targets prediction	**Hao Tong** Leveraging interactome and transcriptome to enhance genomic prediction in plant breeding
1640 - 1700	**Andrea Doeschl-Wilson** Estimating and dissecting host genetic variation underlying infectious disease transmission – methodology and empirical evidence		**Yixuan He** Multi-trait and multi-ancestry polygenic risk score approach improves genetic discovery and risk prediction of respiratory diseases	**Xiandong Ding** An efficient analysis method for integrating multiple omics data based on deep learning
1700 - 1720	**Owen Powell** Improving the prediction of non-additive effects with hierarchical genomic prediction models		**Lin Qing** Multi-ancestry genome-wide association study meta-analysis deciphers the genetic architecture of male fertility in pig	**Julia Sidorenko** Reconciling linkage and association studies of complex traits
1730 - 1815	**Naomi Wray** Quantitative Genetics of Psychiatric Disorders			

Wednesday

Time	Audimax	Arcaded Courtyard	Big HS	HS33
0820 - 1000	**Jacqueline Sztepanacz** Estimating genetic variation and selection in high-dimensional data **Guy Sella** A population genetic interpretation of genome-wide association studies in humans			
1000 - 1030		Coffee break		
1030 - 1245	**Jack Dekkers** Implementation of a Mechanistic Growth Model for Pigs into Bayesian Methods for Genomic Prediction and GWAS **Christine Baes** Quantitative Genetic Solutions for Optimizing Livestock Sustainability: Innovations, Genomic Applications, and Future Directions **Gustavo de los Campos** Improving cross-ancestry PGS Prediction through Transfer Learning using Informative Penalized Regressions and Bayesian Mixture Models			

Thursday

Time	Audimax	Arcaded Courtyard	Big HS	HS33
0820 - 1000	**Julien Ayroles** Transcriptional dynamics under selection: unravelling polygenic adaptation and stress responses **Michael Goddard** Identifying causal variants for histone modification			
1000 - 1030		Coffee break		
1030 - 1200	**Po-Ru Loh** Influences of genomic structural variation on human complex traits **Joelle Mbatchou** Using large language models for rare variant association testing in large-scale biobanks			
1400 - 1600		Poster Session 3		
1600 - 1620	**Al Depope** Light-speed whole genome association testing and prediction via Approximate Message Passing		**Leke Victor Aiyesa** A new unrestricted assessment toward utilizing individual plant phenotypes and genotypes for breeding	**Anna Hewett** Inbreeding depression throughout the growth period of wild Swiss barn owls
1620 - 1640	**Xia Shen** Modelling the genetic architecture of complex traits via stratified high-definition likelihood		**Michelle Stitzer** Transposable element abundance subtly contributes to lower fitness in maize	**Richard Bernstein** Effective population size in honeybees from pedigree and SNP data
1640 - 1700	**Matias Schrauf** Altered Prior Mean of Allelic Effects: An Approach for Adequately Considering Gene Edited Variants within Genomic Predictions		**Neda Rahnamae** Can hybridization allow the emergence of a Super-Genotype in Arabis floodplain species?	**Elizabeth Mittell** The effects of a missing fraction on selection in adult size traits in a wild population
1700 - 1720	**Dom Waters** Reduced rank factor analytic models for capturing genotype by environment interactions in livestock		**Yvonne Wientjes** Changes in allele frequency and GWAS results across years in two pig populations under selection	**Kelly Swarts** Isolating adaptive variation from natural forest trees
1730 - 1815	**Ed Buckler** From Climate Change to AI: Improving Agriculture by Learning from Global Biological Diversity			
1815 - 2100		Evening Reception		

Friday

Time	Audimax	Arcaded Courtyard	Big HS	HS33
0820 - 1000	**Loic Yengo** Convergence of heritability estimates from orthogonal experimental designs **Augustine Kong** Participation bias in genetic studies and estimate adjustments			
1000 - 1030		Coffee break		
1030 - 1200	**Lingzhao Fang** The Farm Animal Genotype-Tissue Expression (FarmGTEx) Project for Advancing Agriculture and Biomedicine **Amelie Baud** The Hologenome 2.0			
1400 - 1600		Poster Session 4		
1600 - 1620	**Lars Rönnegård** Warning: Selection for decreased variability in milk yield may lead to asocial cows!		**Natalia Leite** Marker Effect P-Value for Large Genotype Populations with the Algorithm for Proven and Young	**Tom Druet** Unravelling the genetic architecture of height and muscular development traits in Belgian Blue cattle and using it for genomic prediction
1620 - 1640	**Christie Warburton** IBS versus IBD - new insights from whole genome sequence data		**Anthony Long** X-QTL mapping using multi-parent synthetic populations is powerful and efficient conditional on experimental design	**Martin Johnsson** The structure of potentially functional genetic variation in cattle
1640 - 1700	**Ilse Krätschmer** Direct, indirect and epigenetic effects in families		**Teresa McGee** Increasing power in association mapping with genetic replicates by recognizing variance heterogeneity and exploring implications of near zero-variance	**Emre Karaman** Incorporating prior biological information into genomic predictions: An example from mastitis in Danish Jersey and Nordic Red cattle
1700 - 1720	**Thomas Ellis** The Effect of Population Structure Correction on GWAS Before and After Random Mating		**Nick Machnik** Causal inference for multiple risk factors and diseases from genomics data	**Naveen Kadri** Detection of QTL for global recombination rate in Fleckvieh cattle
1730 - 1800	**Closing remarks and early career poster and talk prizes**			