



Integrating quantitative and molecular genetics to develop new breeding methods in maize and sorghum

October 7 – 9, 2019

TUM School of Life Sciences Weihenstephan

PROGRAM

Monday, October 7, 2019		
12:00	Registration, Lunch	
13:30	Welcome	
Session: C	haracterize, maintain and broaden genetic diversity Chair: Violeta Anđjelković	
14:00	Matthew Hufford, Iowa State University Genome assembly and comparative analysis of the maize NAM founder lines	
14:30	Georg Haberer, Helmholtz Center Munich European flint genomes complementing the maize pan- and core-genome	
14:40	Cinta Romay, Cornell University Unraveling diversity for genomics and breeding	
15:20	Armin Hölker, Technical University of Munich Maize doubled haploid libraries derived from landraces make native diversity accessible	
15:40	Manfred Mayer, Technical University of Munich Identification of novel alleles for elite germplasm improvement	
16:00	Coffee break	
	Chair: Jean-François Rami	
16:30	Ana Galiano, University of Hohenheim Harnessing Brazilian germplasm for the improvement of resistance to NCLB in European maize programs	
16:50	Mihai Miclăuş, Romanian National Research and Development Institute for Biological Sciences Uncovering the genetic structure of SE European maize through a GBS approach on 2,236 inbred lines	
17:00	Mon-Ray Shao, Donald Danforth Plant Science Center High-resolution 3D phenotyping of diverse maize root and sorghum inflorescence architectures	
17:10	David Pot, CIRAD A sorghum biomass quality genetic atlas	
17:40	Paul Chege, Szent István University Diversity analysis of some selected Hungarian and East African Sorghum (Sorghum bicolor (L.) Moench) genotypes using SSR markers	
17:50	Matthieu Falque, INRA Linkage-based detection of copy-number variants	
18:20	Elise Tourrette, INRA Using increased recombination to accelerate genomic selection programs	
18:30	Michelle Stitzer, UC Davis Using the genomic ecosystem of transposable elements to understand maize diversity	





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Tuesday, October 8, 2019

Session: Genotype by environment interactions on different scales Chair: Chris-Carolin Schön		
09:00	Frank Hochholdinger, University of Bonn	
	Transcriptomic response of European maize to cold stress	
09:30	Karina van der Linde, University of Regensburg	
	Small secreted proteins in male inflorescence development and pathogenicity	
09:50	Caroline Gutjahr, Technical University of Munich	
	Understanding arbuscular mycorrhiza responsiveness in maize	
10:20	Coffee break	
11:00	Emilie Millet, Wageningen University	
	Dissecting GxE and QTLxE of maize yield in contrasting scenarios of light, heat and water deficit	
11:30	Ioannis Tokatlidis, Democritus University of Thrace	
	Major reasons for maize breeding to advance crop stability via plant yield efficiency	
11:50	Nadir Abu Samra Spencer, INRA	
	A common genetic gain for hybrid maize (1952-2015) across environmental scenarios	
12:10	Italo Granato, INRA	
	Traits measured in a phenotyping platform disentangle the genetic yield maintenance in specific drought-prone environmental scenarios	
12:30	Lunch	
	Chair: Silvio Salvi	
13:45	Pedro Revilla, CSIC	
	Genetic analysis of cold tolerance in maize	
14:15	Stella Eggels, Technical University of Munich	
	The relationship between carbon isotope discrimination and stomatal properties in maize	
14:25	Viktoriya Avramova, Technical University of Munich	
	Fine mapping of a genomic segment associated with the traits carbon isotope composition, water use efficiency and drought sensitivity in maize (<i>Zea mays</i> L.)	
14:45	Jana Kholova, ICRISAT	
	Cross-disciplinary efforts to improve crop production/resilience in complex SAT environments	
15:15	Meeting EUCARPIA Maize and Sorghum section members (Lecture Hall 17, 30 min.)	
	Poster session	
15:15	<i>Coffee break</i> (Foyer Liesel-Beckmann-Str. 2)	





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Tuesday, October 8, 2019 cont.

Session: New avenues in selection and breeding through integration of molecular tools		
	Chair: Alain Charcosset	
17:00	Aaron Lorenz, University of Minnesota	
	Broadening the scope of selection through genomic prediction	
17:30	Marco Lopez-Cruz, Michigan State University	
	Penalized family and selection indices	
17:50	Elaheh Vojgani, University of Goettingen	
	Accounting for epistasis improves genomic prediction of phenotypes within and across environments	
18:10	Christina Lehermeier, RAGT	
	Improving genetic gain by marker-guided selection of crosses	
19:00	Conference dinner	





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Wednesday, October 9, 2019

Session: N	lew avenues in selection and breeding through integration of molecular tools cont. Chair: Silke Wieckhorst
09:00	Laurence Moreau, INRA Genomic prediction in early stages of a maize breeding program: comparison of testcross and factorial designs
09:30	Torsten Pook, University of Goettingen MoBPS – Modular Breeding Program Simulator
09:50	Medhat Mahmoud, University of Goettingen G-hat: an R package for identifying selection on complex traits
10:00	Antoine Allier, RAGT Improving short and long term genetic gain by accounting for within family variance in optimal cross selection
10:10	Coffee break
10:50	Gustavo de los Campos, Michigan State University
	Extracting genetically accurate phenotypes from high throughput phenotype data using penalized selection indices
11:20	Emma Mace, University of Queensland The road from sequence to consequence: extracting value from genomics for breeding
11:50	Fred van Eeuwijk, Wageningen University Genomic evaluation of sorghum parental lines is enhanced by multi-trait analysis of progeny performance
12:10	Lunch
	Chair: Domagoj Šimić
13:30	Randall Wisser, University of Delaware From dissection to selection for environmental adaptation in maize: transforming exotic populations into future breeds
14:00	Stéphane Nicolas, INRA Genotyping-by-sequencing and SNP arrays are complementary for detecting quantitative trait loci by tagging different haplotypes in association studies
14:20	Alain Charcosset, INRA Disentangling group specific QTL allele effects from genetic background epistasis using admixed individuals in GWAS: an application to maize flowering
14:40	Julie Fievet, INRA The geometry of heterosis
15:00	Albrecht Melchinger, University of Hohenheim Doubled-haploid lines from landraces are useful for maize breeding and genetic research
15:30	Discussion
16:00	End





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