

Synbreed Colloquium

March 4 -6, 2015

Lecture Hall 17 / HS17

Wissenschaftszentrum Weihenstephan,
Technische Universität München



Wednesday March 4, 2015

12:00	Registration	
	<i>Session 1: Evolution of genome-based prediction</i>	<i>Chair: Hans-Rudolf Fries</i>
13:00	Welcome	
13:30	Predicting complex traits in cattle	<i>Mike Goddard</i>
14:15	Evolution of genomic selection in the Synbreed era	<i>Malena Erbe</i>
14:45	Genome-based prediction in maize - Lessons learnt from five cycles of selection	<i>Chris-Carolin Schön</i>
<i>15:15</i>	<i>Coffee break</i>	
	<i>Session 2: Impact of genome-based research</i>	<i>Chair: Natalia de Leon</i>
15:45	Impact of five years Synbreed on the maize breeding and research program at KWS	<i>Milena Ouzunova</i>
16:15	Taking genomics to the farm: Challenges and opportunities	<i>Hans-Rudolf Fries</i>
16:45	Genome-wide selection and its application in poultry breeding	<i>Rudolf Preisinger</i>
17:15	Breeding drought tolerant maize for the US corn-belt	<i>Mark Cooper</i>
<i>18:30</i>	<i>Dinner</i>	
19:30	Poster session	

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Thursday March 5, 2015

<i>Session 3: Advanced statistical methods</i>		<i>Chair: Daniel Gianola</i>
09:00	Graphical models applied to quantitative genetics and genomics	<i>Guilherme Rosa</i>
09:45	Evaluation of the performance of machine learning methods for genomic prediction using simulated and empirical data sets	<i>Joseph Ogotu</i>
10:15	Advanced methodology to exploit genomic information for estimation and prediction	<i>Georg Thaller</i>
<i>10:45</i>	<i>Coffee break</i>	
<i>Session 4: Beyond the additive model</i>		<i>Chair: Henner Simianer</i>
11:15	Genomic prediction of hybrid performance	<i>Albrecht Melchinger</i>
11:45	Estimation of dominance effects in genomic evaluation models	<i>Kay-Uwe Götz</i>
12:15	Genomics in commercial pig breeding	<i>Pieter Knap</i>
<i>13:00</i>	<i>Lunch</i>	
<i>Session 5: Diversity is beautiful</i>		<i>Chair: Aurelien Tellier</i>
14:00	European maize genomics: Demography, adaptation and selection	<i>Maud Tenaillon</i>
14:45	Population genomic analysis of genetic variation in maize landraces	<i>Karl Schmid</i>
15:15	Untangling mutation rate and effective population size using jointly pedigree information and genomic data	<i>Florence Parat</i>
15:45	Genome-wide pattern and magnitude of genetic diversity in a wide range of diverse chicken breeds	<i>Steffen Weigend</i>
<i>16:30</i>	<i>Bus departure Social event and dinner in Munich</i>	

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Friday March 6, 2015

<i>Session 6 : Genome discovery and selection</i>		<i>Chair: Karl Schmid</i>
08:30	Seeing triple: Transcriptional coordination in the polyploid wheat genome	<i>Klaus Mayer</i>
09:15	Genomic signatures of long term selection programs in maize	<i>Natalia de Leon</i>
10:00	Population structure and genetic diversity of DH-libraries of European flint maize landraces and their use in association mapping of agronomic traits	<i>Juliane Böhm</i>
<i>10:30</i>	<i>Coffee break</i>	
11:00	Molecular differences in the flint and dent populations in maize	<i>Georg Haberer</i>
11:30	Footprints of selection in the genomes of livestock populations	<i>Henner Simianer</i>
12:00	Mapping and functional dissection of loci underlying three separate comb phenotypes in chicken	<i>Johan-Carl Rubin</i>
<i>12:45</i>	<i>End</i>	