XVIth meeting of the Eucarpia Section Biometrics in Plant Breeding

Hotel "De Wageningsche Berg", Wageningen NL 9 – 11 September 2015

Wednesday 9 September

07:30	**Registration**	
08:30	**WELCOME**	
08:30	Chair of Local Organizing Committee (M. Bink)	
08:40	President of Eucarpia section Biometrics for Plant Breeding (F. van Eeuwijk)	
08:50	Representative of Eucarpia Board (S. van der Heijden)	
09:00	**SESSION 1**	**Genomic and marker assisted breeding** *Chair: Marco Bink*
09:00	**John Hickey (invited)**	Sequence to Phenotype: Allocation of Resources
09:40	Chris Gaynor	Genomic Selection for Grain Yield in Kansas Wheat
10:00	Emi Tanka	On the joint use of pedigree and marker information for genomic selection in wheat breeding
10:20	**Coffee break**	
10:50	**SESSION 2**	**Genomic and marker assisted breeding** *Chair: Laurence Moreau*
10:50	**Luc Janss**	Genomic analysis in tetraploid potato using genotyping-by-sequencing
11:20	Willem Kruijer	Marker-Based estimation of heritability for plant traits
11:40	Christina Lehermeier	Assessment of genetic heterogeneity in structured plant breeding populations using multivariate whole-genome regression models
12:00	Daniela Bustos	Improving prediction accuracy by using models adapted to traits genetic architecture, and by considering the genetic distances to define the training set
12:20	**Group Picture**	
12:30	**Lunch at hotel**	
13:30	**SESSION 3**	**Genomic and marker assisted breeding** *Chair: Fred van Eeuwijk*
13:30	**Peter Visscher (keynote)**	Genomics and big data in human populations: combining genetics and epigenetics to predict phenotypes
14.20	**Roel Veerkamp**	Genomic selection in animal breeding: a success story
15:00	**Coffee break**	
15:30	**SESSION 4**	**Genomic and marker assisted breeding** *Chair: Ian Mackay*
15.30	Héloïse Giraud	QTL detection in a reciprocal recurrent design for silage in maize
15.50	Marcos Malosetti	Predictions for new genotypes and/or environments: models and designs
16:10	Jong Jiang	Modelling Epistasis in Genomic Selection
16.30	Hélène Muranty	Genomic selection in apple: a multi-year pilot study
16:50	**SESSION 5**	**Various themes** *Chair: Marcos Malosetti*
16:50	Donghui Ma (VSNi)	IBP - Breeding Management System (Sponsored Demo)
17:05	Poster Flashes	**1 slide & 1 minute each**
17:30	**Poster session**	*(with drinks & food)*

Thursday 10 September

08:00	Registration	
08:30	**SESSION 6**	**Implementaton of breeding strategies in public and private sector** *Chair: Hans-Peter Piepho*
08:30	**Neil Haussman (invited)**	Future Breeding Systems: view from DuPont Pioneer
09:10	**Andres Gordillo**	Genomic selection strategies and validation in hybrid maize and rye
09:40	Jaap Buntjer	Strategic use of genomic prediction models for parent selection in breeding programs.
10:00	**Coffee break**	
10:30	**SESSION 7**	**Analysis and use of high throughput data** *Chair: Chris Maliepaard*
10:30	**Dave Marshall**	The data challenges from the application of high throughput technologies in plant breeding and genetics
11:00	**Marco van Schriek**	Exploitation of digital phenotype markers for prediction of brassica napus field seed yield
11:30	Christine Hackett	Linkage map construction in blackcurrant using genotyping by sequencing data
11:50	Pawel Krajewski	On recommendations for metadata and data handling in plant phenotyping
12:10	Heike Sprenger	Discovery of Transcript and Metabolite Markers for the Breeding of Drought Tolerant Potato Cultivars using High Throughput Technologies
12:30	**Lunch at hotel**	
13:30	**Excursions**	(choices to be made via website or at arrival, return at hotel ~18:00 hours)
19:00	**Conference Dinner**	(hotel "De Wageningse Berg")

Friday 11 September

08:30	**SESSION 8**	**Exploitation of genetic resources**
		Chair: Carlotta Vaz Patto
08:30	**Jens Riis-Jacobsen**	Accelerate genetic gain by taking advantage of additional data sources and
	(invited)	integrated data analysis – case studies from maize and wheat breeding at CIMMYT
09:10	Keith Gardner	A high density genetic linkage map for wheat using an eight-founder MAGIC population
09.30	Andreas Maurer	Modelling the genetic architecture of flowering time control in barley through nested association mapping
09:50	**Business Meeting**	**Eucarpia section Biometrics for Plant Breeding**
10:20	**Coffee break**	
10:50	**SESSION 9**	**Experimental design and analysis of phenotyping trials**
		Chair: Pawel Krajewski
10:50	**Alison Smith (invited)**	Experimental designs for expensive multi-phase traits
11:30	**Hans Peter Piepho**	The generation of efficient row-column designs for field trials
12:00	Fred van Eeuwijk	P-spline models for spatial variation in agricultural field trials
12:20	**Lunch at hotel**	
13:30	**SESSION 10**	**Various themes**
		Chair: Dietrich Borchardt
13:30	**Emma Huang (invited)**	Meta-alleles in multiparental populations
14:10	Peter Bourke	High-density linkage mapping and the double-reduction landscape in tetraploid potato
14:30	Chaozi Zheng	Multilocus haplotype reconstruction in outcrossing tetraploids
14:50	**Concluding remarks**	
15:00	**Farewell drinks**	