EUCARPIA

29 Aug – 1 Sep 2016
Zurich/Switzerland

20th General Congress / **Plant Breeding: the Art of Bringing Science to Life**

Program

The following is the current tentative program. Exact locations will be confirmed later. Some times may change. Check back for updates.

Sunday 28. August, 2016

14.00 to 20.00	Registration desk open
17.45 – 18.45	Board meeting

Monday 29. August, 2016

8.00 – 12.00	Registration (continued)

Opening session

Chair: Achim Walter

9.00 – 9.30	Welcome addresses **Lino Guzzella**, President of ETHZ, Switzerland **Bernard Lehmann,** Director of Federal Office of Agriculture, Switzerland **Beat Boller**, EUCARPIA President
9.30 – 10.15	**John Bradshaw,** James Hutton Institute, UK **– Introductory lecture** *Plant breeding: Past, present and future*
10.15 – 10.45	*Coffee break*

Plenary Session Genomics and Bioinformatics 1

Chair: Beat Keller

10.45 – 11.25	**Nils Stein,** IPK Gatersleben, Germany **– Keynote lecture** *Big genomes, big data, big progress? What is the impact of access to reference genome sequences in barley, wheat and rye?*
11.25 – 11.45	**Yonatan Elkind**, The Hebrew University of Jerusalem, Israel *Genomic assisted selection and classical plant breeding – synergy or competition?*
11.45 – 12.00	**Coraline Praz**, University of Zurich, Switzerland *Transcriptomics to understand host adaptation in cereals powdery mildews*
12.00 – 12.15	**Verena Knorst**, Agroscope, Switzerland *Wisdom of crowds: pooled sequencing identifies genomic regions associated with disease resistance in ryegrass*
12.15 – 12.30	**Martin Mascher**, IPK Gatersleben, Germany *BARLEX – the barley draft genome explorer*
12.30 – 13.45	*Lunch*

Plenary Session Genomics and Bioinformatics 2

Chair: Bruno Studer

13.45 – 14.25	**Torben Asp,** Aarhus University, Denmark **– Keynote lecture** *Towards genomic selection in an outbreeding crop, perennial ryegrass*
14.25 – 14.45	**Daniela Bustos-Korts**, Wageningen UR, The Netherlands *Integrating high-throughput phenotyping technologies in a multi-trait genomic prediction model*
14.45 – 15.00	**Vincent Garin**, Wageningen UR, The Netherlands *QTL detection in multi-parent population using different types of QTL effects and cross specific residual terms models*

15.00 – 15.15	**Carine Rizzolatti**, Syngenta, France *Molecular characterization of the cytoplasmic male sterility system underlying the breeding and production of hyvido hybrids in barley*
15.15 – 15.30	**Rianne Van Binsbergen**, Wageningen UR, The Netherlands *Utilizing low-coverage sequence data in tomato recombinant inbred lines (S. lycopersicum x S. pimpinellifolium)*
15.30 – 16.00	*Coffee break*

Plenary Session Stress tolerance 1 (abiotic stress)

Chair: Michele Stanca

16.00 – 16.40	**Delphine Fleury,** Australian Centre for Plant Functional Genomics, Australia **– Keynote lecture** *Making genotype x environment interaction accessible to breeding for drought resistance*
16.40 – 17.00	**Edith Lammerts van Bueren**, Louis Bolk Institute, The Netherlands *Obstacles and challenges when breeding for nitrogen use efficiency in vegetable crops*
17.00 – 17.15	**Ulrike Lohwasser**, IPK Gatersleben, Germany *Genome wide association mapping approach searching for frost tolerance in wheat (Triticum aestivum L.)*
17.15 – 17.30	**Ivo Rieu**, Radboud University, The Netherlands *Tomato likes it hot, but pollen not - understanding heat-tolerance of male fertility in tomato*
17.30 – 17.45	**Matthias Wissuwa**, JIRCAS, Japan *Pup1 and beyond: Developing rice adapted to infertile soils in Africa*

Flash presentations (cross-cutting topics)

Chair: Andreas Hund

17.45 – 18.30	Flash presentations of 3 min. each; corresponding posters will be displayed in the following poster session

Dhaka Ram Bhandari, Justus Liebig University, Germany
Localization of metabolites in plant tissues using high-resolution mass spectrometry imaging
Yong-Bi Fu, Plant Gene Resources, Canada
A new lab guide on genotyping-by-sequencing for plant genetic diversity analysis
Maja Mazur, Agricultural Institute Osijek, Croatia
Applying segregation distortion approach in QTL analysis of three non-BSSS doubled haploid populations in maize
Monica Menz, Syngenta, France
Hapmaps and its application in plant breeding
Sara Giulia Milner, IPK Gatersleben, Germany
BRIDGE: Biodiversity informatics for harnessing barley genetic diversity hosted at the genebank of IPK Gatersleben
Mahbubjon Rahmatov, Swedish Univ. of Agricultural Sciences, Sweden
Development and characterization of a new wheat-rye Robertsonian translocation with Sr59 resistance to stem rust

Gil Ronen, NR Gene, Israel
Better Breeding Decision using high throughput de novo assembly and advanced Genomic Big Data Analytics
Florian Schröper, Fraunhofer IME, Germany
How next-generation sequencing can improve and speed up breeding of new crop varieties
Chaozhi Zheng, Wageningen UR, The Netherlands
RABBIT: reconstructing ancestry blocks bit by bit in experimental populations

18.30 – 19.15	Poster session – cross-cutting topics
19.15	*Welcome reception*

Tuesday 30. August, 2016

Plenary Session Stress tolerance 2 (biotic stress) – COST session

Chair: Richard Visser

8.30 – 9.10	**Richard Oliver,** Curtin University, Australia **– Keynote lecture** *Cause and effects; bottlenecks in the discovery and deployment of effectors and markers for the control of cereal Dothideomycete diseases*
9.10 – 9.30	**Bülent Uzun**, Akdeniz University, Turkey *Breeding pipeline for resistance to phyllody phytoplasmas in sesame*
9.30 – 9.45	**Claude Emmanuel Koutouan**, University of Angers, France *Can the variation of secondary metabolite contents be part of carrot resistance to Alternaria dauci?*
9.45 – 10.00	**Javier Sanchez**, University of Zurich, Switzerland *Association mapping of durable resistance to wheat powdery mildew*
10.00 – 10.15	**Kaile Sun**, Wageningen UR, The Netherlands *Down-regulation of Arabidopsis DND1 orthologs in potato and tomato leads to broad-spectrum resistance to late blight and powdery mildew*
10.15 – 10.45	*Coffee break*

Plenary Session Secondary metabolites

Chair: Jaime Prohens

10.45 – 11.25	**Johann Novak,** University of Veterinary Medicine, Austria **Keynote lecture** *Optimizing plant secondary metabolite production*
11.25 – 11.45	**Olivier Viret**, Agroscope, Switzerland *Stilbenes biomarkers to bread resistant grape varieties against fungal diseases*
11.45 – 12.00	**Ferenc Bekes**, FBFD PTY LTD, Australia *Breeding less allergenic spelt wheat with low FODMAP content*
12.00 – 12.15	**Roland Kölliker**, Agroscope, Switzerland *Improving performance and tannin content of the forage legume sainfoin (Onobrychis viciifolia)*
12.15 – 12.30	**Carol Wagstaff**, University of Reading, UK *Using the L. sativa x L. serriola lettuce mapping population to direct breeding for flavour and nutrition*
12.30 – 13.45	*Lunch*

Crop specific parallel sessions

Speakers and titles for each session available further down after the plenary program.

13.45 – 15.30 Parallel oral presentations

1. Tuber and industrial crops – *Dan Milbourne*
2. Cereals – *Andreas Börner*
3. Fodder crops – *Dirk Reheul*
4. Maize and Sorghum – *Alain Charcosset*
5. Vegetables – *Yuling Bai*
6. Fruit, Ornamentals, Medicinal, Aromatic – *José Vouillamoz*
7. Legumes – *Antonio de Ron*

Special session on occasion of the **International Year of Pulses**

15.30 – 16.00 Coffee break

16.00 – 16.45 Parallel flash presentations

1. Wheat – *Fabio Mascher*
2. Other cereals – *Andreas Börner*
3. Fodder crops and Maize – *Dirk Reheul*
4. Oil and Protein (Legumes) crops *Bülent Uzun*
5. Fruit, Ornamentals, Medicinal, Industrial – *Johan van Huylenbroeck*
6. Vegetables – *Yuling Bai*

16.45 – 17.45 Poster session: Crop specific topics

17.45 – 18.45 EUCARPIA General assembly (for members only)

From 18.45 Free evening in Zurich

Wednesday 31. August, 2016

Chair: François Tardieu

Plenary Session Phenomics 1

8.30 – 9.10	**Matthew Reynolds,** CIMMYT, Mexico – **Keynote lecture** *Phenotyping for Plant Breeding: combining precision with throughput*
9.10 – 9.30	**Achim Walter**, ETH Zurich, Switzerland *Field Phenotyping Platform (FIP) - an automated multi sensor system for plant phenotyping in the field – first results*
9.30 – 9.45	**Catherine Giauffret**, INRA AgroImpact, France *Association mapping for transition to autotrophic growth under chilling conditions in maize*
9.45 – 10.00	**Chantal Le Marié**, ETH Zurich, Switzerland *Imaging of maize root traits in multiple field environments reveals high heritability but limited genotype-specific response to low nitrogen*
10.00 – 10.15	**Marvellous Zhou**, South African Sugarcane Res. Inst., South Africa *Ideotype based breeding for sugarcane yield: a case study of using logistic regression models to identify optimum trait combinations in different breeding populations*
10.15 – 10.45	Coffee break

Plenary Session Phenomics 2

Chair: Achim Walter

10.45 – 11.25	**François Tardieu,** INRA Montpellier, France **– Keynote lecture** *Crop modelling as a basis for genetic plant improvement*
11.25 – 11.45	**Jana Kholova**, Int. Crops Res. Inst. for the Semi-Arid Tropics, India *Enhancement of SAT agricultural production; development of trait-based environment specific breeding pipeline at ICRISAT*
11.45 – 12.00	**Kristina Jonaviciene**, Lithuanian Res. Centre for Agric.and Forestry *Modelling the growth of perennial ryegrass under water limiting conditions*
12.00 – 12.15	**Marco Maccaferri**, University of Bologna, Italy *Whole genome QTL search for root system architecture in tetraploid wheat*
12.15 – 12.30	**Dina St. Clair**, University of California, Davis, USA *Genetics and genomics of water stress tolerance in wild tomato*
12-30 – 19.00	Lunch box and departure for excursions – ending at conference dinner site
From 19.00	Conference dinner at Jucker Farm, Jona, Lake Zurich

Thursday, 1. September, 2016

Plenary Session Genetic resources 1 (conservation)

Chair: Beat Boller

8.30 – 9.10	**Ola Westengen,** University of Life Sciences, Norway **Keynote lecture** *Crops and culture: conserving the seed heritage*
9.10 – 9.30	**Andreas Börner**, Inst. of Plant Genetics and Crop Plant Res., Germany *Conservation and exploitation of plant genetic resources – the view of a Genebank manager*
9.30 – 9.45	**Shelagh Kell**, International Treaty on PGRFA, UK *Bottlenecks in the PGRFA sustainable use system: stakeholders' perspectives*
9.45 – 10.00	**Eva-Maria Sehr**, Austrian Institute of Technology, Austria *Genetic diversity of Austrian flax accessions – a case study for ex situ germplasm characterisation*
10.00 – 10.15	**Muhammet Sakiroglu**, Kafkas University, Turkey *Assessing global patterns of genetic diversity and population structure of tetraploid gene pool of Alfalfa (Lucerne)*
10.15 – 10.45	*Coffee break*

Plenary Session Genetic resources 2 (pre-breeding)

Chair: Shelagh Kell

10.45 – 11.25	**Hei Leung,** IRRI, Philippines **– Keynote lecture** *Multi-parent populations for dissection of complex traits in rice*
11.25 – 11.45	**Beat Keller**, University of Zurich, Switzerland *Molecular diversity of fungal disease resistance genes in cereals and their applications in breeding*
11.45 – 12.00	**Rashed Alarfaj**, University of Reading, UK *QTL identification and phenotyping of strawberry fruit of an octoploid population for quality traits*
12.00 – 12.15	**Antoine Botrel**, Syngenta, France *Supervised genetic group classification for plant breeding*
12.15 – 12.30	**Jaime Prohens**, Universitat Politècnica de València, Spain *Introgressiomics: a new paradigm for crop improvement and adaptation to climate change*
12.30 – 13.45	*Lunch*

Plenary Session Plant-Microbe interactions

Chair: Roland Kölliker

13.45 – 14.25	**German Spangenberg,** DEPI Victoria, Australia **– Keynote lecture** *Systems biology and molecular breeding of grass-endophyte symbiota*
14.25 – 14.45	**Friederike Trognitz**, Austrian Institute of Technology, Austria *Genotype-specific seed microbiota of different wheat accessions and their functional characteristics*
14.45 – 15.00	**Iva Cholakova**, Hasselt University, Belgium *Plant-growth promoting and drought tolerance traits of bacteria isolated from highly drought resistant Pistacia terebinthus: a comparison between spring and autumn isolated communities*
15.00 – 15.15	**Pierre Hohmann**, Res. Inst. of Organic Agriculture, Switzerland *Breeding for symbioses – Mycorrhizae as a case study*
15.15 – 15.30	**Maryam Zarean**, Isfahan University of Technology, Iran *Epichloe endophyte increases seed set in tall fescue through self-pollination*
15.30 – 16.00	*Coffee break*

Plenary Session Innovation vs. Regulation

Chair: Beat Boller

16.00 – 16.40	**Richard Visser,** WUR, The Netherlands **– Keynote lecture** *Innovation vs. regulation – Maintaining biodiversity and breeding innovative cultivars*

16.40 – 17.30 “opinion statements” and extended public discussion

Stakeholders on stage:

- Representative of public research into plant breeding: *Eva Reinhard, Federal office of Agriculture, Switzerland*
- Multinational breeding company: *TBC*
- SME breeding company: *Stephanie Franck, Saatzucht Oberlimpurg / Chair of Bund Deutscher Pflanzenzüchter BDP*
- Seed trade: *Michael Keller, Secretary General, International Seed Federation*
- NGO dealing with environmental concerns: *TBC*
- Politician: *TBC*

17.30 – 18.00	Closing

Crop specific parallel sessions details

Oral presentations

1. Tuber and industrial crops – *Chair Dan Milbourne*

13.45 – 14.00	**Awang Maharijaya**, Bogor Agricultural University, Indonesia *Screening of 14 potato genotypes for their adaptation to tropical medium altitude conditions*
14.00 – 14.15	**Dan Milbourne**, Teagasc, Ireland *Stability of resistance conferred by pyamiding two QRLs for G. pallida Pa2/3*
14.15 – 14.30	**Friederike Trognitz**, AIT, Austria *Diversity of starch related genes among potato cultivars*
14.30 – 14.45	**Louise Andersson**, Syngenta Seeds, Sweden *Transcriptional dynamics during the sugar beet, Beta vugaris ssp. vulgaris - Rhizoctonia solani interaction*
14.45 – 15.00	**Susanne Barth**, Teagasc, Ireland *Genetic diversity in a large Miscanthus germplasm collection*
15.00 – 15.15	**Lothar Frese**, JKI, Germany *Genetic diversity of Patellifolia patellaris from Southeast Spain, a crop wild relative of cultivated beets*
15.15 – 15.30	TBC

2. Cereals – *Chair Andreas Börner*

13.45 – 14.00	**Peter Dracatos**, University of Sydney, Australia *The quest for durable resistance to rust diseases in barley*
14.00 – 14.15	**Juan Herrera**, Agroscope, Switzerland *Identifying the best variety at each site with climatic-limitation covariates*
14.15 – 14.30	**Nusrat Khan**, Murdoch University, Australia *Sugar metabolism in bread wheat for drought tolerance*
14.30 – 14.45	**Borislav Kobiljski**, Biogranum, Serbia *WheatOfChange - challenging the wheat yield stagnation*
14.45 – 15.00	**Marion Röder**, IPK, Germany *Association genetics and validation strategies in European wheat varieties*
15.00 – 15.15	**Thirumeni Saminadane**, Pandit Jawaharlal Nehru College, India *Efficiency of molecular marker tags in improving salt tolerance in rice using Forward Breeding MAS approach*
15.15 – 15.30	**Zerihun Tadele**, University of Bern *Breeding towards improving an African indigenous crop: the case of Tef*

3. Fodder crops – *Chair Dirk Reheul*

13.45 – 14.00	**Joanna Chojnicka**, Institute of Plant Genetics, Poland *Advanced genotyping in three successive generations of the allotetraploid Festuca pratensis × Lolium perenne hybrid*

14.00 – 14.15	**Chloé Manzanares**, ETH Zurich, Switzerland *Development of TILLING in outcrossing forage crops*
14.15 – 14.30	**Sarah Palmer**, Aberystwyth University, UK *A breeder's perspective of exploiting the potential that genomics have to offer*
14.30 – 14.45	**Michael Ruckle**, ETH Zurich, Switzerland *Development of high energy red clover*
14.45 – 15.00	**Franz Xaver Schubiger**, Agroscope, Switzerland *Genetic analysis of resistance to crown rust in a genotype of perennial ryegrass*
15.00 – 15.15	**Daniel Thorogood**, Aberystwyth University, UK *Identifying loci involved in the pollen rejection response at the stigma surface in perennial ryegrass – update and progress*
15.15 – 15.30	Discussion of Fodder Crops and Amenity Grasses Section affairs

4. Maize and Sorghum – *Chair Alain Charcosset*

13.45 – 14.00	**Roxana-Elena Calugar**, Agr. Res. and Devel. Station Turda, Romania *The study of cytoplasmatic diversification role on some productivity elements on maize*
14.00 – 14.15	**Alain Charcosset**, INRA, France *Genetics of hybrid performance in maize: QTL detection for biomass production in a reciprocal multiparental design*
14.15 – 14.30	**Francesco Emanuelli**, University of Bologna, Italy *Fine mapping and cloning of a major QTL for flowering time on maize chromosome 3*
14.30 – 14.45	**Abebe Menkir**, IITA, Nigeria *Mining novel alleles for maize provitamin A enrichment and product delivery*
14.45 – 15.00	**Ioannis Tokatlidis**, Democritus University of Thrace, Greece *The role of intra-crop competition in efficiency of resource use and breeding*
15.00 – 15.15	**Ingrid Vilmus**, CIRAD, France *Paving the way towards the development of biomass sorghum: a transdisciplinary approach for the development of new sorghum varieties*
15.15 – 15.30	**Linda Zamariola**, University of Bologna, Italy *Fine mapping and characterization of JAT, a major locus regulating the transition from juvenile to adult phase in maize*

5. Vegetables – *Chair Yuling Bai*

13.45 – 14.00	**Michela Appiano**, Wageningen UR, The Netherlands *Genome-wide study of the tomato SlMLO gene family and its functional characterization in response to the powdery mildew fungus Oidium neolycopersici*
14.00 – 14.15	**Lorenzo Barchi**, University of Torino, Italy *A high quality eggplant genome sequence: a new tool for the analysis of Solanaceae family evolution and for the molecular deciphering of complex traits*

14.15 – 14.30	**Andrew Beacham**, Harper Adams University, UK *Developing methods to assess and quantify abiotic stress responses in brassica oleracea and tipburn tolerance in lettuce (Lactuca sativa)*
14.30 – 14.45	**Jim Monaghan**, Harper Adams University, UK *A genetic approach to improving postharvest quality in lettuce*
14.45 – 15.00	**Ayse Ozer**, Selcuk University, Turkey *Determination of genes involved in drought mechanism in melon genetic resources*
15.00 – 15.15	**Harry Paris**, Agricultural Research Organization, Israel *Perspectives on cucurbit crop history*
15.15 – 15.30	**Rafael Perl-Treves**, Bar-Ilan University, Israel *The Fom-1-Prv pair of melon resistance genes: lessons from expression and interaction studies*

6. Fruit, Ornamentals and Medicinal/Aromatic plants – *Chair José Vouillamoz*

13.45 – 14.00	**Simone Schuetz**, Agroscope, Switzerland *Accelerated introgression of wild apple fire blight resistance originating from Malus x robusta 5 by the method "Fast Track"*
14.00 – 14.15	**Silvia Vezzulli**, Fondazione Edmund Mach, Italy *Innovative strategies towards marker-assisted pre-breeding for downy and powdery mildew resistance in grapevine*
14.15 – 14.30	**Ellen De Keyser**, Inst. for Agricultural and Fisheries Res., Belgium *Genomics in azalea: defence against broad mite (Polyphagotarsonemus latus) infection as a case study*
14.30 – 14.45	**Sonia Demasi**, University of Torino, Italy *Azalea adaptation to adverse pH conditions: evaluation of potential resources for breeding*
14.45 – 15.00	**Geert van Geest**, Wageningen UR, The Netherlands *Digital phenotyping for postharvest performance and development of a high-throughput genotyping platform for hexaploid chrysanthemum*
15.00 – 15.15	**Cecilia Bester**, Agricultural Research Council, South Africa *Honeybush breeding: revealing the mysteries of this South African indigenous crop*
15.15 – 15.30	**Matteo Caser**, University of Torino, Italy *Irrigation practices differently affect the emission of biogenic volatile organic compounds in Helichrysum petiolare and Salvia sinaloensis*

7. Legumes – *Chair Antonio de Ron*

13.45 – 14.00	**Antonio de Ron**, MBG-CSIC, Spain *In situ conservation of bean germplasm from Northwestern Argentina*
14.00 – 14.15	**Claire Domoney**, John Innes Centre, UK *Unlocking and enhancing nature's diversity to benefit breeding strategies for diverse end uses in pea*
14.15 – 14.30	**Irene Jacob**, Bavarian State Research Center for Agriculture, Germany *Evaluation of new breeding lines of white lupin with improved resistance to anthracnose*
14.30 – 14.45	**Diego Rubiales**, CSIC, Spain *Resistance to powdery mildew in pea germplasm*

14.45 – 15.00	**Svein Solberg**, The World Vegetable Center, Taiwan *Salt tolerance screening of the AVRDC mungbean (Vigna radiata) collection*
15.00 – 15.15	**Rouxlene Van der Merwe**, University of the Free State, South Africa *Grain yield potential and stability of large-seeded vegetable-type soybean genotypes*
15.15 – 15.30	**Johann Vollmann**, BOKU University Vienna, Austria *Polyamines in legumes: Components with a possibly strong health potential and their respective breeding options*

Poster flash presentations

1. Wheat

16.00 – 16.05	**Julien Bonneau**, University of Melbourne, Australia *Nicotianamine synthase genes as a valuable genetic resource for improving bread wheat growth and nutrition*
16.05 – 16.10	**Alexey Doroshkov**, Fed. Res. Inst. of Cytology and Genetics, Russia *The manifestation and phytohormone response of leaf pubescence genes in bread wheat*
16.10 – 16.15	**Dario Fossati**, Agroscope, Switzerland *Lr22a gene is effective and does not alter other disease resistances, yield or bread making quality*
16.15 – 16.20	**Keith Gardner**, NIAB, UK *A large-scale association mapping analysis of wheat resistance to multiple fungal pathogens across three years in multiple locations in NW Europe*
16.20 – 16.25	**Alma Kokhmetova**, Inst.of Plant Biol. and Biotechnology, Kazakhstan *Leaf rust evaluation and molecular screening in wheat cultivars produced in Kazakhstan*
16.25 – 16.30	**Ghasemali Nazemi**, Islamic Azad University, Iran *Prioritizing QTLs for heat stress tolerance using cell membrane stability in durum wheat*
16.30 – 16.35	**Sriram Padmanaban**, University of Southern Queensland, Australia *Variations in the D-genome chromosomes of hexaploid/tetraploid wheat crosses analysed utilising cytology and molecular markers*
16.35 – 16.40	**Myroslava Rubtsova**, IPK, Germany *Influence of individual bread wheat chromosomes on double haploids (DHs) production*
16.40 – 16.45	**Giuseppe Sciara**, University of Bologna, Italy *Saturating QSBM.UBO-2BS for resistance to soil-borne cereal mosaic virus (SBCMV) with novel KASPr markers and recombinant inbred lines*

2. Other cereals

16.00 – 16.05	**Gabriela Alandia**, University of Copenhagen, Denmark *Sowing vegetable proteins for the European diet: It's time for buckwheat*
16.05 – 16.10	**Maja Boczkowska**, National Research Institute, Poland *Landraces and obsolete cultivars of common oat – valuable and unused genetic resources*
16.10 – 16.15	**Gilles Charmet**, INRA, France *WHEALBI: WHEAt and barley legacy for breeding improvement : An EU project to link genomics and agronomy*
16.15 – 16.20	**Anna Florence**, SRUC, UK *Variation in leaf traits in spring barley (Hordeum vulgare L.)*
16.20 – 16.25	**Yuji Kishima**, Hokkaido University, Japan *Different cold sensitivities in rice unvailed by anther morphologies and genome-wide expressions*

16.25 – 16.30	**Timo Knürr**, Natural Resources Institute, Finland *Genomic prediction in a Finnish breeding programme of six-row barley*
16.30 – 16.35	**Maria Jose Martinez Martin**, Aberystwyth University, UK *Analysis of the genetic and environmental factors influencing grain quality in oats*
16.35 – 16.40	**Ievina Sturite**, NIBIO, Norway *Genotypic and environmental impact on spring creals yield and quality*
16.40 – 16.45	**William Thomas**, James Hutton Institute, UK *Genetics of malting barley ‘processability’*

3. Fodder crops and Maize

16.00 – 16.05	**Martina Birrer**, Agroscope, Switzerland *Separation of endophytic and epiphytic phyllosphere bacterial communities of Lolium spp.*
16.05 – 16.10	**Gintaras Brazauskas**, Res. Cen. for Agric. and Forestry, Lithuania *Freezing tolerance of diploid versus tetraploid in perennial ryegrass*
16.10 – 16.15	**Istvan Nagy**, Aarhus University, Denmark *Sequencing and comparative analysis of mitochondrial genomes of fertile and male-sterile lines in perennial ryegrass (Lolium perenne L.)*
16.15 – 16.20	**Dawid Perlikowski**, Polish Academy of Sciences, Poland *Root system performance under water deficit conditions in Lolium multiflorum/Festuca arundinacea introgression forms*
16.20 – 16.25	**Dejan Sokolović**, Institute for forage crops, Serbia *Improvement of drought tolerance of forage perennial ryegrass by breeding of root characteristics and deep root production*
16.25 – 16.30	**Elzbieta Czembor**, Plant Breeding and Acclimatization Inst., Poland *Breeding maize for resistance to fusarium ear rot: impact of plant morphology for disease development and deoxynivalenol formation*
16.30 – 16.35	**Sekip Erdal**, Bati Akdeniz Agricultural Research Institute, Turkey *Popcorn genetic resources and breeding In Turkey*
16.35 – 16.40	**Frank Liebisch**, ETH Zurich, Switzerland *Automated field phenotyping of early vigour and senescence progress in soybean and maize*
16.40 – 16.45	**Carmen D. Vana**, Agr. Res. and Devel. Station Turda, Romania *Evaluation of restoration patterns (Rf) of male sterile cytoplasms (cms) of some early maize local landraces from Transylvania-Romania*

4. Oil and protein (legumes) crops

16.00 – 16.05	**Lucia Hlavačková**, University of Agriculture in Nitra, Slovakia *MicroRNA analysis of flax (Linum usitatissimum L.) genotypes in regard to alpha-linolenic acid content*
16.05 – 16.10	**Anna Kostyn**, University of Wroclaw, Poland *Antisense oligodeoxynucleotide treatment as a new method of gene expression manipulation in flax (Linum usitatissimum)*
16.10 – 16.15	**Ana Marjanović-Jeromela**, Inst. of Field and Vegetable Crops, Serbia *Dissection of year related climatic variables and their effect on winter oilseed rape (Brassica napus L.) development and yield*

16.15 – 16.20	**Katarzyna Mikolajczyk**, Plant Breeding and Acclimat. Inst. Poland *Marker assisted breeding of new winter oilseed rape lined (Brassica napus L.) with changed seed oil fatty acid composition*
16.20 – 16.25	**Marta Preisner**, University of Wroclaw, Poland *Identification of cinnamyl alcohol dehydrogenase isoforms in flax and preliminary assessment of their specificity in response to the biotic and abiotic stresses*
16.25 – 16.30	**Saeed Rauf**, University of Sargodha, Pakistan *Evaluation of sunflower (Helianthus annuus L.) single cross hybrids under heat stress condition*
16.30 – 16.35	**Allison Miller**, Saint Louis University, USA *Global inventory and evaluation of wild perennial cereal, pulse and oilseed species for pre-breeding and domestication*
16.35 – 16.40	**Ilknur Tindas**, Nigde University, Turkey *Physiological responses of soybean cultivars under iron deficiency: A case study in turkey*
16.40 – 16.45	**Engin Yol**, Akdeniz University, Turkey *Flowering time diversity for U.S. groundnut mini-core collection produced under Mediterranean climate type*

5. Fruit, Ornamentals, Medicinal, Industrial

16.00 – 16.05	**Lorenzo León**, IFAPA Centro "Alameda del Obispo", Spain *Variability for oil quality components in an olive progeny 'Olivière' x 'Arbequina'*
16.05 – 16.10	**Vassilis Papasotiropoulos**, Technological Univ. of Western Greece *Sensory, chemical and molecular analysis of fresh strawberries (Fragaria × ananassa Duch.) over different cultivars in Western Greece, reveals factors affecting eating quality*
16.10 – 16.15	**Carina Hieger**, AIT, Austria *Comparative transcriptomics of Rosa corymbifera Laxa roots with regard to replant disease*
16.15 – 16.20	**Galya Petrova**, Bulgarian Academy of Sciences, Bulgaria *Genotoxic effects of heavy metals on intergeneric Helianthus × Echinacea hybrid lines*
16.20 – 16.25	**Yeo Jin Youn**, Sangmyung University, South Korea *Ectopic expression of AHL24 in chrysanthemum plants delayed senescence and enhanced stress tolerance*
16.25 – 16.30	**Tommaso Martinelli**, CREA-CIN, Italy *Towards Silybum marianum's domestication: establishment and screening of a mutagenized population*
16.30 – 16.35	**Lars Gernot Otto**, IPK, Germany *Towards the development of a sterile chamomile variety (Matricaria recutita L.) using breeding, molecular and genomic tools*
16.35 – 16.40	**Daljit S.Virk**, PBS International, UK *Comparing the efficacy of polyester tents and isolation chambers for hybridisation in Miscanthus*
16.40 – 16.45	TBC

6. Vegetables

16.00 – 16.05	**Charlotte Allender**, University of Warwick, UK *Who is sowing our seeds? The Role of the UK vegetable genebank in supporting plant breeding and research*
16.05 – 16.10	**Sergio Lanteri**, University of Torino *Whole genome resequencing in Cynara cardunculus: detection of intra-specific variability and the identification/annotation of novel polymorphisms*
16.10 – 16.15	**Athanasios Mavromatis**, Aristotele University, Greece *Investigation for suitability of three new interspecific rootstocks for eggplant grafting aiming to breeding purposes*
16.15 – 16.20	**Mas Muniroh Mohd Nadzir**, Wageningen UR, The Netherlands *Development of a new screening method for resistance towards Clavibacter michiganensis subsp. michiganensis (Cmm) in tomato*
16.20 – 16.25	**Florent Perrin**, Research Institute of Horticulture and Seeds, France *Changes in carotenoid metabolism in response to biotic and abiotic stresses in various carrot genotypes*
16.25 – 16.30	**Justin Roberts**, Harper Adams University, UK *Identification of quantitative trait loci (QTL) linked to increased lateral root emergence and growth in an intra-specific Lactuca sativa cross for the improvement of lettuce transplants*
16.30 – 16.35	**Cristina Silvar**, Universidade da Coruña, Spain *Deciphering old diversity in the origins of pepper (Capsicum spp)*
16.35 – 16.40	**Ridwani Sobir**, Bogor Agricultural University, Indonesia *Genetic Inheritance resistance to Yellow Virus in melon (Cucumis melo L.)*
16.40 – 16.45	TBC