

Scientific program of

2nd Symposium on Genomics of Plant Genetic Resources (GPGR2)

24-27 April 2010, Palazzo dei Congressi, BolognaFiere, Bologna, Italy

Saturday, April 24

08:30-09:45. Registration and poster mounting

09:45-12:00. Session 1: Opening session

Co-Chairs: *Emile Frison (Bioversity International, Rome, Italy) and Roberto Tuberosa (University of Bologna, Italy)*

09:45-10:15. Welcome addresses

10:15-10:45. Opening keynote presentation

Emile Frison (Bioversity International, Rome, Italy). Building a global plant genetic resources system

10:45-12:00. Invited presentations

10:45-11:10. *Orlando de Ponti (International Seed Federation, Nyon, Switzerland). Germplasm exploitation and ownership: Who owns what?*

11:10-11:35. *Michele Morgante (University of Udine, Italy). From genomics to breeding: How to make the best use of genetic resources*

11:35-12:00. *Jerome Salse (UMR INRA-UBP, Clermont-Ferrand, France). Comparative genomics as a tool for trait dissection*

12:00-13:00. Opening ceremony

13:00-14:15. Lunch & Posters viewing

14:15-16:15. Session 2: Harnessing plant diversity: From sequence to function

Co-Chairs: *Suk-Ha Lee (Seoul National University) and Stefania Grillo (CNR, Italy)*

14:15-15:30. Invited presentations

14:15-14:40. *Suk-Ha Lee (Seoul National University, Seoul, Korea). Sequencing wild soybean genome reveals soybean crop domestication history*

14:40-15:05. *Riccardo Velasco (IASMA, San Michele all'Adige, Italy). Through the genome sequence: The origin of the cultivated apple*

15:05-15:30. *Scott Jackson (Purdue University, Lafayette, IN, USA). Genomic exploration of diversity in the genus *Glycine* (soybean) and related crop legumes*

15:30-16:15. Short communications

15:30-15:45. *Bicheng Yang (BGI-Shenzhen, Shenzhen, China). Whole genome resequencing for crop*

improvement

15:45-16:00. *Sonia Negrão* (ITQB/IBET, Oeiras, Portugal). Use of EcoTILLING to identify natural allelic variants of rice candidate genes involved in salinity tolerance

16:00-16:15. *Tanveer ul Haq* (College of Agriculture, Dera Ghazi Khan, Pakistan). Spatial and temporal quantitative trait loci (QTLs) mapping of ions accumulation on chromosome-1 of rice (*Oryza sativa* L.) under salt stress

16:15-16:45. Coffee break

16:45-18:45. Session 2: Harnessing plant diversity: From sequence to function

Co-Chairs: Masahiro Yano (NIAS, Japan) and Enrico Pe' (Scuola Superiore Sant'Anna, Italy)

16:45-18:00. Invited presentations

16:45-17:10. *Masahiro Yano* (NIAS, Tsukuba, Japan). Genomics-assisted allele mining and its integration to rice breeding

17:10-17:35. *Richard Flavell* (CERES, Red Oaks, CA, USA). Creating new diversity using synthetic transgenes to improve crops

17:35-18:00. *Martin Ganai* (TraitGenetics, Gatersleben, Germany). The 50K maize Infinium chip - design and use for maize diversity analysis

18:00-18:45. Short communications

18:00-18:15. *Michael Deyholos* (University of Alberta, Edmonton, Canada). Whole-genome shotgun sequence assembly and other genomic resources for flax (*Linum usitatissimum*)

18:15-18:30. *Robert Henry* (Southern Cross University, Lismore, Australia). Whole genome sequencing as a tool for plant genetic resource analysis

18:30-18:45. *Bhupendra Chaudhary* (Gautam Buddha University, Greater Noida, India). Expression partitioning of homoeologs during development and evolution of allopolyploid cotton (*Gossypium*)

19:00-19:45. Congress keynote presentation

Gebisa Ejeta (Purdue University, Lafayette, IN, USA). The sustenance of human livelihood via genetics and genetic resources

20:00-21:30. Opening reception with local food and wine tasting; Posters viewing

Sunday, April 25

08:45-10:40. Session 3. Harnessing plant diversity: Genomics-based applications

Co-Chairs: Jizeng Jia (CAAS, Beijing, China) and Antonio Blanco (University of Bari, Italy)

08:45-10:00. Invited presentations

08:45-09:10. *Jean Christophe Glaszmann* (CIRAD, Montpellier, France). Multiple scale analysis of genetic diversity in sorghum

09:10-09:35. *Albrecht Melchinger* (University of Hohenheim, Stuttgart, Germany). Genomics approaches to unravel the genetic basis of heterosis

09:35-10:00. *Richard Visser* (University of Wageningen, The Netherlands). Exploiting genetic resources for plant breeding in the 21st century

10:00-10:45. Short communications

10:00-10:15. *Andrew Flavell* (University of Dundee, Dundee, UK). The genetic diversity and evolution of field pea (*Pisum*) studied by high-throughput retrotransposon-based insertion polymorphism (RBIP) marker analysis

10:15-10:30. *Jun Zou* (Huazhong Agricultural University, Wuhan, China). Impacts of interspecific hybridization on genome structure and agronomic traits via retrotransposon activation in *Brassica napus*

10:30-10:45. *Huaan Yang* (Department of Agriculture and Food Western Australia, South Perth, Australia). Development of molecular markers for large scale implementation for marker-assisted selection in lupin breeding

10:45-11:15. Coffee break

11:10-13:00. Session 3. Harnessing plant diversity: Genomics-based applications

Co-Chairs: Milena Ouzunova (KWS, Germany) and Elisabetta Frascaroli (University of Bologna, Italy)

11:10-12:00. Invited presentations

11:10-11:35. *Antoni Rafalski* (DuPont Agricultural Biotechnology Group and Pioneer Hi-Bred International, Wilmington, USA). Genomic tools for the analysis of genetic diversity

11:35-12:00. *Stefano Tartarini* (University of Bologna, Italy). Toward the fine mapping of Plum Pox Virus (Sharka) resistance QTLs from two different sources in apricot

12:00-13:00. Short communications

12:00-12:15. *Pietro Piffanelli* (PTP, Lodi, Italy). EURIGEN: Characterization of European rice germplasm for stress response traits

12:15-12:30. *Le Hung Linh* (Agricultural Genetics Institute, Tuliem-Hanoi, Vietnam). Mapping QTL for spikelets per panicle and yield components using an NIL from an interspecific cross between *Oryza sativa* and *O. minuta*

12:30-12:45. *Silvio Salvi* (IASMA, San Michele all'Adige, Italy). LD estimation, analyses of diversity and domestication in apple

12:45-13:00. *Francis Ogonnaya* (ICARDA, Aleppo, Syria). Recent progress in the utilisation of synthetics for wheat improvement

13:00-14:15. Lunch & Posters viewing

14:15-16:00. Session 4. Genomics of Triticeae genetic resources (with the support of COST Action FA0604 Tritigen WG 1)

Co-chairs: Ikmet Budak (Sabanci University, Turkey) and Luigi Cattivelli (CRA, Italy)

14:15-15:30. Invited presentations

14:15-14:40. *Karl Schmid* (University of Hohenheim, Germany). Towards natural selection mapping of useful genes in plant germ plasm

14:40-15:05. *Alan H. Schulman* (University of Helsinki, Finland). Mining Triticeae genes with the aid of *Brachypodium*

15:05-15:30. *Eduard Akhunov* (Kansas State University, Manhattan, USA). Genome-wide patterns of SNP variation in polyploid wheat

15:30-16:00. Short communications

15:30-15:45. *Shiveta Sharma* (Christian-Albrechts University of Kiel, Germany). Mapping of QTL contributing to root lesion nematode resistance in barley

15:45-16:00. *Andreas Börner* (IPK, Gatersleben, Germany). Association mapping of wheat germplasm employing historical data

16.00-16.30. Coffee break

16:30-17:50. Session 4. Genomics of Triticeae genetic resources (with the support of COST Action FA0604 Tritigen WG 1)

Co-chairs: Robbie Waugh (SCRI, UK) and Patrizia Galeffi (ENEA, Italy)

16:30-17:20. Invited presentations

16:30-16:55. *Takao Komatsuda* (NIAS, Tsukuba, Japan). Functional diversification of transcription factors for the formation of barley spikes

16:55-17:20. *Robbie Waugh* (SCRI, Dundee, UK). Manipulating the resolution of whole genome association scans in barley using stratified germplasm collections

17:20-17:50. Short communications

17:20-17:35. *Song Weining* (Northwest A&F University, Yangling, Shaanxi, China) One site vs. the world: The genetic diversity of one natural population of wild barley compared to barley varieties from different countries

17:35-17:50. *Fedor Konovalov* (Vavilov Institute of General Genetics, Moscow, Russia). SSAP-based phylogenetic analysis reveals different amplification history of *BARE-1* and *Jeli* LTR retrotransposon families in A-genome diploid wheats

18:00-19:30. Round table on “Educating a new generation of plant breeders”

Moderator: *Chike Mba* (FAO, Rome, Italy)

Speakers: *Zoltan Bedo* (EUCARPIA), *Léon Broers* (KWS, Germany), *Sam Eathington* (Monsanto, USA), *Gebisa Ejeta* (Purdue University, USA), *Albrecht Melchinger* (Univ. of Hohenheim, Germany), *Alain Murigneux* (Limagrain, France), *Richard Visser* (Plant Research Institute, The Netherlands)

Monday, April 26

08:45-10:40. Session 5. Genomics-assisted crop improvement for food security in developing countries
Co-chairs: Chike Mba (FAO, Rome, Italy) and Enrico Porceddu (University of Tuscia, Italy)

08:45-09:40. Invited presentations

08:45-09:00. *Enrico Porceddu* (University of Tuscia, Viterbo, Italy). A doctoral program to harness the value of genetic resources in developing countries

09:00-09:15. *Edward Runge* (Texas A&M University, USA). The Monsanto's Beachell-Borlaug Initiative for food security in developing countries

09:15-09:40. *Sarah Davidson* (Cornell University, Ithaca, NY, USA). The Borlaug Global Rust Initiative: Reducing the genetic vulnerability of wheat to rust

09:40-10:40. Short communications

09:40-09:55. *Ahmed El Oualkadi* (INRA, Equipe "Diversité, Génétique et Génomique Vigne", Montpellier, France). Genetics resources of *Vitis vinifera* in the north of Morocco (Rif region): Characterization and conservation

09:55-10:10. *Yinghua Huang* (USDA-ARS Plant Science Research Laboratory, Stillwater, OK, USA) Toward safeguarding sorghum production against biotic stresses: Uses of worldwide germplasm collection and genomics-based approaches

10:10-10:25. *Zerihun Tadele* (University of Bern, Switzerland). Genomic tools for improving the cereal crop tef (*Eragrostis tef*)

10:25-10:40. *Alganesh Tesema Gellaw* (Institute of Biodiversity Conservation, Addis Ababa, Ethiopia). Molecular diversity in Ethiopian tetraploid wheat

10:40-11:10. Coffee break

11:10-13:00. Session 5. Genomics-assisted crop improvement for food security in developing countries
Co-chairs: David Bergvinson (Bill & Melinda Gates Foundation, USA) and Roberto Papa (University of Ancona, Italy)

11:10-12:00. Invited presentations

11:10-11:35. *David Bergvinson* (The Bill & Melinda Gates Foundation, Seattle, USA). Leveraging plant genetic resources for Africa

11:35-12:00. *Rajeev Varshney* (ICRISAT, Hyderabad, India). Establishing genomics-assisted breeding foundation in chickpea for enhancing crop productivity in Africa and Asia

12:00-13:00. Short communications

12:00-12:15. *Khaled Masmoudi* (Plant Molecular Genetic Laboratory, Sfax, Tunisia). Ions transport activity related to plant adaptation to salt stress

12:15-12:30. *Fahriye Ertugrul* (TUBITAK Marmara Research Center, Kocaeli, Turkey). Use of expressed sequence tag resources to reveal multiplex quantitative gene expression profiles in diploid and polyploid wheat genotypes for salt stress tolerance

12:30-12:45. *Sundeep Kumar* (Sardar Vallabh Bhai Patel University of Agriculture and Technology, Modipuram, India). Molecular and pathological characterization of slow-rusting genes against leaf rust in wheat (*Triticum aestivum* L. em Thell)

12:45-13:00. *Rattan Yadav* (IBERS, Aberystwyth University, United Kingdom). Progress and prospects of increasing drought tolerance in pearl millet using genetics and genomics approaches.

13:00-14:30. Lunch & Posters viewing

14:30-16:30. Session 6. Genomics for increased sustainability of Triticeae crops production (with the support of COST Action FA0604 Tritigen WG 1)

Co-chairs: Alan Schulman (University of Helsinki, Finland) and Nicola Pecchioni (University of Modena and Reggio Emilia, Italy)

14:30-15:45. Invited presentations

14:30-14:55. *Jizeng Jia* (CAAS, Beijing, China). Core collection-based genomic stocks in wheat

14:55-15:20. *Peter Langridge* (ACPF and University of Adelaide, Australia). Genetic resources and genomic approaches to improve abiotic stress tolerance in cereals

15:20-15:45. *Tzion Fahima* (University of Haifa, Israel). Wild emmer wheat genetic resources: From genetic diversity to map-based cloning for increased sustainability of Triticeae crops

15:45-16:30. Short communications

15:45-16:00. *Nicola Pecchioni* (University of Modena and Reggio Emilia, Italy). Dissection of quantitative resistance to leaf rust (*Puccinia brachypodii*) in *Brachypodium distachyon*, the model plant for Triticeae

16:00-16:15. *Melda Kantar* (Sabanci University, Istanbul, Turkey). Identification and quantification of barley miRNAs and their targets in response to drought stress

16:15-16:30. *Stuart Lucas* (Sabanci University, Istanbul, Turkey). Subtleties of the wheat drought response displayed by a DRE-binding protein from *Triticum dicoccoides*

16:30-17:00. Coffee break

17:00-18:50. Session 6. Genomics for increased sustainability of Triticeae crops production (with the support of COST Action FA0604 Tritigen WG 1)

Co-chairs: Beat Keller (University of Zurich, Switzerland) and Valeria Terzi (CRA, Italy)

17:00-17:50. Invited presentations

17:00-17:25. *Beat Keller* (University of Zurich, Switzerland). Allelic diversity of fungal disease resistance genes in wheat

17:25-17:50. *Patrick Schweizer* (IPK, Gatersleben, Germany). Converging evidence for genes of basal defense in barley

17:50-19:05. Short communications

17:50-18:05. *Aaron Fait* (Ben-Gurion University of the Negev, Boqer Campus, Israel). Exploitation of diversity in nuclear-cytoplasm interaction using alloplasmic wheat lines

18:05-18:20. *Ciro De Pace* (University of Tuscia, Viterbo, Italy). Deployment of either a whole or dissected wild nuclear genome into the wheat gene pool meets the breeding challenges posed by the sustainable farming systems

18:20-18:35. *André Laroche* (Agriculture and Agri-Food Canada, Research Centre, Lethbridge, Canada). NextGen sequencing of the transcriptome of triticale

18:35-18:50. *Marco Maccaferri* (University of Bologna, Italy). Identification of agronomically valuable

alleles in durum wheat through linkage and association mapping

18:50-19:05. *Enrico Francia* (University of Modena and Reggio Emilia, Italy). Towards physical mapping and sequencing the *FrH2* (*Frost resistance-H2*) region of barley chromosome 5H

20:00-22:30. Social dinner

Tuesday, April 27

08:45-10:50. Session 7. Genetic resources for nutritional quality

Co-chairs: Joe Tohme (CIAT, Colombia) and Domenico La Fiandra (University of Viterbo, Italy)

08:45-09:35. Invited presentations

08:45-09:10. *Joe Tohme* (HarvestPlus; hosted at CIAT, Cali, Colombia). Strategies to develop and deploy biofortified crops

09:10-09:35. *Peter R. Shewry* (Rothamsted Research, Harpenden, UK). Improving the health benefit of wheat

09:35-10:50. Short communications

09:35-09:50. *Marta Wilton de Vasconcelos* (Catholic University of Porto, Portugal). Effects of *AtFRO2* expression in the nutritional enhancement of soybean (*Glycine max* L.)

09:50-10:05. *Marion S. Röder* (IPK, Gatersleben, Germany). Exploiting the genomic sequences of rice and *Brachypodium* for delimiting a grain size QTL in wheat

10:05-10:20. *Simonetta Agostina Angioi* (University of Sassari, Italy). The genetic make-up of European landraces of common bean

10:20-10:35. *Owen Hoekenga* (Robert W. Holley Center for Agriculture and Health, USDA-ARS, Ithaca, NY, USA). Iron biofortification of maize grain

10:35-10:50. *Yamuna Rani* (University of Agricultural Sciences, GKVK, Bangalore, India). Biofortification of finger millet for high zinc

10:50-11:20. Coffee break

11:20-13:15. Session 7. Genetic resources for nutritional quality

Co-chairs: Francois Baulfourier (INRA, France) and Marina Carcea (INRAN, Italy)

11:20-11:45. Invited presentation

Fabio Virgili (INRAN, Rome, Italy). Nutrigenomics: New functions for “old” molecules

11:45-13:15. Short communications

11:45-12:00. *Mario Motto* (CRA-Maize Research Unit, Bergamo, Italy). Gene discovery to improve grain quality-related traits in maize

12:00-12:15. *Qing-Yao Shu* (Zhejiang University, Hangzhou, China). Low phytate rice and soybean: Mutant generation, characterization and gene discovery

12:15-12:30. *Barbara De Nardi* (CRA-VIT – Research Centre for Grapevine Production, Conegliano, Treviso, Italy). Transcriptomic and metabolite analyses of genes implicated in traits relevant to grapevine quality

12:30-12:45. *Christoph U. Germeier* (Julius Kühn Institute, Quedlinburg, Germany). *Avena* genetic resources for quality in human consumption (AVEQ) – a European project on nutritional quality

12:45-13:00. *Søren K. Rasmussen* (University of Copenhagen, Denmark). Mutations in genes controlling the metabolism of inositol phosphates in cereals

13:00-13:15. *Luigi Cattivelli* (CRA-Genomic Research Centre, Fiorenzuola d'Arda, Italy). Exploitation of crop diversity to improve food quality at Agricultural Research Council (CRA) of Italy

13:15-14:30. Lunch & Posters viewing

14:30-16:40. Session 8. The next challenges

Co-chairs: Antoni Rafalski (DuPont, USA) and Chiara Tonelli (University of Milano, Italy)

14:30-16:35. Invited presentations

14:30-14:55. *Maarten Koornneef* (Max Planck Institute, Koln, Germany). Arabidopsis natural variation as model for the use of plant genetic resources

14:55-15:20. *Ulrich Schurr* (Institute of Phytosphere Research, Julich, Germany). Plant Phenotyping: quantitative analysis of plant structure and function on mechanistic, high-throughput and field level

15:20-15:45. *Patrick Giavalisco* (Max-Planck-Institute of Molecular Plant Physiology, Potsdam, Germany). Metabolomics: Tools and applications

15:45-16:10. *Serena Varotto* (University of Padova, Italy). Understanding epiallele formation and inheritance in response to environmental cues in plants

16:10-16:35. *Giorgio Valle* (University of Padova, Italy). Perspectives of plant genomes analysis

16:40-18:20. Session 9. Closing session

Co-Chairs: Andreas Graner (IPK, Germany) and Francesco Salamini (IASMA, Italy)

16:40-17:20. Invited presentations

16:40-17:00. *Carmen de Vicente* (The Generation Challenge Program; hosted at CIMMYT, Texcoco, Mexico). Capacity building in genomics of plant genetic resources within the Generation Challenge Program

17:00-17:20. *Annette Schneegans* (KBBE, EC, Brussels, Belgium). EU-funded research opportunities on genomics of plant genetic resources

17:20-17:50. Closing keynote presentation

Andreas Graner (IPK, Gatersleben, Germany). Exploiting the diversity of crop plants: Present state and future challenges

17:50-18:05. Closing scientific remarks

Francesco Salamini (IASMA, San Michele all'Adige, Italy)

18:05-18:10. Presentation of the venue for the GPGR3 Congress

To be announced

18:10-18:20. Closing of the GPGR2 Congress

Emile Frison (Bioversity International, Rome, Italy) and *Roberto Tuberosa* (University of Bologna, Italy)