



66th ANNUAL CONGRESS ITALIAN SOCIETY OF AGRICULTURAL GENETICS

Bari, 5-8 September 2023

SCIENTIFIC COMMITTEE

Società Italiana di Genetica Agraria

Edgardo Filippone (President), Silvio Salvi (Vicepresident), Daniele Rosellini (Secretary),
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Elisabetta Mazzucotelli (Councillors)

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Luigi Ricciardi, Claudio De Giovanni, Chiara Delvento, Valentina Fanelli, Agata Gadaleta,
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Concetta Lotti

*Università degli Studi di Foggia – Dipartimento di Scienze Agrarie, Alimenti, Risorse Naturali
e Ingegneria*

PROGRAMME

TUESDAY, SEPTEMBER 5th

13:00 – 14:30 Registration

14:30 - 14:50 Opening ceremony

Chairpersons: Filippone E., Ricciardi L., Lotti C.

Welcome addresses by Institutional and Local Authorities

14:50 - 15:00 Communication from EIT-FOOD Projectmanager at UNIBA

De Ruggeri B.

EIT Food: Innovation for a healthy and sustainable food system

15:00 - 16:45 Session 1 - Omics to study and use genetic resources in plant breeding

Chairpersons: Ambrosone A., Mazzucotelli E.

15:00 – 15:30 Invited Lecture

Iorizzo M.

Omics approach to uncover the origin of high carotenoid orange carrots

15:30 – 15:45 Forestan C., Bozzoli M., Maccaferri M., Tuberosa R., Mazzucotelli E., Desiderio F., Faccioli P., Cattivelli L., Ens J., Sharpe A., Pozniak C., Chawla H., Walkowiak S., Pirona R., Ceriotti A., Morgante M., Masci S., Sestili F., Giuliano G., Gadaleta A., Pè M.E., Pecchioni N., Bassi F.M., Distelfeld A., Rusholme-Pilcher R., Hall A., Swarbreck D., Spannagl M., Navratilova P., Šimková H., Silvestri M., Zastrow-Hayes G., Llaca V., Fengler K., The Svevo Platinum Consortium, The Tetraploid Wheat Pangenome Consortium

Upgrading the Durum wheat Genomic Resources: from the Platinum-quality Svevo genome assembly and annotation to the tetraploid wheat pangenome

15:45 – 16:00 Miculan M., Zuccolo A., Fabbian L., Zhou Y., Rivera L.F., Copetti D., Talag J.D., McNally K., Henry A., Wing R.A.

Disentangling the genome wide contribute of structural variations to drought stress resistance in the model species *Oryza sativa*

16:00 – 16:15 Gabelli G., Palumbo F., Boni A.G., Ferrari G., Beretta M., Barcaccia G.

Deciphering the recombination spots scenario in a MAGIC population of cultivated and wild tomato

16:15 – 16:30 Tripodi P., Beretta M., Peltier D., Kalfas I., Vasilikiotis C., Laidet A., Briand G., Aichholz C., Zollinger T., van Treuren R., Scaglione D., Goritschnig S.

Development and application of single primer enrichment technology (SPET) SNP assay for population genomics analysis and candidate gene discovery in lettuce

16:30 – 16:45 Gaccione L., Toppino L., Sulli M., Tumino G., Alonso D., Aprea G., Tassone M.R., Boyaci H.F., Lin Y., Lanteri S., Prohens J., Portis E., Rotino G.L., Giuliano G., Barchi L.

Genome-wide association study for agronomically relevant traits and fruit quality-related metabolites in a worldwide eggplant core collection

16:45 – 17:15 Coffee Break and Poster Viewing

17:15 – 18:45 Session 1 - (cont.)

17:15 – 17:30 Americo S., Ferrari G., Desiderio F., Guerra D., Beretta M., Lo Piero A.R., Sicilia A., Morelli G., Cattivelli L., D'Orso F.

Unveiling the position and effects on salt stress resilience of wild *S. pennellii* genome in *S. pennellii* x *S. lycopersicum* introgression lines through integrated DNA and RNA sequencing approach

17:30 – 17:45 Tafuri A., Pirona R., Fricano A., Mazzucotelli E., Cagliani L.R., Gasser M., Giordano M., Zuccaro M., Ravaglia S., Consonni R., Thomas A., Gilardi F., Ceriotti A., Baldoni E.

Metabolite characterization of durum wheat grain for association studies: exploring the natural variation of free asparagine content

17:45 – 18:00 Delvento C., Arcieri F., Marcotrigiano A.R., Guerriero M., Fanelli V., Dellino M., Curci P.L., Bouwmeester H., Lotti C., Ricciardi L., Pavan S.

High-density linkage mapping and genetic dissection of resistance to broomrape (*Orobanche crenata* Forsk.) in pea (*Pisum sativum* L.)

18:00 – 18:15 Bono G.A., Giaume F., Vicentini G., Mineri L., Betagnon G., Fornara F., Brambilla V.

Molecular control of flowering at the rice shoot apex

18:15 – 18:30 Foresti C., Amato A., Fattorini C., D'Inca E., Vitulo N., Zenoni S.

NACs intra-family hierarchical regulatory network orchestrating grape berry ripening

18:30 – 18:45 General Discussion

19:00 - 20:30 Welcome Cocktail

WEDNESDAY, SEPTEMBER 6th

09:00 – 10:45 Session 2 – Breeding for resilience: addressing climate change in plant genetics

Organized by Next Generation SIGA

Chairpersons: Broccanello C., Di Marsico M.

09:00 – 09:30 Invited Lecture

Dixon L.

Adapting cereal development to changing climates

09:30 – 09:45 Persello A., Rotasperti L., Torricella V., Ballabio F., Betti A., Tadini L., Camilloni C., Hansson M., Rossini L., Horner S.D., Salvi S., Pesaresi P.

Pale-green crops for a new sustainable agriculture

09:45 – 10:00 Bubici G., Batelli G., Cellini F., Costa A., De Palma M., Grillo S., Melillo M.T., Petrozza A., Prigigallo M.I., Ruocco M., Sportelli G., Stabolone L., Summerer S., Veronico P., Cillo F.

A phenomics approach to drought and pathogen responses in a tomato genotype collection

10:00 – 10:15 De Sario F., Liu C., Bozzoli M., Forestan C., Ratti C., Bruschi M., Novi J.B., Campana M., Sciara G., Ormanbekova D., Corneti S., Confortini A., Viviani A., Stefanelli S., Giulini A., Bardelli T., Novarina E., Gadaleta A., Mazzucotelli E., Desiderio F., Viola P., Invernizzi C., Oliveri F., Mastrangelo A.M., Marone D., Roncallo P., Bassi F., Perovic D., Cattivelli L., Tuberosa R., Maccaferri M.

The Global Durum Genomic Resource in use: a collaborative genomics initiative to leverage genetic resources for increasing and characterizing the breeding value of durum varieties

10:15 – 10:30 Colanero S., Martignago D., Loukili I., Sutti A., Landoni B., Cioffi S., Bosc A., Tonelli C., Galbiati M., Conti L.

Engineering water use in tomato by generating *SlMyb60* mutants using a CRISPR-Cas9-based approach

10:30 – 10:45 General Discussion

10:45 – 11:15 Coffee Break and Poster Viewing

11:15 – 13:15 Session 3 - Innovative methods and tools in plant genetics and breeding

Chairpersons: Lotti C., Pavan S.

11:15 – 11:45 Invited Lecture

Bai Y.

Impaired plant susceptibility genes in resistance breeding: from concept to cultivars

11:45 – 12:00 Bettinelli P., Bianco L., Fontana P., Moser M., Pindo M., Nicolini D., Costantini L., Stefanini M., Hausmann L., Vezzulli S.

Black rot resistance of grapevine: from organ-specific QTL mapping to the sequencing of the donor towards candidate gene identification

12:00 – 12:15 Li R., Cui L., Martina M., Moglia A., Bracuto V., Meijer-Dekens F., Wolters A.A., Bai Y., Acquadro A.

Less is more: CRISPR/Cas9-based mutations in DND1 gene enhance tomato resistance to powdery mildew with low fitness costs

12:15 – 12:30 Caproni L., Altman T., Ferguson J., Heuermann M., Kromdijk J., Pè M.E., Dell'Acqua M.

Combining phenomics approaches from pot to plot to identify candidate genes for photosynthesis improvement in the multi parent MAGIC maize population

12:30 – 12:45 Bozzoli M., Bruschi M., Fanelli Carvalho H., Isidro y Sánchez J., Ruggeri M., Meriggi D., Manstretta V., Bartocchetti E., Sgrelli S., Meriggi P., Tuberosa R., Maccaferri M.

INNOVAR project: developing high-throughput phenotyping and genetic methods and technologies to improve accuracy in agriculture and in wheat varietal registration protocols

12:45 – 13:00 Michelotti V., Rossi R., Crosatti C., Mica E., Guerra D., Colombo M., Masiero S., Radchuk V., Cattivelli L., Battaglia R.

Sporophytic control of male fertility, the role of the SWEET4 gene in barley

13:00 – 13:15 General Discussion

13:15 – 13:30 EUCARPIA: current progressive future opportunity for plant breeding

Ercolano M.R.

13:30 – 14:30 Lunch Break

14:30 – 16:45 Session 4 - Underground genetics: roots and their interactions

In memory of Marina Tucci

Chairpersons: Beretta M., Salvi S.

14:30 – 15:00 Invited Lecture

Laplaze L.

Targeting root traits to improve tolerance to vegetative drought episodes in pearl millet (*Pennisetum glaucum* L.)

15:00 – 15:15 Puglisi D., Carletti G., Delbono S., Cattivelli L., Fricano A.

Shovelomics and clear pot analyses highlight extensive natural genetic variation for root system architecture in barley

15:15 – 15:30 Daddiego L., Bianco L., Alagna F., Lopez L., Panara F., Fantini E., Facella P.

Differential expression patterns of cryptochrome and circadian clock genes between roots and leaves in *Medicago truncatula*

15:30 – 15:45 Scintu D., Shtin M., Svolacchia N., Sabatini S., Dello Ioio R., Di Mambro R.

Exploring root programmed cell death as a mechanism for heat stress resilience

15:45 – 16:15 Invited Lecture

Pieterse C.M.J.

The root microbiome and plant immunity

16:15 – 16:30 General Discussion

16:30 – 17:00 SIGA Young Research Award 2023

Dedicated to Francesco D'Amato and Gian Tommaso Scarascia Mugnozza

Chairpersons: Filippone E., Rosellini D.

Rotasperti L.

The barley mutant happy under the sun 1 (hus1): An additional contribution to pale green crops

Iohannes S.D.

Data-driven, participatory characterization of farmer varieties discloses teff breeding potential under current and future climates

Award ceremony

17:00 – 17:45 Coffee Break and Poster Viewing

17:45 – 19:30 SIGA General Assembly

THURSDAY, SEPTEMBER 7th

09:00 – 10:15 Session 5 - Exploring the plant epigenomes

Chairpersons: Comino C., Varotto S.

09:00 – 09:30 Invited Lecture

Zilberman D.

Long-term epigenetic inheritance and phenotypic diversity in natural populations

09:30 – 09:45 Bevilacqua I., Moffa L., Varotto S., Chitarra W., Nerva L.

Harnessing genome editing to elucidate the role of histone variant H2A.Z in grapevine

09:45 – 10:00 Liva M., Magris G., Di Gaspero G., Schwoppe R., Catacchio C.R., Daponte A., Ventura M., Morgante M.

Analysis of genetic and epigenetic structure and variability of grapevine centromeres through the use of long read sequencing and T2T assemblies

10:00 – 10:15 General Discussion

10:15 – 11:30 Coffee Break and Poster Viewing

11:30 – 12:30 Session 6 – Fruit and forest trees genomics, genetics and breeding

Chairpersons: Giannino D., Montemurro C.

11:30 – 12:00 Invited Lecture

Gonzalez Martinez S.

Population vulnerability of a keystone Mediterranean tree under future climate – an ecological genomics approach

12:00 – 12:15 Garosi C., Vettori C., Bajc M., Kraigher H., Westergren M., Dovč N., Damjanić R., Sever K., Breznikar A., Gregoric A., Lanščak M., Ivankovic M., Bogunović S., Paffetti D.

Genome-wide SNP association analysis reveals genomic signature of local adaptation in European beech (*Fagus sylvatica* L.)

12:15 – 12:30 Alicandri E., Sebastiani B., Paolacci A.R., Sorgonà A., Manti F., Bosignore C.P., Badiani M., Ciaffi M.

Terpenoids and the expression of terpene synthase genes are coherently and selectively modulated in Calabrian pine (*Pinus nigra* subs. *laricio*) in response to pine processionary moth (*Thaumetopoea pityocampa*) infestation

13:00 – 14:30 Lunch Break

14:30 – 17:15 Session 6 - (cont.)

14:30 – 15:00 Invited Lecture

Decroocq V.

Genetic diversity and use of stone fruit tree wild relatives for a more sustainable fruit production

15:00 – 15:15 Cominelli E., Beritognolo I., Cardoni S., Forti C., Cherubini M., Leonardi L., Leone P.A., Sparvoli F., Biffani S., Stella A., Toschi I., Cesari V., Chiozzotto R., Cirilli M., Pozzi C., Mattioni C.

Chestnut cultivation development in Lombardy: leveraging native genetic resources in two pilot areas

15:15 – 15:30 Costa F., Busatto N., Sayantan P., Vittani L., Populin F., Khomenko I., Biasioli F., Vrhovsek U., Aharoni A., Zanella A.

System genetics approach disclosed the genetic architecture of the chilling injury disorder superficial scald in apple

15:30 – 15:45 Simoni S., Castellacci M., Usai G., Giordani T., Natali L., Cavallini A., Besnard G., Mascagni F.

Genomic dynamics of olive trees in the Mediterranean basin: insights from the repetitive component evolution

15:45 – 16:00 Bonghi C., Canton M., Joseph J., Marconi G., Forestan C., Varotto S.

The bud peach dormancy dilemma

16:00 – 16:15 da Silva Linge C., Baccichet I., Chiozzotto R., Gasic K., Fu W., Byrne D., Rawandoozi Z., Worthington M., Bassi D., Cirilli M., Hardner C., Rossini L.

Unlocking genetic diversity for peach fruit acidity through global GWAs and genomic prediction-based selection

16:15 – 16:30 Michelotti V., Gentile A., Scortichini M., Lucioli S., Caboni E., Tacconi G.

Application of a CRISPR/CAS9 vector in *A. chinensis* var. *chinensis* to induce

Pseudomonas syringae pv. *actinidiae* resistance/tolerance

16:30 – 16:45 Sicilia A., Villano C., Di Serio E., Aversano R., Ferlito F., Nicolosi E., Lo Piero Angela R.

Transcriptome analysis reveals plasticity of gene expression in wine grape cultivars grown at different latitudes in southern Italy

16:45 – 17:00 Bolognesi G., Crespan M., Broccanello C., Delfino P., Mora R., Marini M., Gardiman M., Giust M., Tomasi D., Bellin D.

Genome wide association analysis of phenology related traits in *Vitis vinifera* L.

17:00 – 17:15 General Discussion

17:15 – 17:45 Coffee Break and Poster Viewing

17:45 – 19:45 Parallel Poster Sessions

20:30 Social Event (Sala Zonno, Molo S. Nicola 3, Bari)

FRIDAY, SEPTEMBER 8th

09:30 – 12:15 Session 7 - Updates and upgrades in genome editing

Chairpersons: Lanubile A., Nigro D.

09:30 - 10:00 Invited Lecture

Cereseto A.

Expanding the genome editing toolbox by unlocking RNA guided nucleases using massive metagenomic data

10:00 - 10:15 Vicentini G., Bertagnon G., Giaume F., Fornara F., Brambilla V.
Controls of stem elongation by the flowering pathway in rice

10:15 - 10:30 Vaccino P., Sansoni F., Volante A., Zampieri E., Salvi S., Camerlengo F., Pierbattista S., Valè G., Crosatti C., Toppino L., Bono G.A., Fornara F., Pecchioni N.
A new rice plant ideotype through genome editing: the SUSRICE project

10:30 - 10:45 Maioli A., De Marchi F., Valentino D., Gianoglio S., Patono D., Miloro F., Bai Y., Comino C., Lanteri S., Lovisolo C., Acquadro A., Moglia A.
New insights on the role of SIDMR6-1 in drought avoidance in tomato

10:45 - 11:00 Nicolìa A., D'Agostino N., Tamburino R., Festa G., Sannino L., Aufiero G., Paparo R., Arimura S., Scotti N., Cardì T.
Molecular and phenotypic characterization of potato plants edited in the mitochondrial genome by mitoTALEN and mitoTALECD approaches

11:00 - 11:15 Salvagnin U., Giacomelli L., Scintilla S., Rouppe van der Voort J., Zeilmaier T., Moser C.
Reduced susceptibility to downy mildew of DMR6 gene-edited grapevine plants and development of DNA-free edited mutants

11:15 - 11:30 Moffa L., Bevilacqua I., Pagliarani C., Gambino G., Perrone I., Velasco R., Lovisolo C., Nerva L., Chitarra W.
Improving grape resilience to drought exploiting the CRISPR/Cas technology: functional characterization of the target gene through Spray Induced Gene Silencing (SIGS)

11:30 - 12:00 Invited Lecture
Granell A.
Genome editing for better, healthier tomatoes

12:00 - 12:15 General Discussion

12:15 - 12:30 Closing Ceremony
Chairpersons: Filippone E., Salvi S.

SNP GENOTYPING TO EXPLORE GENETIC DIVERSITY: THE CASE OF MONTENEGRIN DURUM WHEAT LANDRACES

VELIMIROVIĆ V.*, JOVOVIĆ Z.*, PEROVIĆ D.**, LEHNERT H.***, MIKIĆ S.****, MANDIĆ D.*****, PRŽULJ N.*****, MANGINI G.*****, FINETTI-SIALER M.***** *)

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durum wheat landraces, Rogosija, genetic diversity, SNP array

Landraces of durum wheat (*Triticum turgidum* subsp. *durum*), were the main cereals of Montenegro until the mid-20th century, where they were collectively recognized as Rogosija. After the Second World War, the introduction of high-yielding common wheat cultivars threatened the survival of Rogosija landraces, that were almost extinct in farmers' fields. Starting from 1955, sampling of durum wheat accessions in Montenegrin regions allowed the conservation of a Rogosija durum collection in the Montenegro Plant Gene Bank. This assortment represents an unexplored durum wheat germplasm that can be analyzed for the identification of valuable alleles, useful to increase the wheat crop adaptability to climate change. Aims of this study were: i) to estimate the genetic diversity and population structure of the Rogosija collection using SNP markers; ii) to investigate correlation between genetic clusters and the Montenegro ecogeographic conditions. The collection was analyzed with a high-throughput genotyping system based on the 25K Illumina SNP wheat array. A total of 6,915 high-quality SNPs were retained and mapped on the durum genome. Principal components and phylogenetic analyses discriminated two different genetic durum clusters. Analysis of molecular variance revealed that 16% of the total variation was due to differences among the genetic clusters, whereas the remaining variance occurred within clusters. To estimate whether the genetic clusters detected are related to Montenegrin ecogeographic regions, the durum accessions were geo-referenced and evaluated according to ecological data of the collecting sites. Interestingly, one genetic cluster included samples located around Lake Skadar, while the second genetic cluster comprised accession sampled in the Montenegrin littoral coast. This result suggests that the Rogosija durum collection stored in the Montenegro Plant Gene Bank enclosed two Rogosija durum populations, evolved in two different eco-geographic micro-areas.