



LXVI SIGA ANNUAL CONGRESS

CLIMATE-SMART PLANTS TO FEED THE FUTURE

BARI, 5 - 8 SEPTEMBER, 2023

PROGRAMME

TUESDAY, SEPTEMBER 5

13:00 – 14:30 Registration

14:30 – 14:50 Opening ceremony

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

Welcome address by Institutional and Local Authorities

14:50 – 15:00 Communication from EIT-FOOD Project manager at UNIBA

De Ruggieri 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	<i>Forestan C., Bozzoli M., Maccaferri M., Tuberosa R., Mazzucotelli E., Francesca D., 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</i> Upgrading the durum wheat genomic resources: from the platinum-quality Svevo genome assembly and annotation to the tetraploid wheat pangenome
15:45 – 16:00	<i>Miculan M., Zuccolo A., Fabbian L., Zhou Y., Rivera L.F., Copetti D., Talag J.D., McNally K., Henry A., Wing R.A.</i> Disentangling the genome wide contribute of structural variations to drought stress resistance in the model species <i>Oryza sativa</i>
16:00 – 16:15	<i>Gabelli G., Palumbo F., Boni A.G., Ferrari G., Beretta M., Barcaccia G.</i> Deciphering the recombination spots scenario in a MAGIC population of cultivated and wild tomato
16:15 – 16:30	<i>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.</i> 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	<i>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.</i> 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	<i>Americo S., Ferrari G., Desiderio F., Guerra D., Beretta M., Lo Piero A.R., Sicilia A., Morelli G., Cattivelli L., D'Orso F.</i> Unveiling the position and effects on salt stress resilience of wild <i>S. pennellii</i> genome in <i>S. pennellii</i> x <i>S. lycopersicum</i> introgression lines through integrated DNA and RNA sequencing approach

17:30 – 17:45	<i>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.</i> Metabolite characterization of durum wheat grain for association studies: exploring the natural variation of free asparagine content
17:45 – 18:00	<i>Delvento C., Arcieri F., Marcotrigiano A.R., Guerriero M., Fanelli V., Dellino M., Curci P.L., Bouwmeester H., Lotti C., Ricciardi L., Pavan S.</i> High-density linkage mapping and genetic dissection of resistance to broomrape (<i>Orobanche crenata</i> Forsk.) in pea (<i>Pisum sativum</i> L.)
18:00 – 18:15	<i>Bono G.A., Giaume F., Vicentini G., Miner I., Betagnon G., Fornara F., Brambilla V.</i> Molecular control of flowering at the rice shoot apex
18:15 – 18:30	<i>Foresti C., Amato A., Fattorini C., D'Incà E., Vitulo N., Zenoni S.</i> NACs intra-family hierarchical regulatory network orchestrating grape berry ripening
18:30 – 18:45	General discussion
19:00 – 20:30	Welcome cocktail

WEDNESDAY, SEPTEMBER 6

09:00 – 10:45	Session 2 – Breeding for resilience: addressing climate change in plant genetics <i>Organized by Next Generation SIGA</i> <i>Chairpersons: Broccanello C., Di Marsico M.</i>
09:00 – 09:30	Invited Lecture <i>Dixon L.</i> Adapting cereal development to changing climates
09:30 – 09:45	<i>Persello A., Rotaspertti L., Torricella V., Ballabio F., Betti A., Tadini L., Camilloni C., Hansson M., Rossini L., Horner S.D., Salvi S., Pesaresi P.</i> Pale-green crops for a new sustainable agriculture
09:45 – 10:00	<i>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., Stavolone L., Summerer S., Veronico P., Cillo F.</i> A phenomics approach to drought and pathogen responses in a tomato genotype collection
10:00 – 10:15	<i>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.,</i>

	<i>Invernizzi C., Oliveri F., Mastrangelo A.M., Marone D., Roncallo P., Bassi F., Perovic D., Cattivelli L., Tuberosa R., Maccaferri M.</i>
	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	<i>Colanero S., Martignago D., Loukili I., Sutti A., Landoni B., Cioffi S., Bosc A., Tonelli C., Galbiati M., Conti L.</i>
	Engineering water use in tomato by generating <i>SlMyb60</i> 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 <i>Chairpersons: Lotti C., Pavan S.</i>
11:15 – 11:45	Invited Lecture <i>Bai Y.</i> Impaired plant susceptibility genes in resistance breeding from concept to cultivars
11:45 – 12:00	<i>Bettinelli P., Bianco L., Fontana P., Moser M., Pindo M., Nicolini D., Costantini L., Stefanini M., Hausmann L., Vezzulli S.</i> Black rot resistance of grapevine: from organ-specific QTL mapping to the sequencing of the donor towards candidate gene identification
12:00 – 12:15	<i>Li R., Cui L., Martina M., Moglia A., Bracuto V., Meijer-Dekens F., Wolters A.A., Bai Y., Acquadro A.</i> Less is more: CRISPR/Cas9-based mutations in <i>DND1</i> gene enhance tomato resistance to powdery mildew with low fitness costs
12:15 – 12:30	<i>Caproni L., Altman T., Ferguson J., Heuermann M., Kromdijk J., Pè M.E., Dell'Acqua M.</i> 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	<i>Bozzoli M., Bruschi M., Fanelli Carvalho H., Isidro y Sánchez J., Ruggeri M., Meriggi D., Manstretta V., Bartocetti E., Sgrelli S., Meriggi P., Tuberosa R., Maccaferri M.</i> 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	<i>Michelotti V., Rossi R., Crosatti C., Mica E., Guerra D., Colombo M., Masiero S., Radchuk V., Cattivelli L., Battaglia R.</i> Sporophytic control of male fertility, the role of the <i>SWEET4</i> gene in barley
13:00 – 13:15	General discussion
13:15 – 13:30	EUCARPIA: current progressive future opportunity for plant breeding <i>Ercolano M.R.</i>

13:30 – 14:30	Lunch break
14:30 – 16:45	Session 4 – Underground genetics: roots and their interactions <i>In memory of Marina Tucci</i> Chairpersons: Beretta M., Salvi S.
14:30 – 15:00	Invited Lecture <i>Laplace L.</i> Targeting root traits to improve tolerance to vegetative drought episodes in pearl millet (<i>Pennisetum glaucum</i> L.)
15:00 – 15:15	<i>Puglisi D., Carletti G., Delbono S., Cattivelli L., Fricano A.</i> Shovelomics and clear pot analyses highlight extensive natural genetic variation for root system architecture in barley
15:15 – 15:30	<i>Daddiego L., Bianco L., Alagna F., Lopez L., Panara F., Fantini E., Facella P.</i> Differential expression patterns of cryptochrome and circadian clock genes between roots and leaves in <i>Medicago truncatula</i>
15:30 – 15:45	<i>Scintu D., Shtin M., Svolacchia N., Sabatini S., Dello Ilio R., Di Mambro R.</i> Exploring root programmed cell death as a mechanism for heat stress resilience
15:45 – 16:15	Invited Lecture <i>Pieterse C.M.J.</i> The root microbiome and plant immunity
16:15 – 16:30	General discussion
16:30 – 17:00	SIGA Young Research Award 2023 <i>Dedicated to Francesco D'Amato and Gian Tommaso Scarascia Mugnozza</i> Chairpersons: Filippone E., Rosellini D. <i>Rotasperti L.</i> The barley mutant <i>happy under the sun 1 (hus1)</i> : An additional contribution to pale green crops <i>Iohannes S.D.</i> Data-driven, participatory characterization of farmer varieties discloses teff breeding potential under current and future climates <i>Award ceremony</i>
17:00 – 17:30	Coffee break and poster viewing
17:45 – 19:30	SIGA General Assembly

THURSDAY, SEPTEMBER 7

09:00 – 10:15	Session 5 – Exploring the plant epigenomes <i>Chairpersons: Comino C., Varotto S.</i>
09:00 – 09:30	Invited Lecture <i>Zilberman D.</i> Long-term epigenetic inheritance and phenotypic diversity in natural populations
09:30 – 09:45	<i>Bevilacqua I., Moffa L., Varotto S., Chitarra W., Nerva L.</i> Harnessing genome editing to elucidate the role of histone variant H2A.Z in grapevine
09:45 – 10:00	<i>Liva M., Magris G., Di Gaspero G., Schwope R., Catacchio C.R., Daponte A., Ventura M., Morgante M.</i> 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 <i>Chairpersons: Giannino D., Montemurro C.</i>
11:30 – 12:00	Invited Lecture <i>Gonzalez-Martinez S.</i> Population vulnerability of a keystone Mediterranean tree under future climate – an ecological genomics approach
12:00 – 12:15	<i>Garosi C., Vettori C., Bajc M., Kraigher H., Westergren M., Dovč N., Damjanić R., Sever K., Breznikar A., Gregoric A., Lanšćak M., Ivankovic M., Bogunović S., Paffetti D.</i> Genome-wide SNP association analysis reveals genomic signature of local adaptation in European beech (<i>Fagus sylvatica</i> L.)
12:15 – 12:30	<i>Alicandri E., Sebastiani B., Paolacci A.R., Sorgonà A., Manti F., Bosignore C.P., Badiani M., Ciaffi M.</i> Terpenoids and the expression of terpene synthase genes are coherently and selectively modulated in Calabrian pine (<i>Pinus nigra</i> subs. <i>laricio</i>) in response to pine processionary moth (<i>Thaumetopoea pityocampa</i>) infestation
13:00 – 14:30	Lunch break
14:30 – 17:15	Session 6 – (cont.)
14:30 – 15:00	Invited Lecture <i>Decroocq V.</i> Genetic diversity and use of stone fruit tree wild relatives for a more sustainable fruit production

15:00 – 15:15	<i>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.</i> Chestnut cultivation development in Lombardy: leveraging native genetic resources in two pilot areas
15:15 – 15:30	<i>Costa F., Busatto N., Sayantan P., Vittani L., Populin F., Khomenko I., Biasioli F., Vrhovsek U., Aharoni A., Zanella A.</i> System genetics approach disclosed the genetic architecture of the chilling injury disorder superficial scald in apple
15:30 – 15:45	<i>Simoni S., Castellacci M., Usai G., Giordani T., Natali L., Cavallini A., Besnard G., Mascagni F.</i> Genomic dynamics of olive trees in the Mediterranean basin: insights from the repetitive component evolution
15:45 – 16:00	<i>Bonghi C., Canton M., Joseph J., Marconi G., Forestan C., Varotto S.</i> The bud peach dormancy dilemma
16:00 – 16:15	<i>da Silva Linge C., Baccichet I., Chiozzotto R., Gasic K., Fu W., Byrne D., Rawandozi Z., Worthington M., Bassi D., Cirilli M., Hardner C., Rossini L.</i> Unlocking genetic diversity for peach fruit acidity through global GWAs and genomic prediction-based selection
16:15 – 16:30	<i>Michelotti V., Adele G., Scorticchini M., Lucioli S., Caboni E., Tacconi G.</i> Application of a CRISPR/CAS9 vector in <i>A. chinensis</i> var. <i>chinensis</i> to induce <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> resistance/tolerance
16:30 – 16:45	<i>Sicilia A., Villano C., Di Serio E., Aversano R., Ferlito F., Nicolosi E., Lo Piero Angela R.</i> Transcriptome analysis reveals plasticity of gene expression in wine grape cultivars grown at different latitudes in southern Italy
16:45 – 17:00	<i>Bolognesi G., Crespan M., Broccanello C., Delfino P., Mora R., Marini M., Gardiman M., Giust M., Tomasi D., Bellin D.</i> Genome wide association analysis of phenology related traits in <i>Vitis vinifera</i> 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 8

09:30 – 12:15	Session 7 – Updates and upgrades in genome editing <i>Chairpersons: Lanubile A., Nigro D.</i>
09:30 – 10:00	Invited Lecture <i>Cereseto A.</i> Expanding the genome editing toolbox by unlocking RNA guided nucleases using massive metagenomic data
10:00 – 10:15	<i>Vicentini G., Bertagnon G., Giaume F., Fornara F., Brambilla V.</i> Controls of stem elongation by the flowering pathway in rice
10:15 – 10:30	<i>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.</i> A new rice plant ideotype through genome editing: the SUSRICE project
10:30 – 10:45	<i>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.</i> New insights on the role of <i>SIDMR6-1</i> in drought avoidance in tomato
10:45 – 11:00	<i>Nicolia A., D'Agostino N., Tamburino R., Festa G., Sannino L., Aufiero G., Paparo R., Arimura S., Scotti N., Cardi T.</i> Molecular and phenotypic characterization of potato plants edited in the mitochondrial genome by mitoTALEN and mitoTALECD approaches
11:00 – 11:15	<i>Salvagnin U., Giacomelli L., Scintilla S., Rouppe van der Voort J., Zeilmaker T., Moser C.</i> Reduced susceptibility to downy mildew of DMR6 gene-edited grapevine plants and development of DNA-free edited mutants
11:15 – 11:30	<i>Moffa L., Bevilacqua I., Pagliarani C., Gambino G., Perrone I., Velasco R., Lovisolo C., Nerva L., Chitarra W.</i> 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 <i>Granell A.</i> Genome editing for better, healthier tomatoes
12:00 – 12:15	General discussion

12:15 – 12:30 Closing ceremony
Chairpersons: Filippone E., Salvi S.