



Piacenza, 6 - 9 September 2022

**ON MENDEL'S FOOTSTEPS
FROM GENES TO FORK**

SCIENTIFIC PROGRAMME

TUESDAY, SEPTEMBER 6

- 13:00 – 14:30 Registration**
- 14:30 – 15:00 Opening ceremony**
Chairpersons: Filippone E., Marocco A., Cattivelli L.
Welcome address by Institutional and Local Authorities
- 15:00 – 16:45 Session 1 – One health – Plant genes for human health**
Chairpersons: Ambrosone A., Comino C.
- 15:00 – 15:30 Invited Lecture**
Bosch D.
Plant terpene biosynthesis genes for human health. Application via genome editing in chicory; the EU-CHIC project
- 15:30 – 15:45 Diretto G., Frusciante S., Ahrazem O., Gomez-Gomez L., Rambla J.L., Granell A., Argandona J., Moraga A., Lobato-Gomez M., Presa S.**
Engineering high levels of saffron apocarotenoids in tomato
- 15:45 – 16:00 Cacciulli A., Salonia F., Pindo M., Stefani E., Amenta M., Caruso M., Licciardello C.**
Colourimetric, genetic, transcriptomic and metabolomic approaches on four lycopene-rich citrus varieties for broad applications in biotechnology
- 16:00 – 16:15 Colombo F., Bertagnon G., Sangiorgio S., Singh S., Pilu R.**
Chasing the main pleiotropic effects in low phytic acid1-1 mutant: a sustainable solution to non-renewable phosphorus

16:15 – 16:30	<i>Botticella E., Testone G., Buffagni V., Palombieri S., Lucini L., Giannino D., Lafiandra D., Sestili F.</i> Tailoring starch biosynthesis in wheat hits crucial kernel metabolic pathways as disclosed by multiple omics approaches
16:30 – 16:45	<i>Simoni S., Vangelisti A., Clemente C., Tavarini S., Usai G., Mascagni F., Natali L., Angelini L.G., Cavallini A., Giordani T.</i> Transcriptomic analysis of <i>Stevia rebaudiana</i> (Bertoni) provides novel insights into steviol glycosides and phenolic compounds biosynthesis and accumulation
16:45 – 17:10	Coffee break and online poster viewing
17:10 – 19:00	Session 2 – One health – Developing the holobiont concept <i>Chairpersons: Mastrangelo A.M., Salvi S.</i>
17:10 – 17:40	Invited Lecture <i>Hochholdinger F.</i> Genetic control of maize root formation and its interaction with the rhizosphere
17:40 – 17:55	<i>Bertola M., Righetti L., Gazza L., Ferrarini A., Fornasier F., Cirlini M., Lolli V., Galaverna G., Visioli G.</i> Evolution of rhizosphere microbial communities' composition and activity during perennial wheat crops cultivation
17:55 – 18:10	<i>Vangelisti A., Cela F., Simoni S., Avio L., Turrini A., Sbrana C., Incrocci L., Pardossi A., Natali L., Cavallini A., Giordani T.</i> Arbuscular symbiosis in soilless culture: transcriptomic and biochemical analyses in <i>Lactuca sativa</i> plants
18:10 – 18:25	<i>Cuccurullo A., Yoneyama K., Bouwmeester H., D'Agostino N., Festa G., Camerlengo F., Contaldi F., Cardi T., Nicolia A.</i> Phenotypic comparison of CRISPR/Cas9 tomato mutants targeting genes responsible for the biosynthesis of strigolactones
18:25 – 18:40	<i>Martinelli F., Vergata C., Ferrini F., Moura B., Buti M., Baccelli I., Mengoni A., Vaccaro F.</i> Hidden plant responses to urban particulate matter
18:40 – 19:00	General discussion

WEDNESDAY, SEPTEMBER 7

09:00 – 10:45	Session 3 – Phytohormones, sensing and signaling <i>Chairpersons: Beretta M., Leone A.</i>
09:00 – 09:30	Invited Lecture <i>Caño-Delgado A.I.</i> Deciphering the role of brassinosteroids in plant adaption to climate change
09:30 – 09:45	<i>Vicentini G., Bignardi A., Moore S., Cazzaniga F., Pirota M., Giaume F., Gomez-Ariza J., Pierce S., Fornara F., Brambilla V.</i> <i>PREMATURE INTERNODE ELONGATION 1 (PINE1) represses GIBBERELLIN sensitivity in the rice stem</i>
09:45 – 10:00	<i>Busatto N., Moretto M., Farneti B., Populin F., Vrhovsek U., Comisso M., Sonego P., Biasioli F., Guzzo F., Fontana P., Costa F.</i> The ripening initiation of apple fruit is regulated by a hormonal circuit sustained by auxin
10:00 – 10:15	<i>Simoni L., Simeoni F., Conti L., Tonelli C., Castorina G., Skirycz A., Galbiati M.</i> The AtMYB60 transcription factor integrates ABA and oxylipin signalling in guard cells
10:15 – 10:30	<i>Giulietti S., De Lorenzo G., Savatin D.</i> Insights into the Arabidopsis NPK1-related Protein kinases (ANPs) role in danger signaling
10:30 – 10:45	General discussion
10:45 – 11:15	Coffee break and online poster viewing
11:15 – 13:00	Session 4 – Comparative genomics and pangenomics <i>Chairpersons: Maccaferri M., Mazzucotelli E.</i>
11:15 – 11:45	Invited Lecture <i>Wulff B.</i> Sustainable control of disease resistance – the case for GM wheat
11:45 – 12:00	<i>Bozzoli M., Bruschi M., Nefzaoui M., Prestera M., Thomelin P., Ober E., Quiroz Chávez J., Ramirez Gonzalez R., Gaurav K., Arora S., Uauy C., Brande W., Tuberosa R., Maccaferri M.</i> Exploiting the full potential of a low-linkage disequilibrium, fully re-sequenced <i>Agilops tauschii</i> collection for GWAS targeting root system architecture
12:00 – 12:15	<i>Guerra D., Viottini G., Li C., Naz A., Mascher M., Stein N., Cattivelli L., Tondelli A.</i> A gene duplication at the Blp1 locus is associated with the black grain phenotype in barley
12:15 – 12:30	<i>Toppino L., Sirangelo T.M., Tassone M.R., Bagnaresi P., Lopatriello G., Delledonne M., Rotino G.L.</i> Genomic and transcriptomic investigation about <i>Fusarium oxysporum</i> f. sp. <i>melongenae</i> resistance in '305E40' eggplant line

12:30 – 12:45	<i>Rossato M., Marcolungo L., De Antoni L., Lopatriello G., Bellucci E., Cortinovis G., Frascarelli G., Nanni L., Bitocchi E., Bett K., Ramsay L., Konkin D.J., Delledonne M., Papa R.</i> CRISPR-Cas9-based repeat depletion for high-throughput genotyping of complex plant genomes
12:45 – 13:00	General discussion
13:00 – 14:30	Lunch break
14:30 – 16:30	Session 5 – New routes to plant adaptation and sustainable agriculture <i>Chairpersons: Dell'Acqua M., Lanubile A.</i>
14:30 – 15:00	Invited Lecture <i>Dubcovsky J.</i> Reverse genetic tools and their utilization to dissect grain yield components in wheat
15:00 – 15:15	<i>Forestan C., Rosignoli S., Sciara G., Bruschi M., Sangiorgi G., Ormanbekova D., Tuberosa R., Maccaferri M., Salvi S.</i> Exploring the molecular bases of Root Growth Angle and its regulation in barley and wheat
15:15 – 15:30	<i>Gómez-Álvarez E.M., Tondelli A., Nghi K.N., Viktoriia V., Valè G., Perata P., Pucciariello C.</i> Barley germination after flooding events depends on hypoxia-induced secondary dormancy
15:30 – 15:45	<i>Guche M.D., Pilati S., Dalla Costa L., Moser C., Guella G., Trenti F., Lanubile A., Marocco A.</i> Functional study of lipoxygenase-mediated resistance against <i>Aspergillus flavus</i> and <i>Fusarium verticillioides</i> infection in maize
15:45 – 16:00	<i>D'Incà R., Mattioli R., Tomasella M., Tavazza M., Macone A., Tavazza R., Martignago D., Incocciati A., Fraudentali I., Cona A., Angelini R., Nardini A., Tavladoraki P.</i> CRISPR/Cas9-mediated mutagenesis of a polyamine oxidase gene increases tomato plant tolerance to drought stress
16:00 – 16:15	<i>Licciardello C., Scalabrin S., D'Amante G., Russo M.P., Caruso P., Vidotto M., Alves M.N., Wulff N.A., Vendramin V., Ollitrault P., Peña L.</i> <i>Eremocitrus glauca</i> , a genetic source to fight against Huanglongbing, a highly destructive citrus disease
16:15 – 16:30	General discussion

16:30 – 17:00 SIGA Young Research Award 2022
Chairpersons: Filippone E., Rosellini D.

Puglisi D.

Genomic prediction of grain yield in a barley MAGIC population
modeling genotype per environment interaction

Magris G.

The genomes of 204 *Vitis vinifera* accessions reveal the origin of
European wine grapes

Award ceremony

17:00 – 17:30 Coffee break and online poster viewing

17:30 – 19:30 SIGA General Assembly

THURSDAY, SEPTEMBER 8

09:00 – 11:00	Session 6 – Genetics and beyond: from Mendel to epigenomics Organized by Next Generation SIGA Chairpersons: Cassibba V., Mascagni F.
09:00 – 09:30	Invited Lecture <i>Benoit M.</i> Impact of structural and epigenetic variation on quantitative traits during tomato domestication
09:30 – 09:45	<i>Usai G., Ventimiglia M., Marturano G., Vangelisti A., Simoni S., Cavallini A., Giordani T., Natali L., Zuccolo A., Mascagni F.</i> Exploring a model for the formation of novel genes from transposons in plants
09:45 – 10:00	<i>de Sario F., Bozzoli M., Forestan C., Sakuma S., Gabay G., Milner S.G., Snowdon R., Salvi S., Tuberosa R., Schnurbusch T., Maccaferri M.</i> Fine mapping and characterization of Grain Number Increase-2 locus (GNI-A2) in durum wheat
10:00 – 10:15	<i>Novi J.B., Mazzucotelli E., Desiderio F., Pourkhorshid Z., Viola P., Invernizzi C., Oliveri F., Randazzo B., Mastrangelo A.M., Marone D., Roncallo P., Campana M., Bozzoli M., Meriggi D., Omar I., Baidani A., Ozkan H., Bashour I., Sharif Ragab Mohamed E., Gadaleta A., El Amil R., Nazari K., Bassi F., Cattivelli L., Tuberosa R., Maccaferri M.</i> Multienvironment assessment and GWAS of the global durum genomic resource for resistance to yellow rust
10:15 – 10:30	<i>Mineri L., Cerise M., Giaume F., Vicentini G., Martignago D., Chiara M., Galbiati F., Sergi E., Spada A., Horner D., Fornara F., Brambilla V.</i> A common set of genes responding to florigenic and photoperiodic induction at the shoot apical meristem of rice
10:30 – 10:45	<i>Puglisi D., Lopatriello G., Grosso V., Caruso M., Bazzano M., Scuderi G., Catara A., Caruso P., Rossato M., Licciardello G., Licciardello C.</i> The transcriptome of <i>Citrus aurantium</i> sequenced and assembled by using a hybrid approach: a novel basis to investigate the cross-protection mechanism of Citrus tristeza virus
10:45 – 11:00	<i>Paolo D., Rossato M., Testone G., Frugis G., Di Vittori V., Liberatore C., Galbiati M., Cominelli E., Locatelli F., Delle donne M., Cortinovis G., Bellucci E., Bitocchi E., Rodriguez M., Attene G., Aragao F., Porch T.G., Papa R., Sparvoli F.</i> Genetics of domestication in common bean (<i>Phaseolus vulgaris</i> L.): an approach for the analysis of candidate genes via TILLING-by-sequencing
11:00 – 11:30	Coffee break and online poster viewing
11:30 – 12:30	Session 6 – (cont.)

11:30 – 11:45	<i>Zhu W., Yang L., Wu D., Meng Q., Deng X., Huang G., Chen X., Ferrández C., Liang W., Dreni L., Zhang D.</i> Rice SEPALLATA genes <i>OsMADS5</i> and <i>OsMADS34</i> cooperate to limit inflorescence branching by repressing the <i>TERMINAL FLOWER1</i> -like gene <i>RCN4</i>
11:45 – 12:00	<i>Macharia M.W., Tamang A., Caproni L., Miculan M., Pe' M.E., Dell'Acqua M.</i> Genetic structure of maize landraces from the Himalayan region
12:00 – 12:15	<i>Joseph J., Canton M., Aiese Cigliano R., Bonghi C., Varotto S.</i> A transcriptomic study on peach floral and vegetative buds during winter dormancy
12:15 – 12:30	General discussion
12:30 – 14:30	Lunch break
14:30 – 16:45	Workshop – Coordinamento delle politiche di conservazione e utilizzo delle risorse genetiche vegetali per attività di ricerca e di miglioramento genetico <i>Discussants: Ercolano M.R., Giannino D.</i>
14:30 – 16:30	<i>Mazzucato A.</i> Agro-biodiversità: l'impatto delle visioni generali e particolari <i>Tucci M.</i> La tutela, gestione e valorizzazione delle RGVAA nel groviglio dei regolamenti internazionali, nazionali e regionali. La concertazione del progetto ABC <i>Laghetti G.</i> I progetti, i programmi e le visioni del Consiglio Nazionale delle Ricerche <i>Verde I.</i> Il programma RGV FAO: visioni e problematiche sul reperimento, conservazione, utilizzo e condivisione delle risorse genetiche vegetali del CREA <i>Giuliano G.</i> Una proposta di infrastruttura Europea dedicata alle RGVAA <i>Papa R.</i> Il progetto "INCREASE": collezioni intelligenti di risorse genetiche di leguminose alimentari per i sistemi agroalimentari europei <i>Maccaferri M.</i> Il coordinamento italiano delle "Global Durum Resources", un progetto collaborativo mondiale: dalle risorse agli utilizzatori finali <i>Goritschnig S.</i> Progetto EVA: caratterizzazione e valutazione delle RGVAA delle banche europee mediante partenariati internazionali pubblico-privati <i>Lipparini A.</i> La posizione di Assosementi sull'impiego delle RGVAA

Manzella D.

La normativa internazionale in evoluzione: risorse genetiche, dati e nuove prospettive per la condivisione dei benefici

16:30 – 16:45 **Conclusioni**
Cardi T.

16:45 – 17:30 **Coffee break and online poster viewing**

17:30 – 19:00 Parallel Poster Sessions in presence

20:30 **Social Event** (*Collegio Alberoni, Via Emilia Parmense 77, Piacenza*)

FRIDAY, SEPTEMBER 9

09:30 – 12:00	Session 7 – SIGA on Mendel's footsteps <i>Chairpersons: Cattivelli L., Masci S.</i>
09:30 – 09:45	<i>Nicolia A., Festa G., D'Agostino N., Scotti N., Arimura S., Cardi T.</i> Mitochondrial DNA editing in potato
09:45 – 10:00	<i>Dal Corso G., Galati S., Giannelli G., Fragni R., Buschini A., Furini A., Visioli G.</i> The involvement of DNA methylation in enhancing heavy metal hypertolerance
10:00 – 10:15	<i>Populin F., Vittani L., Stuerz S., Buehlmann A., Khomenko I., Biasioli F., Vrhovsek U., Masuero D., Zanella A., Busatto N., Costa F.</i> Comparative analysis of 'Granny Smith' and 'Ladina' apple cultivars in relation to the onset of the postharvest disorder superficial scald
10:15 – 10:30	<i>Vannozzi A., Perin C., Palumbo F., Sandri M., Zuccolotto P., Zenoni S., Barcaccia G., Pindo M., Cestaro A., Sonego P., Lucchin M.</i> Dissecting the effect of soil on berry transcriptional plasticity in two Italian grapevine varieties (<i>V. vinifera</i> L.)
10:30 – 10:45	<i>Casarini S., Bertazzon N., Sirangelo T.M., Filippini L., Cattivelli L., Angelini E., Bagnaressi P.</i> The study of three grapevine clones to uncover the genetic traits responsible for the low susceptibility to <i>Flavescence dorée</i>
10:45 – 11:00	<i>Bonarrigo M., Palombieri S., Potestio S., Sestili F., Lafiandra D., Miceli C., Messina B., Russo G., Masci S.</i> Evaluation of genetic diversity of Sicilian autochthonous tetraploid wheat varieties by gluten protein analysis
11:00 – 11:15	<i>Vitale P., Laidò G., Dono G., Pecorella I., Ramasubramanian V., Lorenz A., De Vita P., Pecchioni N.</i> Multivariate genomic prediction for agronomic traits in durum wheat under two field managements
11:15 – 11:45	Invited Lecture <i>Morgante M.</i> The evolving definition of a gene in the context of modern plant breeding
11:45 – 12:00	General discussion
12:00 – 12:15	Closing ceremony <i>Chairpersons: Filippone E., Salvi S.</i>