

PlantEd

Genome editing in plants

Cost Action CA18111

4th PlantEd Conference

18-20 September 2023

Porto, Portugal

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Book of Abstracts

Book of Abstracts of the 4th PlantEd Conference

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Committees

Scientific Committee

Dennis Eriksson, Swedish University of Agricultural Sciences, Sweden

Isabel Mafra, REQUIMTE-LAQV/Faculty of Pharmacy, University of Porto, Portugal

Götz Hensel, Heinrich-Heine-University, Dusseldorf, Germany

Katrijn Van Laere, EV ILVO, Belgium

Dragana Miladinovic, Institute of Field and Vegetable Crops, Serbia

Jeremy Sweet, JT Environmental Consultants, UK

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Matina Tsalavouta, University of Liverpool, UK

Vladislava Galovic, Institute of Lowland Forestry and Environment- ILFE, Serbia

Anna Coll, National Institute of Biology, Slovenia

Ankica Kondic-Spika, Institute of Field and Vegetable Crops, Serbia

Sebastien Carpentier, KU Leuven , Belgium

Local Organising Committee

Isabel Mafra, REQUIMTE-LAQV/FFUP, Portugal

Joana Costa, REQUIMTE-LAQV/FFUP, Portugal

Caterina Villa, REQUIMTE-LAQV/FFUP, Portugal

Carla Teixeira, REQUIMTE-LAQV/FFUP, Portugal

Isabel Ferreira, REQUIMTE-LAQV/FFUP, Portugal

Scope

The 4th PlantEd Conference (COST Action 18111) will be held over three days, with open scientific sessions on genome editing technology in plants, followed by PlantEd Working Group (WG) sessions and a Management Committee (MC) meeting. The conference will be a hybrid event, with a limited number of participants physically present, combined with live streaming (Zoom). The PlantEd conference, a network for plant genome editing research across Europe and beyond, is an excellent platform for disseminating information, discussion, and connections and updating the latest research and innovation.

The PlantEd Conference, being a network for research on plant genome editing across Europe and beyond, is an excellent platform for dissemination, discussions and connections, and for updating on the latest research and innovation forefront.

Topics to be covered: The conference will host sessions on the application of genome editing in various types of economically important plants (cereals, oil crops, roots and tubers, legumes, fruits and vegetables, trees, algae), as well as the latest technological advancements for genome editing in plants.

The conference will take place towards the end of the action and final grant period, which marks the closing of PlantEd activities, identifying the main achieved outcomes, but most importantly, planning/on-going activities by the prospection of new resources.

Venue

[Faculty of Pharmacy, University of Porto \(FFUP\)](#)

Rua Jorge Viterbo Ferreira, 228

4050-313 Porto

[DIRECTIONS](#)



The conference will have the support of the [Associated Laboratory REQUIMTE](#) and [Faculty of Pharmacy, University of Porto](#).

Supporters

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Financial supporters



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Programme

4th PlantEd Conference

Porto, Portugal – September 18-20, 2023

Monday 18 Sept		Session Chair: Dennis Eriksson
	08:00-09:00	Registration
	09:00-09:30	Welcome Local Organizer – Isabel Mafra ; REQUIMTE- LAQV, Faculty of Pharmacy, University of Porto/Portugal Welcome Executive Board of Faculty – Marcela Segundo ; Faculty of Pharmacy, University of Porto/Portugal Welcome COST Action Chair – Dennis Eriksson ; Swedish University of Agricultural Sciences/Sweden
	09:30-10:00	Keynote: Dirk Bosch and Katarina Cankar ; Wageningen University/The Netherlands <i>Genome editing to improve health benefits of root chicory</i>
	10:00-10:20	Justyna Boniecka , Department of Genetics, Nicolaus Copernicus University in Toruń/Poland <i>CRISPR/Cas9-directed editing of RelA/SpoT Homologs in tomato (Solanum lycopersicum L.)</i>
	10:20-10:40	Zoe Hilioti , Institute of Applied Biosciences/CERTH/Greece <i>Tomato breeding by design using non-transgenic genome editing</i>
Session I – GE applications and molecular mechanisms	10:40-11:20	Coffee break and poster session
	11:20-11:40	Daria Navrotska , Institute of Molecular Biology and Genetics of the National Academy of Sciences of Ukraine/Ukraine <i>Brachypodium distachyon DOF transcription factor gene analysis and genome editing</i>
	11:40-12:00	Tjaša Lukan , Department of Biotechnology and Systems Biology, National Institute of Biology/Slovenia <i>CRISPR/Cas9-mediated miRNA editing in tetraploid potato</i>
	12:00-12:20	Yordan Dolapchiev , The Sainsbury Laboratory/United Kingdom <i>Efficient targeted gene insertions in diploid potatoes</i>
	12:20-12:40	Katrijn Van Laere , ILVO - Plant Sciences Unit/Belgium <i>CRISPR-based visualisation of centromere sequences in chicory</i>
	12:40-13:50	Lunch
Monday 18 Sept		Session Chair: Isabel Mafra
	13:50-14:20	Keynote: Sílvia Coimbra ; Faculty of Sciences, University of Porto/Portugal <i>CRISPR - Bridging fundamental knowledge and novel technology to increase rice heat tolerance</i>
	14:20-14:40	Cecilia Sarmiento , Tallinn University of Technology/Estonia <i>Optimized Lolium perenne L. protoplasts isolation and transformation for CRISPR-Cas9 downstream applications</i>
Session II – Improving resistance to abiotic stress	14:40-15:00	Muneeb Hassan Hashmi , University of Siegen, Siegen/Germany <i>Establishment of highly efficient and reproducible Agrobacterium-mediated transformation system for tomato (Solanum lycopersicum L.)</i>
	15:00-15:20	Luca Nerva , CREA - Research Centre for Viticulture and Enology/Italy <i>Improving grape resilience to climate change exploiting the CRISPR/Cas technology: different approaches to face drought</i>
	15:20-16:00	Coffee break and poster session
	16:00-17:30	PlantEd Working Group meeting (WG1-WG5 together)

Tuesday 19 Sept		Session Chair: Götz Hensel
Session III – Improved technologies	09:30-09:50	Hilal Betul Kaya , Manisa Celal Bayar University/Turkey <i>Optimizing protoplast isolation and transformation efficiency for enhanced plant genome editing in grapevine</i>
	09:50-10:10	William de Martines , Wageningen University and Research/The Netherlands <i>Exploring alternative approaches for efficient gene targeting in plants: high fidelity nonhomologous end-joining with CRISPR-Cas12a in potato protoplasts</i>
	10:10-10:30	Angelo Ciacciulli , CREA OFA Acireale/Italy <i>New genomic techniques in citrus, step-by-step solutions for more efficient and successful procedures</i>
	10:30-11:10	Coffee break and poster session
Session IV – Nutritional improvement and characterisation	11:10-11:40	Keynote: Nélide Leiva Eriksson ; University of Lund/Sweden <i>Nutritional enrichment of sweetpotato with highly bioavailable iron</i>
	11:40-12:00	Ellen Slaman , VIB-Ugent/Belgium <i>In-depth characterization of Cas9 specificity in tomato using high-throughput amplicon sequencing, GUIDE-seq and whole genome resequencing</i>
	12:00-12:20	Concetta Licciardello , CREA/Italy <i>A dual single-guide RNA approach used to edit the b-cyclase 2 gene in anthocyanin-rich sweet orange varieties</i>
	12:20-12:40	Fabio D'Orso , Research Centre for Genomics and Bioinformatics/Italy <i>HQT gene editing to study chlorogenic acid metabolism and its physiological role in tomato</i>
	12:40-13:50	Lunch
Tuesday 19 Sept		Session Chair: Vladislava Galovic
Session V – Improving resistance to biotic factors	13:50-14:20	Keynote: Johan Hunziker ; INRAE/France <i>Gene editing in potato to enhance PVY resistance</i>
	14:20-14:40	Éva Csaba , ELKH Centre for Agricultural Research/Hungary <i>Studying potato resistance and susceptibility factors against pathogens with the use of genome editing</i>
	14:40-15:00	Senne Van den Broeck , KU Leuven/Belgium <i>Gene editing in triploid banana cultivars</i>
	15:00-15:20	Kim Hebelstrup , Department of Agroecology, Aarhus University/Denmark <i>De novo domestication of wild tuber-bearing Solanum species</i>
	15:20-16:00	Coffee break and poster session
	16:00-17:30	Management Committee meeting
	19:30	Social dinner
Wednesday 20 Sept		Session Chair: Katrijn Van Laere
Session VI – Regulation and public perception	09:00-09:30	Keynote: Elke Vereecke ; EV ILVO/Belgium <i>Increase the production of industrially valuable compounds in the microalgae Chlorella – the GeneBEcon approach</i>
	09:30-09:50	Juan Vives-Vallés , University of the Balearic Islands - INAGEA/Spain <i>Preliminary analysis of the European Commission Proposal for a Regulation on the production and marketing of plant reproductive material</i>
	09:50-10:10	Tomasz Zimny , Institute of Law Studies, Polish Academy of Sciences/Poland <i>The new NGT legislation proposal of the European Union. Analysis of selected EU and national regulatory obstacles for the introduction and market viability of NGT plant products</i>
	10:10-10:30	Anna Linkiewicz , Cardinal Wyszyński University in Warsaw/Poland <i>The awareness of the Polish society on new genomic techniques</i>
	10:30-11:00	Coffee break and poster session

	11:00-11:15	Agnés Ricroch ; AgroParisTech and University of Paris Saclay/France <i>“Roadmap for Plant Genome Editing” – a Springer book production from PlantEd</i>
Session VII - STSM	11:15-11:30	Vladislava Galovic ; University of Novi Sad, Institute of Lowland Forestry and Environment/Serbia <i>Overview on the 4-year STSM activities</i>
	11:30-11:45	Alvaro Valenzuela , Fondazione Edmund Mach/Italy <i>Leveraging system biology and new breeding technologies for water stress tolerance in grapevines</i>
	11:45-12:00	Karam Mostafa , Ondokuz Mayıs University/Turkey and Agriculture Research Center/Egypt <i>Application of multiplexed CRISPR-ACT3.0 gene activation system in tomato roots for enhancing resistance against plant-parasitic nematodes</i>
	12:00-12:15	Kubilay Yıldırım , Ondokuz Mayıs University, Department of Molecular Biology and Genetics, Samsun/Turkey <i>Development of resistant sunflower lines to broomrape using crispr-cas9</i>
	12:15-12:30	Sara Yasemin , Siirt University/Turkey <i>Exploring the role of snrk2 genes in salinity stress response of Petunia axillaris through CRISPR-based genome editing</i>
	12:30-12:45	Poster prizes
	12:45-13:00	Closing of conference

Multiplex genome editing and trait improvement for complex multicrop systems

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Breeding for diverse crop rotations involves selecting objectives that often overlap with current breeding programs. However, in the context of diverse crop rotations, a new target population of environments emerges, necessitating selection strategies to maximize genetic gain. The primary breeding goal remains productivity, but additional factors specific to diverse crop rotations, such as yield stability, postharvest quality, and traits associated with disease and insect pests, need to be considered. Occasionally, crops are bred for unexplored regions or novel crops are developed, such as perennial grain crops like intermediate wheatgrass, winter oilseeds like pennycress, and cover crops like hairy vetch. In these cases, breeding efforts may focus on crucial domestication traits such as seed shattering and harvestability.

Improving performance in a multicrop system can enhance breeding efficiency by identifying traits that can be observed in monoculture. Breeders can then select for these traits in multicrop systems without establishing a dedicated multicrop nursery, known as a "trait-informed approach." This approach proves particularly useful when heritability is low due to environmental heterogeneity. However, in the absence of highly correlated and observable traits, direct selection in multicrop systems becomes necessary to achieve optimal genetic gain. As high-throughput phenotyping technology advances, breeding programs can improve efficiency even when additional nurseries and trials are required. Collaboration with engineers to develop high-throughput phenotyping platforms suitable for complex multicrop systems presents further opportunities.

Complex traits like yield and disease tolerance often require edits in multiple independent loci. Multiplex genome editing enables the simultaneous modification of multiple, related or unrelated, loci within a single cell and subsequently within a single regenerated plant. Some of these loci may have negative impact on other important traits and it make this technology difficult for application. For example, reducing seed glucosinolates in Brassica plants can be achieved through mutation of glucosinolate transporter genes (GTRs). Previously created low seed glucosinolate germplasms in *B. napus* using gene-editing cannot be utilized for breeding due to their negative effects on other traits, possibly caused by the involvement of edited genes in other trait formation. However, in 2018 researchers demonstrated that CRISPR/Cas9-mediated mutations of three homologous *BnWRKY70* genes in rapeseed increased resistance against *S. sclerotiorum*, offering theoretical guidance and germplasm resources for developing rapeseed varieties with high resistance to *S. sclerotinia* and proving the concept that multiplex genome editing is useful not only for scientific reasons but also for application in breeding.

Acknowledgements: This work is part of the project supported by Ministry of Education, Science and Technological Development of Republic of Serbia, grant number 451-03-47/2023-01/200032, and COST Action CA18111.