

Host groups

Host Groups for the 2023 AGeNT call are the following:

Principal Investigator	Research line	e-mail address and website link
Albert Ferrer and Teresa Altabella	Free and glycosylated sterols play a key role in lipid rafts (LR) formation, which have emerged as central players in plasma membrane-dependent biological processes. Our main research interests are: (i) Understanding the molecular mechanisms underlying the effects of changes in sterol profile on plant development and stress response. (ii) Establishing a working model of LR-based biological processes involved in the phenotypic alterations induced by changes in the membrane sterol composition. (iii) Exploring the effects of changes in the sterol profile on root exudate composition and the rhizosphere microbial community.	teresa.altabella@cragenomica.es albert.ferrer@cragenomica.es https://www.cragenomica.es/research-groups/sterol-and-terpenoid-metabolism-plant-development-and-stress-responses
Àlex Clop	The project seeks to understand the genetic and molecular basis of semen quality in swine. To this end, we will implement whole genome sequencing and single cell multiome analysis (RNA + ATAC) from testes samples belonging to boars from artificial insemination centres with eGBV for semen quality. The main aims are to (i) obtain a single cell atlas of testicular cells in 4 pig breeds and (ii) identify genetic variants with high causative potential related to semen quality and fertility in boars with high genetic merit for production traits.	alex.clop@cragenomica.es https://www.cragenomica.es/research-groups/animal-genomics
Amparo Monfort	Enhancing of disease resistance in cultivated strawberries. Our research aims to improve the specific resistance of fungi and pests such as insects. Leveraging genetic tools such as genotyping and candidate gene analysis, we aim to identify genetic factors associated with disease resistance. This approach not only allows us to unlock the greatest production potential of disease-resistant varieties, but also promotes sustainable strawberry cultivation by reducing the need for chemical treatments. By minimizing treatments, we can mitigate the environmental impact and contribute to a balanced agricultural system.	amparo.monfort@cragenomica.es https://www.cragenomica.es/research-groups/rosaceae-genetics-and-genomics
Ana Montserrat Martín-Hernández	Role of the cell secretory pathway in the resistance/susceptibility to viruses in melon and tomato. Plant viruses alter the endomembrane system and the secretory pathways during the infection. We have found in melon two genes involved in the susceptibility to cucumber mosaic virus (CMV) and have generated CRISPR melon and tomato plants in one of them. These two genes are related to sterol metabolism and are involved in membrane trafficking. We aim to characterize their role during the infection and to generate melon and tomato plants resistant to CMV and other viruses that use the same infection pathway.	montse.martin@cragenomica.es https://www.cragenomica.es/research-groups/plant-viruses
David Caparrós	Elucidating the role of cell wall phenolic metabolites in the production of trichloroanisole (TCA) in <i>Quercus suber</i> . Within a private-public project, we identified several cell wall phenolic metabolites in <i>Quercus suber</i> as putative substrates to generate TCA, an undesirable compound for the cork and wine industry. We propose here to produce these metabolites synthetically coupled to a tag, injected them directly into the cork and determine the appearance of tagged TCA. We will also overproduce these <i>Quercus</i> phenolic metabolites in <i>Arabidopsis</i> to study in vivo the role of these compounds in the production of TCA.	david.caparros@cragenomica.es https://www.cragenomica.es/research-groups/bioengineering-licnocellulosic-biomass-maize
Elena Monte	To understand how photoprotection and growth are regulated under fluctuating light and temperature is key in the current climate context. Our laboratory studies how plants and microalgae sense and respond to their environment, employing cell imaging, photobiology, transcriptomic, epigenetic, and computational approaches to decode fitness optimization. Our research includes processes like the rhythmicity of growth and stomata aperture, photoreceptor and retrograde signaling, leaf growth, or chloroplast biogenesis. Our objective is to understand the basic biology with the further aim to have an impact in the field.	elena.monte@cragenomica.es https://www.cragenomica.es/research-groups/environmental-control-plant-and-algae-growth
Iban Eduardo	In the IRTA's peach and almond breeding programs, marker assisted breeding (MAB) is focused in three areas. Marker assisted selection (MAS) has been implemented for different traits and new markers are being developed. Marker assisted introgression (MAI) is a breeding strategy to increase the genetic variability introgressing new traits from closely related compatible species. Several ILS collections are under development. Finally, the resynthesis strategy is used to develop new cultivars very similar to already existing successful ones with few improved characteristics.	iban.eduardo@cragenomica.es https://www.cragenomica.es/research-groups/rosaceae-genetics-and-genomics
Ignacio Rubio Somoza	Research at the MoRE lab focuses on understanding the evolution of plant-microbe interactions and the underlying molecular processes (i.e., hormone-mediated communication, crosskingdom RNAi...). We also aim to understand the immunity programs specific to each plant cell type and how those impact on viral infection strategies and viral genome plasticity.	ignacio.rubio@cragenomica.es https://www.cragenomica.es/research-groups/molecular-reprogrmning-and-evolution
Igor Florez-Sarasa	Plant primary metabolism under stress. Our group is dedicated to enhancing the understanding of primary metabolism in vegetable crops under changing environmental conditions. Our main expertise is in metabolomics, respiration, photosynthesis and stable isotopes. Gene-edited and transgenic vegetable crops with altered mitochondrial respiration components are being developed to study their role and regulation during climacteric ripening and photosynthesis under stress. The knowledge generated can be used for obtaining crops with improved productivity and fruit quality in the upcoming global change scenarios.	igor.florez@cragenomica.es https://www.cragenomica.es/research-groups/genetics-and-genomics-vegetable-crops
Ivan Reyna-Llorens	The research project aims to investigate the coexistence of C4 and CAM photosynthetic pathways in the <i>Portulaca</i> genus, uncovering the morphological and molecular determinants for a C4-CAM switch, and then engineering a C4-CAM prototype in other plant species, potentially revolutionizing crop resilience and providing valuable insights for crop engineering.	ivan.reyna-llorens@cragenomica.es https://www.cragenomica.es/research-groups/synthetic-biology-and-photosynthesis
Jae-Seong Yang	Computational and Synthetic Biology Group is utilizing high-throughput experimental techniques and machine learning methods to understand the impact of genetic variation on gene expression in microalgae. We are currently seeking post-doctoral candidates with an interest in synthetic biology or metabolic engineering in microalgae, or in transcription and gene silencing mechanisms.	jaeseong.yang@cragenomica.es https://www.cragenomica.es/research-groups/computational-and-synthetic-biology
Jordi Garcia-Mas and Marta Pujol	Genetic dissection of climacteric fruit ripening in melon. We are interested in performing epigenomic studies (DNA methylation and histone modification) in CRISPR/Cas9 knock-out mutants already obtained in two master transcription factors, where climacteric ripening has been abolished. Preliminary data suggest that one of the transcription factors regulates chromatin remodelling in the transition between fruit growth and fruit ripening.	jordi.garcia@cragenomica.es marta.pujol@cragenomica.es https://www.cragenomica.es/research-groups/genetics-and-genomics-vegetable-crops
José Luis Riechmann	Peptides play multiple roles in plants, controlling development and growth or affecting stress responses. However, the genome-wide coding potential of short open reading frames in eukaryotes has been underestimated and overlooked, and the plant peptidome is still largely uncharacterized. We are interested in defining the plant peptidome and in the identification of novel peptides potentially involved in developmental processes, using <i>Arabidopsis</i> flower/inflorescence development and legumes as our experimental systems, to eventually develop peptides as a tool for sustainable agriculture.	joseluis.niechmann@cragenomica.es https://www.cragenomica.es/research-groups/gene-regulatory-networks-plant-development
Josep M ^a Casacuberta	Our research group studies the structure and the evolution of plant genomes. We are investigating the impact that genome structural variation have in phenotypic variation and we are particularly interested in the regulation and impact of transposable elements. We are currently working in capturing the structural variability of crop species in pangenomes, connect structural variability with transcriptional variation, and understanding the molecular determinants of retrotransposon integration in plant genomes. We use a variety of approaches and tools spanning from bioinformatics to molecular biology and biochemistry.	josep.casacuberta@cragenomica.es https://www.cragenomica.es/research-groups/structure-and-evolution-plant-genomes
Josep M ^a Folch	This project will integrate different OMICs to study energy metabolism and immunity in pigs, identifying regulatory gene networks, genes and genetic variants. The main aim is to improve animal disease resistance, production performance, and product quality while maintaining the sustainability of production systems and reducing antibiotic resistance.	josepmaria.folch@cragenomica.es https://www.cragenomica.es/research-groups/animal-genomics
Julia Qüesta	Our lab studies novel epigenetic mechanisms underlying plant developmental transitions and rendering resilience to changing climates. We focus on the role of long non-coding (lncRNAs) and the VAL/Polycomb Repressive Complex system in regulating <i>Arabidopsis</i> development. Furthermore, we are characterizing the epigenomic landscape modulating plant responses to cold temperatures. To this end, we combine innovative methodologies including CRISPR, single molecule imaging, proteomics, transcriptomics and epigenomics.	julia.questa@cragenomica.es https://www.cragenomica.es/research-groups/epigenetics-and-plant-development
L. Maria Lois	SUMO conjugation to proteins is essential during seed development and modulates agronomic traits, such as seed dormancy. Our group is interested in elucidating novel molecular mechanisms involved in SUMO homeostasis with implications in plant evolution and crop productivity.	maria.lois@cragenomica.es https://www.cragenomica.es/research-groups/protein-regulation-development-and-stress

Laura R. Botigué	Laura Botigué is interested in the study of genome evolution during plant domestication and cultivation history. She uses population genetics theory and in modern and ancient DNA to unravel the events and adaptive processes that shaped the genetic variability of modern crops and identify the lost variability that could have agronomic interest. She also studies population structure in crop wild relatives to identify the main contributors of the domestication process.	laura.botigue@cragenomica.es https://www.cragenomica.es/research-groups/genomics-ancient-crops-and-domestication
Marc Valls	Genes controlling the fitness of the plant pathogen <i>R. solanacearum</i> inside and outside the plant host: <i>Ralstonia solanacearum</i> is an emerging plant pathogen that causes major losses in agriculture. We will decipher the genes that are essential for pathogen survival in the soil microbiome and for adaptation to the plant. We will use global gene expression studies combined with synthetic microbiome communities (syncoms) to understand key genes used by the pathogen to complete its life cycle, which may identify targets to control the bacterial wilt disease on crops.	marc.valls@cragenomica.es https://www.cragenomica.es/research-groups/bacterial-plant-diseases-and-plant-cell-death
Marcel Amills	The CAPRAGENE project focuses on the identification of mutations with potential causal effects on goat dairy and health phenotypes by combining whole-genome sequencing of 100 bucks, imputation to 1,400 goats with 50K chip data, and fine mapping of potential causal mutations with Bayesian methods. Moreover, we also expect to identify copy number variation (CNV) segregating in the 1,400 goats and to carry out association studies between selected CNVs and dairy and health phenotypes, thus providing an unprecedented view about the genomic architecture of traits of economic interest in dairy goats.	marcel.amills@cragenomica.es https://www.cragenomica.es/research-groups/animal-genomics
María José Aranzana	The group of Rosaceae Genetics and genomics at Crag works in close collaboration with the apple breeding program at IRTA, developing molecular tools to increase breeding efficiency. We offer a postdoctoral position to establish a methodology for CRISPR-Cas9-based gene editing apple at Crag, with the main objective of gene validation and development of novel genetic resources for breeding. The project will be in close collaboration with Mickael Malnoy at FEM (Fondazione Edmund Mach, Italy), with demonstrated experience in cis-genic and gene edit modification in apple. A secondment at FEM is planned.	mariajose.aranzana@cragenomica.es https://www.cragenomica.es/research-groups/rosaceae-genetics-and-genomics
Nicolas Bologna	DICER-LIKE1 (DCL1) plays a central role in plant miRNA biogenesis, however, its dsRNA substrates have never been directly isolated. By point mutations in their RNaseIII domains, we generated catalytically inactive DCL1. RNA sequencing of DCL1c1 IP allowed us to detect a novel set of DCL1 RNA substrates generated from transposable elements, in addition to miRNA precursors. As a part of this research line, in collaboration with Dr. Yiliang Ding (JIC, UK), the goal of the project is to determine the in vivo single molecule secondary structures and characterize the biological roles of all regions interacting with DCL1.	nicolas.bologna@cragenomica.es https://www.cragenomica.es/research-groups/molecular-biology
Paloma Mas	Our lab focuses on understanding how plants can measure time and use this measurement for improved growth development and responses to stresses such as drought and heat. We propose to use novel gene-editing strategies to specifically manipulate the circadian system in order to obtain plants that are resistant to drought and heat.	paloma.mas@cragenomica.es https://www.cragenomica.es/research-groups/molecular-mechanisms-circadian-clock-function
Robertas Ursache	Our research is focused on uncovering the mechanisms of cell wall remodelling and developing new tools for better plant adaptation. The proposed project aims to create an improved plant gene targeting approach to modulate the activity of secondary cell wall remodelling enzymes. The research will involve both the development of synthetic biology tools and the behavioural analysis of cell wall remodelling genes in native genomic backgrounds using <i>Arabidopsis thaliana</i> as a model, with the goal of adapting the technology to crop species.	robertas.ursache@cragenomica.es https://www.cragenomica.es/research-groups/plant-cell-wall-remodeling-and-adaptation
Salomé Prat	Potato tubers differentiate from the subapical region of underground branches or stolons. Although it is widely accepted that formation of these organs involves a developmental process that is unrelated to formation of storage roots, our preliminary data indicate that both shoot- and root-derived organs originate from the vascular meristem. The proposal aims at using scRNA-Seq to unveil the regulatory pathways switching the pre-set xylem differentiation pathway into a storage parenchyma identity.	salome.prat@cragenomica.es https://www.cragenomica.es/research-groups/light-and-temperature-control-plant-development
Sebastián Ramos-Onsins	The team is focused on (i) the Development of Population statistics and methods to measure the levels and patterns of diversity in domestic and wild diploid and polyploid species; (ii) Development of bioinformatic tools for the scientific community interested in variability studies, and (iii) Genome-wide studies of empirical data, focused on understanding the adaptation process under changes in environmental (domestication, climate change) or genomic (polyploidization) contexts.	sebastian.ramos@cragenomica.es https://www.cragenomica.es/research-groups/statistical-and-population-genomics
Soraya Pelaz	Plants as sessile organisms must maximize their chances to survive adversities by reprogramming their development for adaptation to environmental changes. We aim to deeply explore the potential role of RAV genes on adaptation to environmental conditions, including an evolutionary developmental approach, because tem mutants performed better than wild-types when exposed to abiotic stresses, indicating a key role for RAVs in adaptive growth.	soraya.pelaz@cragenomica.es https://www.cragenomica.es/research-groups/floral-induction-and-development