

2021 International CRAG “Severo Ochoa” PhD Program

The International “Severo Ochoa” PhD Program of the Centre for Research in Agricultural Genomics (CRAG) is advertising four PhD positions in its 2021 call. This is a four-year program beginning in mid 2022. Doctoral students enrolled in this program will obtain their PhD Degree from either the Autonomous University of Barcelona (UAB) or the University of Barcelona (UB). More information about the doctoral program at CRAG can be found here: <https://www.cragenomica.es/crag-phd-program>

If interested in applying to the International CRAG “Severo Ochoa” PhD Program, **please carefully read the Application requirements and procedure** and check out all **available projects**.

Application deadline is **Sunday October 3, 2021**. Shortlisted applicants will be interviewed during October 2021. Successful applicants will start their PhD projects in mid 2022.

This four-year PhD grant is funded by the “National Programme for the Promotion of Talent and its Employability 2021” from the Spanish Ministry of Science and Innovation.

Application requirements and procedure

Eligibility

1. The program is aimed at national and international students who have completed one of the following options by October 2021:

- studies that lead to an official Spanish (or from another country of the European Higher Education Area) university degree in Biology, Biochemistry, Biotechnology, or related areas and that have 300 credits (ECTS), of which at least 60 must correspond to master level.
- a degree in a non-Spanish university not adapted to the European Higher Education Area that gives access to doctoral studies in Biology, Biochemistry, Biotechnology or related areas.

2. Candidates are selected exclusively on merit, on the basis of their curriculum. Academic grades and the curriculum of applicants are evaluated, as well as reference letters and a motivation letter. No selection criteria for positive or negative discrimination are applied.

3. Applicants should have obtained a Bachelor degree after January 2018.

4. Candidates cannot be in possession of a PhD Degree.

5. Candidates cannot have been hired as predoctoral students for more than 12 months before the start of the CRAG “Severo Ochoa” PhD Program

6. Candidates cannot have started a pre-doctoral fellowship funded by the Spanish “Plan Estatal de Investigación, Desarrollo e Innovación Tecnológica” or any previous “Plan Nacional”.

How to apply

Applicants should complete and submit the on-line application through [Cragjobs](#).

Applicants will be asked to upload the following documents:

- Curriculum vitae
- A motivation letter, including a brief summary of work experience and a statement of research interests and career goals (2 pages maximum).
- A scanned copy of the student's certified Academic Record, including a detailed record of study / transcript (a list of attended courses and corresponding grades): these documents must show the grades attained in exam periods.
- Copy of passport (international applicants only).
- Any additional files considered relevant to the application, but please only provide documents that are important to support it. Do not overload the application with certificates and documents of lesser significance.

In addition, applicants must ensure the submission of two reference letters from university lecturers or scientists with whom the applicant has studied or worked. Letters should be sent directly by the referees to PhDprogram@cragenomica.es, and should also be received by the application deadline, **October 3, 2021**. Only letters with official letterhead and signature will be accepted. Candidates are responsible for ensuring that referees submit these letters, and should consider that referees may need some time to prepare and send their letters within the deadline. Applications without reference letters will not be considered.

Please [download](#) referee request.

The doctoral program is in English. Therefore, a good knowledge of English is absolutely required. We encourage candidates to support the application with scores of internationally valid language exams like TOEFL or other tests. However, they are not mandatory: a verifiable education in English, or a reasonably long stay in an English speaking country are also convincing.

In the motivation letter, **applicants should indicate up to two research projects in which they would like to work, in order of preference** (see **Available Projects**, below). Moreover, if candidates have a particular interest in any one of these projects, they should also indicate it. More information on the research activities of each group can be found at Crag website.

Applicants must submit information in English (CV, and motivation letter including summary of work experience). If the certified academic records are not in English, Catalan or Spanish, applicants must also attach a translation in one of these languages.

Applicants must upload all the required documents as **PDF files of less than 10MB**.

Please note that we can only consider applications that are complete.

Selection procedure

Applications will be reviewed through a selection process involving CRAG group leaders, including the Principal Investigators that will host the fellows. Students are preselected according to their written application, grades, and reference letters.

Short-listed candidates will be interviewed during October 2021. Candidates who are accepted for the program will be notified by email shortly after the interview period. These PhD positions are funded by the Spanish Ministry of Science and Innovation (MICIU) and CRAG. CRAG will assist the selected candidates to submit the required documents at the Spanish MICIU website in end October/November 2021. Applicants who have not been successful but have received a positive evaluation will be put on a waiting list to cover possible candidate withdrawals and future positions.

Available Projects

CEX2019-000902-S-21-1 – Improving potato adaptation to climate change via the miR156/miR319 network. (IMPACC)

Principal Investigator: **Ignacio Rubio-Somoza and Salomé Prat**

Micro RNAs (miRNAs) are core elements within the genetic programs that orchestrate plant development and adaptation. Thus, miRNAs have been pointed out as key targets for rational intervention of those programs in order to achieve plant varieties with better performance upon different stresses (i.e. climate change). In plants, miRNAs tend to regulate the expression of transcription factors (TFs) that in turn can engage in common regulatory complexes that govern the expression of common downstream genes. In order to understand what are the processes controlled by miRNA-TF pairs in different organs (root and shoot) from *Arabidopsis thaliana*, we have undertaken a systems biology strategy encompassing RNA- and ChIP-seq approaches, among others. Preliminary results suggest that some of those interacting TFs might regulate sugar metabolism and sink to source transport. On the other hand, miRNAs regulating those TFs have been linked to the regulation of different responses to temperature and light condition changes. Those miRNA-TF pairs are conserved in other plant species, such potato. The topic of this project will be to transfer the knowledge obtained in a model system such as *Arabidopsis* to an important crop such as potato, in order to obtain varieties that cope better with climate change.

CEX2019-000902-S-21-2 – Genetic, molecular and metabolic basis for the links between ethylene synthesis, aroma volatiles and respiration during melon fruit ripening

Principal Investigator: **Jordi Garcia-Mas**

Fleshy fruits are classified into climacteric and non-climacteric depending on their respiratory profile as well as the manner in which they produce ethylene during ripening. Melon has been proposed as an alternative model to understand fruit ripening due to the coexistence of climacteric and non-climacteric varieties. Several QTLs controlling ripening behaviour have been described in melon segregating populations, and the combination of three QTLs involved in ethylene production modulates fruit ripening traits such as ethylene and aroma production. Among aroma constituents, volatile compounds derived from amino acids are major contributors to the unique aroma of melons and branched-chain amino acids (BCAAs) catabolism is tightly linked to mitochondrial metabolism and volatiles production depending on the ripening stage. However, the metabolic links to mitochondrial metabolism remain to be explored and could be a suitable target for metabolic engineering to favour carbon flux from primary precursors to melon volatiles biosynthesis. In plants, mitochondrial respiration is characterized by possessing

alternative respiratory pathways (ARPs) in addition to the classical energy-producing pathway, and ARPs have been suggested to play a crucial role in mediating cross-talk between ethylene response, carbon metabolism, ATP production, and ROS signalling during climacteric ripening. We propose to study ethylene and volatiles synthesis in parallel to respiratory metabolism during fruit ripening in recently developed pyramided introgression lines carrying ethylene related QTLs, and to generate CRISPR-CAS9 melon mutants in candidate genes to evaluate ripening-related traits.

Selected publications:

1. Mayobre C, Pereira L, Eltahiri A, Bar E, Lewinsohn E, Garcia-Mas J, Pujol M (2021). Genetic dissection of aroma biosynthesis in melon and its relationship with climacteric ripening. *Food Chemistry*, <https://doi.org/10.1016/j.foodchem.2021.129484>.
2. Pereira L, Santo Domingo M, Ruggieri V, Argyris J, Phillips MA, Zhao G, Lian Q, Xu Y, He Y, Huang S, Pujol M, Garcia-Mas J (2020). Genetic dissection of climacteric fruit ripening in a melon population segregating for ripening behavior. *Horticulture research* 7:1-18.
3. Florez-Sarasa I, Obata T, Fernandez Del-Saz NS, Reichheld JP, Meyer EH, Rodriguez-Concepción M, Ribas-Carbo M, Fernie AR (2019). The Lack of Mitochondrial Thioredoxin TRXo1 Affects In Vivo Alternative Oxidase Activity and Carbon Metabolism under Different Light Conditions. *Plant and Cell Physiology* 60: 2369-2381.
4. Pereira L, Ruggieri V, Pérez S, Alexiou KG, Fernandez M, Jahrman T, Pujol M, Garcia-Mas J (2018). QTL mapping of melon fruit quality traits using a high-density GBS-based genetic map. *BMC Plant Biology* 16:324.
5. Pereira L, Pujol M, Garcia-Mas J, Phillips MA (2017). Non-invasive quantification of ethylene in attached fruit headspace at 1 p.p.b. by gas chromatography–mass spectrometry. *The Plant Journal* 91:172-183.

CEX2019-000902-S-21-3 – Target specific insertion of LTR retrotransposons for plant breeding

Investigator(s): **Josep M. Casacuberta**

Transposable Elements (TEs) are mobile genetic elements present in the genome of virtually all organisms. TEs have played a major role in evolution, and in particular in that of crops (Lisch, 2013; Olsen & Wendel, 2013). In our lab, we are interested in studying the dynamics of TEs and their impact on crop evolution, as our recent work on melon (Sanseverino et al., 2015; Morata et al., 2018) and almond (Alioto et al., 2020) illustrates. The impact of TEs depends greatly on their insertion specificity. Some TEs, such as the tobacco retrotransposons Tnt1, are known to preferentially insert in gene regions (Vives et al., 2016), and it has been proposed that LTR retrotransposons (LTR-RTs) may target stress-responsive genes (Quadrona et al., 2019), which suggests a particularly important impact of TEs in the evolution of stress responses. However, different LTR-RT families show different genome distribution, and very little is known on how they target genome sites for integration. In recent analyses of the TE dynamics in *Physcomitrium patens* (Vendrell-Mir et al., 2020) and rice (Castanera et al., 2021) we have been able to carefully analyze TE distribution, taking into account the confounding effect of selection that cleans away TE insertions from genic regions. Interestingly, we have identified LTR-RT families showing very different target site preferences while being phylogenetically very closely related. A detailed analysis of the integrases of these LTR-RTs has allowed us to identify a short variable region that could be at the origin of LTR RT target specificity. This region is located in the C-terminal domain of the integrase, which has been recently shown in different yeast LTR-RTs to play a role in protein-protein interactions and target selection (Asif-Laidin et al., 2020). In this project we propose to study the molecular determinants of LTR retrotransposon insertion specificity, with a particular focus on regions of the retrotransposon integrase that may participate in the targeting of these elements.

Selected publications:

1. Alioto T, Alexiou KG, Bardil A, Barteri F, Castanera R, Cruz F, Dhingra A, Duval H, Fernández i Martí Á, Frias L, et al. 2020. Transposons played a major role in the diversification between the closely related almond and peach genomes: results from the almond genome sequence. *Plant Journal* 101: 455–472.
2. Asif-Laidin A, Conesa C, Bonnet A, Grison C, Adhya I, Menouni R, Fayol H, Palmic N, Acker J, Lesage P. 2020. A small targeting domain in Ty1 integrase is sufficient to direct retrotransposon integration upstream of tRNA genes. *EMBO Journal* 39: e104337.
3. Castanera R, Vendrell-Mir P, Bardil A, Carpentier MC, Panaud O, Casacuberta JM. 2021. The amplification dynamics of MITEs and their impact on rice trait variability. *Plant J*.
4. Morata J, Tormo M, Alexiou KG, Vives C, Ramos-Onsins SE, Garcia-Mas J, Casacuberta JM. 2018. The evolutionary consequences of transposon-related pericentromer expansion in melon. *Genome Biology and Evolution* 10: 1584–1595.
5. Vendrell-Mir P, López-Obando M, Nogué F, Casacuberta JM. 2020. Different Families of Retrotransposons and DNA Transposons Are Actively Transcribed and May Have Transposed Recently in *Physcomitrium* (*Physcomitrella*) patens. *Frontiers in Plant Science* 11: 1274.

CEX2019-000902-S-21-4 – Evolution of light-stress responses in plants.

Investigator(s): Ivan Reyna

A central question in plant biology is how plants sense and cope with different light conditions across their lifecycle. While light deficiency can reduce the levels of photosynthesis, too much light irradiance can also inhibit the photosynthetic capacity when parts of the photosynthetic machinery are damaged and not repaired fast enough. Photosynthetic organisms have evolved different mechanisms to monitor and respond to light stress. Some of these mechanisms are ancestral to land plants, likely favouring the movement of chlorophytes to shallow waters and the subsequent adaptation to terrestrial living. Despite this level of conservation, light stress responses are different among plant species, suggesting the downstream gene regulatory networks have evolved dynamically across many lineages. Our group is interested in understanding how global re-arrangements of gene regulatory networks have shaped the evolution of photosynthesis in plants; more specifically, the adaptation of the photosynthetic machinery to different light conditions, and how can we use this knowledge as a principle for engineering more resilient crops. For that end, the laboratory uses a variety of genomics, bioinformatics, phenomics and synthetic biology tools.

Selected publications:

1. Burgess, S. J*, **Reyna-Llorens, I***, Stevenson, S. R., Singh, P., Jaeger, K., & Hibberd, J. (2019). Genome-wide transcription factor binding in leaves from C3 and C4 grasses. *The Plant Cell*.
2. **Reyna-Llorens, I.**, Burgess, S.J., Reeves, G., Singh, P., Stevenson, S.R., Williams, B.P., Stanley, S. and Hibberd, J.M., 2018. Ancient duons may underpin spatial patterning of gene expression in C4 leaves. *Proceedings of the National Academy of Sciences*, 115(8), pp.1931-1936.
3. Yu, Z., Boehm, C. R., Hibberd, J. M., Abell, C., Haseloff, J., Burgess, S. J., & **Reyna-Llorens, I***. (2018). Droplet-based microfluidic analysis and screening of single plant cells. *PLoS ONE* 13(5): e0196810. <https://doi.org/10.1371/journal.pone.0196810>.
4. **Reyna-Llorens, I.**, & Hibberd, J. M. (2017). Recruitment of pre-existing networks during the evolution of C₄ photosynthesis. *Philosophical Transactions of the Royal Society B*, 372(1730), 20160386.
5. Xiong, H., Hua L., Reyna-Llorens, I., Shi, Y., Chen M., Smirnov, N., Kromdijk, J., Hibberd, J., (2021). Photosynthesis-independent production of reactive oxygen species in the rice bundle sheath during high light is mediated by NADPH oxidase. *Proceedings of the National Academy of Sciences*. 118(25) e2022702118. <https://doi.org/10.1073/pnas.2022702118>.