





DEADLINE EXTENDED!!!

2019 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 for 2020. This is a four-year program beginning in early 2020. 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: <u>https://www.cragenomica.es/training/phd-programme</u>

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 **Monday July 15, 2019.** Shortlisted applicants will be interviewed during summer 2019. Successful applicants will start their PhD projects in early 2020.

This four-year PhD grant is funded by the "National Programme for the Promotion of Talent and its Employability 2019" from the Spanish Ministry of Economy and Competitiveness.

Application requirements and procedure

Eligibility:

1. The program is aimed at international students who have completed one of the following options by September 2019:

- 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 2016.

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 <u>CRAGjobs</u>.

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, **July 15, 2019.** 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 <u>download</u> 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 summer 2019. 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 Economy and Competitiveness (MINECO) and CRAG. CRAG will assist the selected candidates to submit the required documents at the Spanish MINECO website in September-October 2019. Applicants who have not been successful but have received a positive evaluation will be put on a waiting list to cover possible renunciations and future positions.

Available Projects

2019 CRAG SO – 1: The cell wall keeps the rhythm to modulate drought responses in maize Principal Investigator: Paloma Mas & David Caparrós-Ruiz

Climate change, and particularly drought, represents the main environmental stress limiting agricultural crop productivity. Maize plants are the highest produced crop worldwide and water deficit negatively affect their growth and productivity (1). Over the last years, the group of D. Caparrós-Ruiz has identified genes and new molecular mechanisms that participate in the production of secondary cell wall (SCW), which is clearly affected by abiotic stresses such as drought (2). Previous studies in the laboratory of P. Mas have also demonstrated that in Arabidopsis thaliana, the circadian clock controls responses to drought (3). Furthermore, preliminary studies also indicate that miss-expression of clock components alters the expression of key SCW genes. Thus, the circadian clock is an ideal starting point to elucidate the main determinants involved in drought responses for biotechnological applications (4, 5). In fact, studies with maize plants grown under environmental stress conditions have shown that maize circadian clock genes closely cluster together with the most enriched networks of lignin and cell wall genes, suggesting a possible connection of the circadian clock with lignin and cell wall genes in response to stress in maize. Based on these data, this PhD project proposes to define the circadian clock function controlling lignin biosynthesis under drought conditions in maize. We will use state-of-the-art technologies including genome editing strategies to examine the cellular specificity of both the clock and SCW gene networks. We will determine how circadian alterations of SCW govern the resistance of maize plants to drought. This is highly relevant to ensure food security for the increasing population.

References

¹Tardieu et al. Plant Physiology 164, 1628-1635 (2014), ²Barnes et al. Molecular Plant 11, 31-46 (2018), ³Legnaioli et al. EMBO J 28, 3745-3757 (2009). ⁴Bendix et al. Molecular Plant 8, 1135-1152 (2015), ⁵Seo et al. Trends in Plant Science 20, 230-237 (2015)

2019 CRAG SO – 2: Computational and biochemical approaches for the analysis of LRR-RLKS involved in peach fruit shape

Principal Investigator: Maria José Aranzana & Ana I. Caño-Delgado

Peach fruit shape is one of the fruit traits highly linked to consumer acceptancy having a great agroeconomic impact. Peaches may have round, flat and intermediate shape like ovate or elliptic. Recent analyses in peach conducted by the group of Dr. Aranzana have identified possible polymorphisms in five homologous LRR-RLK genes that cluster together in the flat shape locus *S* (in chromosome 6), being one of them (Prupe.6G281100m; orthologous to Brassinosteroid insensitive 1-associated receptor kinase (*BAK1*)) a strong candidate for the flat shape¹. The present hypothesis is that some of these LRR-RLK receptors signaling mediate fruit shapes. By identifying the causal polymorphisms of different fruit shapes and validating the role of these RLKs proteins in this trait will not only have a high scientific impact but also of application in breeding programs. The laboratory of Dr. Caño-Delgado has an international reputation in the study of the role Brassinosteroid (BR) signal pathway in plant development and adaptation in plants. Plants perceived BRs by the receptor kinase Brassinosteroid-insensitive 1 like family of receptors (*BRI1*-like), that





dimerizes with *BAK1* to prompt BR signal transduction². By using structural bioinformatics and biochemistry, the lab of Dr. Caño-Delgado is analyzing and modeling protein-protein interactions, as well as predicting protein binding sites using Arabidopsis and Sorghum as model species. This PhD project aims at implementing such approach to investigate how LRR-RLK of the S locus may dimerize participating in signaling mechanisms during fruit development driving differential fruit shapes and will improve our understanding of LRR-RLK function regulating networks during fruit development. This PhD project will investigate the role of LRR-receptor kinases involved in peach fruit shape by combining structural, biochemical and genetic approaches.

References:

¹ López-Girona et al. 2017. Sci Rep. 7(1):6714; ² Kinoshita, Caño-Delgado, 2005. *Nature*. 433(7022):167-71.

2019 CRAG SO – 3: Characterization of ARGONAUTE proteins shuttling processes

Principal Investigator: Nicolas Bologna

In eukaryotes, non-coding RNA pathways are essential during developmental processes, adaptive responses to stress, general innate immune response to viruses and to preserve genomic integrity by controlling transposon activity. To unravel novel RNA functions is essential to understand the ARGONAUTE(AGO) proteins nuclear shuttling process mechanism. AGO proteins are the main responsible of RNA-induced silencing complexes (RISCs) recruiting small RNAs to interact with target mRNA or DNA in order to execute their final functions ranging from post-transcriptional gene silencing, transcriptional gene silencing, chromatin organization, splicing modulation to DNA repair [1]. Recently, we have described a previously unidentified Arabidopsis AGO1 nucleo-cytosolic shuttling pathway required for mature miRNA translocation and for miRNA-mediated silencing. We managed to show that Nt-Coil could serve as flexible platforms affecting AGO subcellular localization and its concomitant final role [2]. In the proposed project, we will perform a detailed analysis to describe features and machinery involved in the nuclear shuttling of ARGONAUTE proteins in Arabidopsis thaliana and Caenorhabditis elegans. The anticipated results will provide a crucial advance in the eukaryotic RNA pathways and gene regulation fields. We are looking for a highly motivated individual who has interest in RNA biochemistry, cell biology and bioinformatics, is fluent in English (both written and oral) and able to integrate in a running laboratory as a team-player. The project will involve collaborations in others laboratories (Cambridge, Zurich and/or Düsseldorf) consequently the student should be motivated to perform short-term stays (~ three months) abroad.

References:

¹Bologna et al. (2014) Annu Rev Plant Biol. 65:473-503; ²Bologna et al. (2018) Molecular Cell 69,709-19.

2019 CRAG SO – 4: Epigenetic control of plant development by VAL transcriptional repressors

Principal Investigator: Julia Qüesta

Plants undergo several phase transitions during their lifecycle; from gametophyte to sporophyte, embryo to vegetative, and vegetative to reproductive development. These transitions rely on the correct timing and sequence of gene expression patterns between individual developmental stages. Remarkably, as plants cannot move, phase transitions must be aligned to the environmental cues of the different seasons. Chromatin is key to control of gene regulation at the transcriptional level. Polycomb Repressive Complexes (PRCs) define chromatin inactive states to ensure the correct execution of the plant developmental program. Understanding how PRCs are recruited to their target genes has been subject of active research over the past years. In *Arabidopsis thaliana*, the VAL B3-domain proteins mediate PRC binding to a key floral repressor during winter to trigger epigenetic silencing, allowing the plants to flower in spring. However, VAL function is not restricted to the floral transition. Following germination, VAL promote seedling establishment by maintaining the embryonic program in the repressed state for the whole plant life. Interestingly, seedling growth and flowering are induced by distinct cues and yet VAL participate in both processes. The central aim of this PhD project is to elucidate how VAL proteins link environmental perception to epigenetic silencing of



key Arabidopsis developmental genes. To this end, epigenomic and transcriptomic approaches will be combined to dissect the VAL regulatory network. In parallel, a forward genetic screen will be conducted to identify the factors or cues that trigger VAL activity. Overall, this multidisciplinary project will advance our knowledge of chromatin silencing mechanisms in Arabidopsis, with findings likely to be broadly important in the development of crop species.

Suggested reading:

Qüesta et al Science (2016) 353:485-488; Csorba et al PNAS (2014) 111:16160–16165; Casal and Qüesta New Phytol (2018) 217:1029-1034.

