

2020 International CRAG “Severo Ochoa” PhD Program

The International “Severo Ochoa” PhD Program of the Centre for Research in Agricultural Genomics (CRAG) is advertising five PhD positions in its 2020 call. This is a four-year program beginning in mid 2021. 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/training/phd-programme>

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 **Tuesday September 15, 2020**. Shortlisted applicants will be interviewed during September 2020. Successful applicants will start their PhD projects in mid 2021.

This four-year PhD grant is funded by the “National Programme for the Promotion of Talent and its Employability 2020” from the Spanish Ministry of Science and Innovation.

Application requirements and procedure

Eligibility

1. The program is aimed at international students who have completed one of the following options by September 2020:
 - 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 2017.
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, **September 15, 2020**. 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.

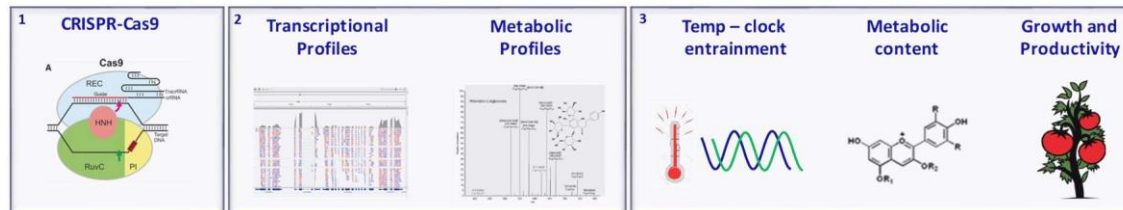
Short-listed candidates will be interviewed during September 2020. Candidates who are accepted for the program will be notified by email shortly after the interview period. These PhD positions are funded by the Spanish Ministry of Science and Innovation (MICIU) and CRAG. CRAG will assist the selected candidates to submit the required documents at the Spanish MICIU website in October 2020. 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

2020 CRAG SO – 1: Circadian timing for improved productivity and nutritional value of tomato plants

Principal Investigator: Paloma Mas

Nearly all photosensitive organisms have evolved a timekeeping mechanism or circadian clock that anticipates and responds to the 24-h environmental changes that occur during the day and night cycle. This timing mechanism works in resonance with the predictable and stressful environmental changes to generate rhythms in growth, physiology and metabolism. Studies in crops of agronomical interest have uncovered the possible beneficial role of the circadian clock on important agricultural traits such as reproduction, biomass or yield. With an annual production of >150 million tons, tomato is the most important fruit-bearing crop worldwide. Its rapid growth cycle and diploid genetics make it an ideal model for both vegetative and fruit development. Similar to other crops, extreme temperatures and water deficits exacerbated by global warming negatively affect tomato development and productivity. Changes in temperature also influences the plant circadian oscillator in a process known as entrainment. In *Arabidopsis thaliana*, light and temperature regulate a number of key clock components. This regulation affects clock entrainment and plant development, reproduction and metabolism in response to changes in photoperiod and temperature. Therefore, we aim to manipulate the circadian timing through down-regulation of essential clock components in order to obtain tomato genotypes with improved nutritional quality, growth and yield under changing temperatures.



Selected Publications:

1. Takahashi N, Hirata Y, Aihara K, Mas P. CELL (2015); 163:148.
2. Chen WW, Takahashi N, Hirata Y, Ronald J, Davis SJ, Nusinow DA, Kay SA, Mas P. NAT PLANTS (2020); 6:416.
3. Huang W, Pérez-García P, Pokhilko A, Millar AJ, Antoshechkin I, Riechmann JL, Mas P. SCIENCE (2012); 336:75.
4. Fung-Uceda J, Lee K, Seo PJ, Polyn S, De Veylder L, Mas P. DEV CELL (2018) 45:101

2020 CRAG SO – 2: REC-RIF Signaling for Photoprotection

Principal Investigator: Elena Monte

Under conditions of excess light, photosynthetic organisms switch modes from light harvesting to energy dissipation to prevent damage. This is especially relevant in a changing climate where photoprotection strategies are becoming increasingly critical. Damage prevention for optimal fitness under stressful light environments requires tight coordination of photoperception, photosynthesis and photoprotection, and the underlying mechanisms are just now beginning to be elucidated. The green algae *Chlamydomonas* is a simple cell type system that offers many advantages for these type of studies, as it has a photosynthetic apparatus that is very similar to that of vascular plants but instead responds uniformly upon exposure to excessive light intensities. Our laboratory is characterizing the signaling events involved in the photoprotection mechanisms, where convergence of light signaling and photoprotective responses is key. We use *Chlamydomonas* as the organism of choice due to its advantages that can accelerate our understanding of the fundamental principles of photoprotection and the worldwide interest in this algae from the industry given its wide range of applications. Through a bioinformatic search in the *Chlamydomonas* genome database, we have identified a novel REC-RIF module as an early signaling candidate for photoprotection under excess light conditions. Our next aim is to validate and characterize this REC-RIF signaling mechanism linking excess light perception to photoprotection responses.

Selected Publications:

1. Duan L, Ruiz-Sola MA, Couso A, Veciana N, Monte E. (2020). Red and blue light differentially impact retrograde signaling and photoprotection in rice. *Philos. Trans. Royal Society B.* 375: 20190402
2. Martín G, Rovira A, Veciana N, Soy J, Toledo-Ortiz G, Gommers CMM, Boix M, Henriques R, Minguet EG, Alabadi D, Halliday KJ, Leivar P, Monte E. (2018). *Current Biology* 28:311-318.
3. Martín G, Leivar P, Ludevid D, Tepperman JM, Quail PH, Monte E. (2016). *Nature Communications* 7:11431.
4. Soy J, Leivar P, González-Schain N, Martín G, Diaz C, Sentandreu M, Al-Sady B, Quail PH, Monte E. (2016). *Proc. Natl. Acad. Sci. U.S.A.* 113:4870-5.

2020 CRAG SO – 3: Computational analysis of ancient dog genomes to unravel archaic population structure

Principal Investigator: Laura Botigué

Dog evolutionary history has been the object of study of many researchers mostly for two reasons: Dogs were the first species to be domesticated, long before than any other animal or plant. They evolved from wolves during the Palaeolithic and have been close human companions ever since. Also, the vast amount of phenotypic variability that exists within dog breeds makes them a unique case study to understand genotype – phenotype associations, including genetic susceptibility to important human diseases. In spite of all the interest that dog population history sparks, little is known about the factors driving genetic diversity in dogs prior to the generation of breeds in the European continent, with evidence pointing to certain degree of population structure and possibly localized gene flow with neighboring regions. Our lab has gathered an outstanding collection of archaeological remains from Europe spanning from the Neolithic to the Middle Ages, and preliminary results have shown that all samples contain high endogenous DNA content. In an international collaboration we are going to analyze the genomic data from these samples together with publicly available data of ancient and modern canids to inquire about events shaping the genetic variability of dog populations through time. We will investigate population structure within the European continent, gene flow with neighboring regions and archaic dog-wolf hybridization. We will use bioinformatics, biostatistics and computational simulations to ultimately build a demographic model for dog populations in Europe in the past. This will allow us to better understand the origins of Victorian dog breeds and compare movements of dog populations with those from humans.

Suggested reading:

1. Botigué et al. Nature Communications (2017)
2. Frantz et al. Science (2016)

2020 CRAG SO – 4: Reverse and Forward engineering the Promoters of Microalgae

Principal Investigator: Jae-Seong Yang

Our group is interested in applying techniques ranging from modern machine learning and computational structural biology to high-throughput experimental methods such as NGS-based screening, to understand how genetic variation affects biological phenotypes (reverse engineering) and design DNA sequences that can generate desired phenotypes (forward engineering). Currently, we are studying how mutations affect heterologous gene expression and transcriptional regulation on microalgae.

Microalgae have a great biotechnological potential for the possibility to be used as bio-factories for the production of value-added compounds and the expression of human-recombinant proteins. In order to facilitate this possibility, we will generate and investigate a massive amount of synthetic promoters that mimic native cis-motif elements and structures of the endogenous promoters. The selected Ph.D. student will be supervised by Dr. Jae-Seong Yang and senior researchers in the group to apply and further develop the state-of-the-art of bioengineering techniques such as ELM-seq (Nat Commun. 2017 Aug 28;8(1):368) and rec-YnH (Nat Commun. 2018 Sep 14;9(1):3747). The PhD student will have opportunities to learn not only experimental synthetic biology but also computational biology. The results will significantly advance our knowledge on fundamental questions about transcriptional regulation in microalgae and will have a direct biotechnological application for industry. At the Institute's level, we are expecting to generate multiple collaborative projects. For example, the expression of plant proteins in microalgae can help their functional analysis, and we could apply promoter properties found in other plant systems.

Selected Publications:

1. Nat Commun. 2017 Aug 28; 8(1):368
2. Nat Commun. 2018 Sep 14; 9(1):3747

2020 CRAG SO – 5: ELF3 regulation of temperature and salt stress responses

Principal Investigator: Salomé Prat

Warm temperatures, drought and salinity cause important crop losses worldwide, limiting the land usable for agriculture. As a result of global warming, the frequency of simultaneous occurrence of elevated temperatures and high salinity has sensibly increased in the Mediterranean area, which urges the need of developing new crops able to cope with these combined stresses. The endogenous clock is pivotal to plant's ability to acclimate to a changing environment, function of the clock ELF3 protein being recently linked to enhanced survival under high salinity. Drought, salt or ABA, all suppress enhanced elongation at warm temperatures, while *elf3* mutants are insensitive to this inhibitory effect. ELF3 integrates light and temperature cues to the entrainment of the clock and to balance growth- and stress-related responses. However, its molecular mechanism of action remains little understood. ELF3 activity is regulated by phyB and the E3 ligase COP1, and mathematical modelling of thermosensitive growth showed that COP1-dependent control of ELF3 activity is critical to temperature-induced elongation during the day. COP1 binds a VP peptide motif in its degradation targets, whereas related VP motifs in the phytochrome and cryptochrome photoreceptors were recently shown occupy the COP1 substrate-binding pocket and inhibit COP1 E3 ligase activity. Interestingly, ELF3 has, two such VP motifs and we aim here at investigate function

of these conserved motifs in ELF3 degradation and/or COP1 inhibition, and in the ELF3-dependent control of thermomorphogenic elongation and tolerance to salt-stress.