crag

BIANNUAL REPORT 2012-2013

From the director

Browsing through this on-line CRAG 2012-2013 Bi-Annual Report will provide you with a summary view of our activities and accomplishments during the period, and a snapshot of today's CRAG. Less apparent, though, is the distance that has been travelled since CRAG started as a much smaller "experiment", slightly over ten years ago: 2013 marked the tenth anniversary of the initial CSIC-IRTA consortium that, under the guidance of its founding director, Pere Puigdomènech, would later become CRAG, and that reached a milestone in 2011 when our facilities at the UAB campus were inaugurated.

The two years covered by this Report represented a period of change -and sometimes of stress and turmoil- for CRAG. They encompass the midst of an economic crisis that brought serious financial strains and that has had profound effects in the research enterprise in Spain and in our Center. They also coincided with the change in directorship at CRAG, which took place in early 2013, and with changes in CRAG's external Scientific Advisory Board. It is because of the efforts of all CRAG members during this period that we secured stability for the Center, and that we achieved the excellent research results reported here: in the Scientific Highlights and in the other sections, and adding up to 160 scientific articles (85% published in first quartile journals) and 26 PhD theses.

Among the changes that were implemented at CRAG in 2012 and 2013, a most prominent one was its reorganization into four scientific programs to further develop the interdisciplinary scientific mission and the inter-institutional nature of CRAG (these programs are: Plant Development and Signal Transduction, Plant Responses to Biotic and Abiotic Stress, Plant Metabolism and Metabolic Engineering, and Plant and Animal Genomics). As it enters its second decade, CRAG will continue to evolve and consolidate, maintaining its focus on conducting excellent science, translating discoveries for the benefit of society, training researchers and students, and engaging in the public dialogue about plant and animal research. Furthermore, whereas still managing the aftermath of the economic crisis, CRAG relies on providing opportunities for young scientists – a priority for the forthcoming years.

José Luis Riechmann

Melon genome sequence

A consortium led by CRAG scientists Pere Puigdomenech (CSIC) and Jordi García-Mas (IRTA), reported the genome sequence of melon (Cucumis melo), an important horticultural crop worldwide. Melon belongs to the cucurbitaceae family, which contains other species of high commercial interest such as cucumber (Cucumis sativus), watermelon (Citrulus lanatus) and zucchini (Cucurbita pepo). Diseases that affect them, such as the mosaic virus in the case of cucumber or fungi, can cause important losses.

A total of 375 Mb of the double-haploid melon line DHL92 were assembled into scaffolds that were anchored to 12 pseudochromosomes by using a SNP genetic map, and 27,427 protein-coding genes were predicted from the assembly. Analysis of the genome sequence did not show recent whole-genome duplications in the melon lineage since the known ancient eudicot gamma triplication. Data also suggested that transposon amplification around 2 My ago may explain the increased size of the melon genome (450 Mb) compared with the close relative cucumber (350 Mb). The genomes of cucumber and melon were compared, suggesting that chromosome fusions followed by rearrangements happened in the cucumber lineage. The DHL92 melon genome was also compared with that of its parental lines, the Piel de sapo line T111 and the Korean accession PI 161375, to estimate sequence variability in the species.

The availability of the genome sequence will allow the improvement of melon breeding strategies, by accelerating the discovery of the genes related with agronomically important traits such as fruit quality and disease resistance.

The research was performed in the framework of the MELONOMICS project, a public-private initiative that was launched in 2009. The genome sequence of melon was the first example of the sequencing of a eukaryote genome performed and coordinated in Spain.

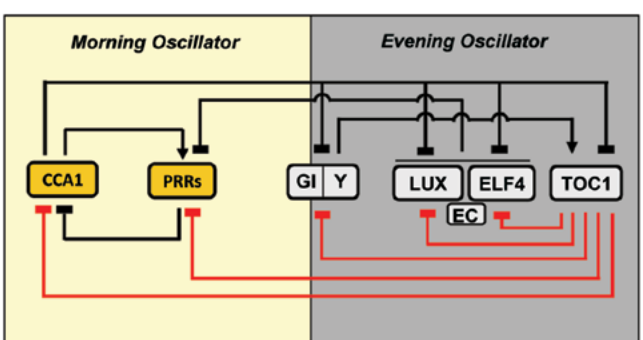
Circadian clock

The beat of time: molecular mechanisms of the plant circadian clock

Plants, as many other organisms, synchronize the timing of their physiology and development by using an endogenous mechanism called circadian clock. Perception of environmental changes during the day-night cycle is crucial for circadian function, which relies on transcriptional feedback loops at the core of a central oscillator.

However, deciphering the oscillator transcriptional regulatory code is a major challenge due to the interplay among clock activators and repressors, which are responsible for the generation of the loops. The team led by CSIC Investigator Paloma Mas has shown that the morning and evening oscillators in the small plant Arabidopsis thaliana are connected through the repressing activity of the key clock component known as TOC1. These results overturn the canonical, long-standing model of the plant circadian clock, in which TOC1 was presumed to be an activator of a reduced number of oscillator genes, not a general repressor of oscillator gene transcription, as has now been demonstrated. The studies were pioneer in using the ChIP-Seq technique to identify the target genes of TOC1. Biochemical, molecular and genetic analysis also allowed to define the regulatory network at the core of the clock in plants.

The team has also demonstrated that chromatin remodeling is a prevalent regulatory mechanism at the core of the clock. The functional properties of chromatin are modulated by various mechanisms, including, among others, posttranslational modifications of histones, incorporation of histone variants and DNA methylation. It has now been shown that the peak-to-trough circadian oscillation is paralleled by the sequential accumulation of different histone marks at the promoters of core clock genes. Mechanistically, histone methylation functions as a transition mark, modulating the progression from circadian activation to repression. Despite divergences in oscillator components, a chromatin-dependent mechanism of clock gene activation appears to be common to both plant and mammal circadian systems.

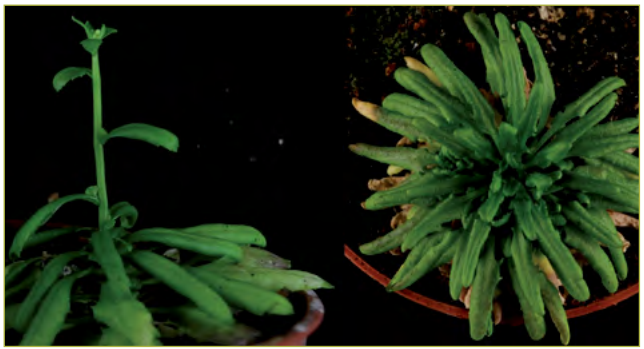


Flowering

New clues about the mechanism that inhibits early flowering in plants

Flowering is controlled by several genetic mechanisms that respond to external stimuli, including the length of day (photoperiod). The vast majority of plants flower and set fruits between spring and summer, when days are longer. Indeed, plants are capable of "differentiating" between those favorable conditions, long days, and unfavorable conditions, short days as in winter, and to respond accordingly by activating the appropriate mechanism.

FT protein is the main promoter of flowering when days are long, and it was known that FT is inhibited by the TEMPRANILLO genes, delaying flowering. In addition, It was also known that when days are unexpectedly shorter - what would happen, for example, if the plant is moved from one country to another and at the time of flowering, the plant finds fewer hours of light - the FT protein does not act, despite that plants need to bloom to perpetuate. In this case, plants have an "auxiliary" mechanism: it is the accumulation of phytohormones, gibberellins, which triggers flowering. However, the mechanisms involved in the regulation of the accumulation of these hormones remained unknown.



The team led by ICREA Research Professor Soraya Pelaz found that it is the same TEM genes that inhibit the synthesis of gibberellins. The results show that TEMPRANILLO genes control flowering both in unfavorable (short days) and favorable conditions (long days). Under adverse conditions, flowering is delayed to achieve the proper time for seed set. Even in favorable conditions, bloom must be adequately postponed for the plant to acquire the necessary reserves for flower and fruit formation. In both cases TEM avoids a precocious flowering.

TEM genes and their function were first discovered in 2008 by the same research team. Since then, TEM genes are being isolated and identified in numerous species, suggesting that this way of controlling flowering time is general to many plant species.

Brassinosteroids

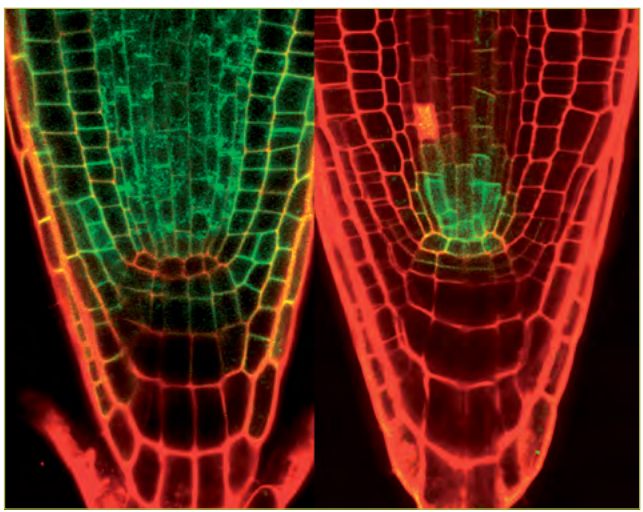
Different functional steroid hormone receptor complexes exist for specific cell types in plants

Plant steroids are called brassinosteroids (BRs) since they were discovered in the pollen of the plant Brassica napus. BRs are essential hormones that regulate plant growth and development, and they are able to regulate a myriad of biological processes such as cell elongation, cell division, cell differentiation, pollen viability, germination and flowering time, among others.

Despite the resemblance of BRs to animal steroids, which are perceived in the nucleus, plant steroid receptors are located at plasma cell membrane. BRI1 (BR insensitive 1) is the main BR receptor that binds the hormone and it is expressed within most cells of the root meristem (image, left). Additionally to BRI1, plants express other BR receptors, called BRL1 (BRI1-like 1) and BRL3 (BRI1-like 3), which specifically localize within the stem cells of the root meristem (image, right).

The group led by CSIC investigator Ana Caño-Delgado identified the BRL3 signalosome complex in planta and characterized its contribution to plant development. Immunoprecipitation and liquid chromatography followed by mass spectrometry of BRL3 receptors identify BRL1 and BAK1 (BRI1 associated kinase 1) proteins as part of the BRL3 signalosome.

The study has uncovered a novel role for the BRL3 signalosome complex in regulating cell division within the Arabidopsis primary root meristem. On one hand, the BRL3 complex promotes root length and division of the root stem cells (specifically, quiescent centre cells which normally display low-rate division) independently from the BRI1 receptor. On the other, the BRL3 complex regulates provascular stem cell division in a distinct manner than BRI1, which suggest that different BR complexes accomplish cell-type specialized functions.

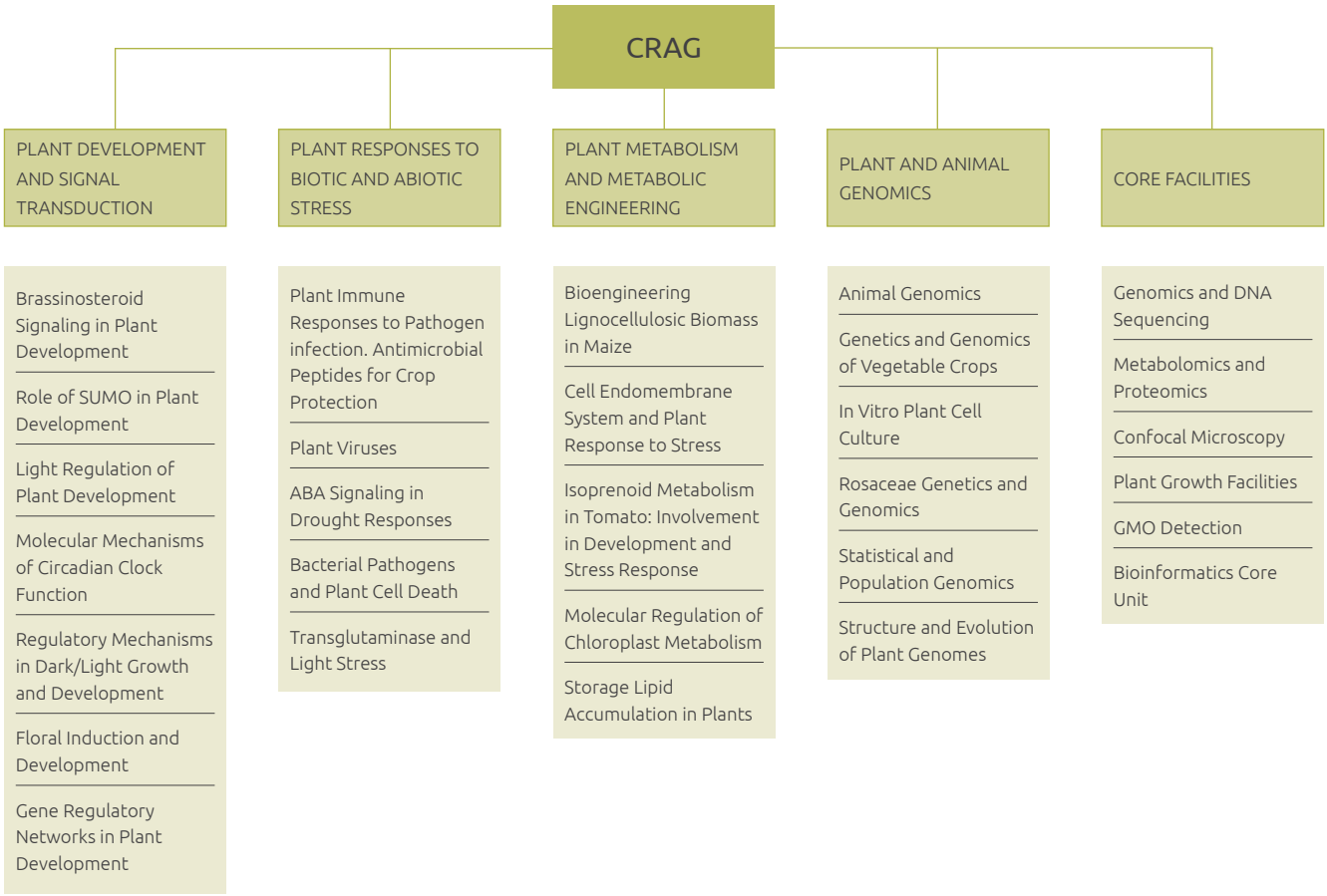


Isoprenoids

Chloroplasts, isoprenoids, and protein quality control

Chloroplasts are the main factory for the production of plant metabolites. Among them, isoprenoids are essential for photosynthesis and plant development, but they also have a great interest to the pharmaceutical and food industries. A team led by CSIC investigator Manuel Rodriguez-Concepción discovered that the activity of the main enzyme regulating the production of chloroplast isoprenoids (named DXS) depends on its interaction with J20, a co-chaperone protein. The work demonstrates that J20 recognizes inactive forms of DXS and transfers them to the molecular chaperone Hsp70. Upon interaction with Hsp70, the misfolded forms of DXS are either refolded back to their enzymatically active form or unfolded for their eventual degradation. This discovery opens the door to new strategies to enrich crops in isoprenoid metabolites of nutritional or industrial interest.

Research at CRAG



Personnel

2012

49 *Researchers*

64 *Predocs*

25 *Administration*

55 *Postdocs*

49 *Technicians*

2013

41 *Researchers*

53 *Predocs*

21 *Administration*

34 *Postdocs*

40 *Technicians*

6 *Career track fellows*

Funding

2012

Core funding
2,637,316.22
External funding
4,722,969.77
Investments
486,664.40
Total budget: 7,846,950.45

7,8 M€

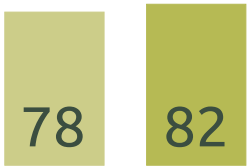
2013

Core funding
2,281,395.02
External funding
3,600,245.91
Investments
153,724.58
Total budget: 6,035,366.34

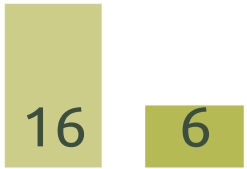
6 M€

Publications statistics

Articles

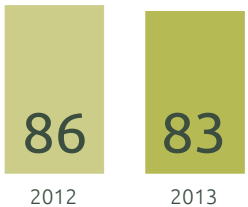


Books and book chapters

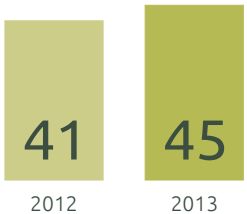


PhD Theses

Articles in 1st quartile journals (%)



Articles in 1st decile journals (%)



Awards

8

CRAG
Centre for Research
in Agricultural Genomics

Campus UAB / Edifici CRAG Bellaterra
Cerdanyola del Vallès, 08193 Barcelona
www.cragenomica.es

To access the full on-line report, please visit:
biannualreport2012-2013.cragenomica.es

CSIC IRTA UAB UB