**Summary of the current research and future directions**

Our research interest focuses on understanding the genetic and molecular mechanisms that control plant developmental transitions, and particularly, two processes with direct impact on crop yield, flowering initiation and seed germination/seedling establishment. Since epigenetic processes are key players in the regulation of plant development and chromatin represents the interphase mediating genome interaction with the environment, the characterization of chromatin-mediated regulatory processes is and will be a corner stone in our research.

Our future research directions are based on previous achievements of the group, and will continue to dissect the role of chromatin remodeling in the regulation of plant development,focusing on **the role of the histone acetyltransferase (HAT) complex NuA4 (NuA4-C) in the regulation of flowering time and other developmental processes in Arabidopsis** (Crevillen et al., 2019; Barrero-Gil et al., 2022; PID2019-104899GB-I00). Our results show that different NuA4-C subunits perform distinct functions in the flowering response to environmental cues such as photoperiod or ambient temperature. Also, mutants affected in particular subunits of NuA4-C display specific phenotypic alterations regarding other developmental traits or environmental responses. In the upcoming years we will keep on elucidating the molecular basis for these specific responses of NuA4-C subunits such as ING2, a flowering promoter under long days (LD) and short days (SD), EAF6, an activator of reproductive growth under SD, and EPL1B, required to induce flowering in low ambient temperature. Furthermore, we will extend the characterization of the two Arabidopsis *HAM* homologs using genomic approaches to further delve into the role of NuA4-C catalytic subunit in the control of plant development. Since HAM proteins are present in additional chromatin remodeling complexes, the comparative analysis with other subunits of this HAT complex will also shed light on NuA4-C-dependent and -independent roles of HAM proteins. Altogether, these analyses will enlighten the relevance of histone acetylation in the regulation of plant development.

Furthermore, our recent work revealed a **novel attenuation mechanism of stress responses during the flowering initiation** mediated by the MRG subunits of NuA4-C (Barrero-Gil et al., 2021). Under our CEPEI´s CHROPTIPLANT initiative and in collaboration with Dr. D. Jiang (IGDB-CAS, China), we are further exploring the basis for this epigenetic switch likely involved in the optimization of plant reproduction and fitness at the expense of costly responses to environmental challenges.

In addition, with the goal of **assisting the agrifood sector in developing crops better suited to withstand increasingly high temperatures**, we are analyzing plant developmental responses to warm ambient temperature in Brassica crops. Our previous analyses identified several differentially expressed genes in Brassica napus (oilseed rape, OSR) varieties displaying differential flowering responses to warmth (Abelenda et al., 2023). One of them, *MBD4*, encodes a novel chromatin remodeling factor induced in both OSR and Arabidopsis upon plant exposure to 28ºC. We are **functionally characterizing this factor that could mediate plant developmental responses to temperature through chromatin** **reorganization** (TED2021-132137B-C21). We are following similar approaches in *B. rapa* (turnips) (Del Olmo et al., 2019) and *B. oleracea* (cabbage, cauliflower) within an international consortium funded by the PRIMA project BrasExplor, focused on the wide exploration of genetic diversity in Brassica species for sustainable crop production.

Besides, we are interested in **understanding at the molecular level the effects that the exposure of mother plants to warm ambient temperature has on the performance of OSR seeds during germination and seedling establishment**, a crucial stage influencing crop yield, in the EpiSeedLink MSCA-Doctoral Network. Environmental conditions experienced by mother plants affect seed performance in the progeny, and chromatin remodeling processes are likely involved in this memory. Our research will follow up on these approaches to **identify molecular and epigenetic mechanisms underlying plant responses to temperature, with the overarching goal of contributing to enhance crop resilience to suboptimal environments.**

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**Relevant research milestones, technical contributions, or awards since 2019** (10 contributions)

1. The differential flowering time responses of OSR varieties to high ambient temperature is mediated through both H2A.Z-dependent and independent molecular mechanisms (Abelenda et al., 2023).

2. Histone H4 acetylation mediated by NuA4-C regulates chloroplast biogenesis coordinating the transcription of nuclear and plastid genomes during chloroplast development in Arabidopsis (Barrero-Gil et al., 2022).

3. An epigenetic switch operated by the NuA4-C MRG subunits attenuate abiotic stress responses during flowering initiation to optimize plant fitness and reproductive success (Barrero et al., 2021).

4. The Arabidopsis YAF9 subunits of NuA4-C modulate flowering time through NuA4-dependent H4 and H2A.Z histone acetylation, but not H2A.Z deposition, at *FLC* chromatin (Crevillén et al., 2019).

5. Participation in the international consortium BrasExplor that, funded by PRIMA EraNet, is focused on the wide exploration of genetic diversity in Brassica species for sustainable crop production.

6. Involvement in the EU MSCA-Doctoral Network EpiSeedLink consortium to explore epigenetic regulation of seed priming mechanisms to improve crop performance under threats caused by climate change.

7. International collaboration in the CEPEI´s CHROPTIPLANT initiative to explore the molecular basis of NuA4-C-mediated integration of stress signals and developmental programs in Arabidopsis plants.

8. Funding for young researchers granted through national (Atracción de Talento CAM, senior and junior; Juan de la Cierva, postdoctoral) and international (CSC-UPM predoctoral, CEPEI) programs.

9. PIs involvement in science management activities: JAJ, coordinator of the Biotechnology subarea of the Agencia Estatal de Investigación (AEI) Area 18: Biosciences and biotechnology; MP, INIA representative in EPSO, member of CBGP Internal Advisory Board.

10. Successful training of PhD fellows (three completed since 2019, and four currently undergoing in our group) and postdoctoral researchers (eight since 2019).