



BioISI - Biosystems & Integrative Sciences Institute

Functional analysis of DRIF, RAD and DIV genes in *Arabidopsis thaliana*

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Abstract / MSc thesis project proposal

The overall plant architecture, seedling development and flowering time are important determinants of the performance of crop plants. Understanding the molecular mechanisms underlying these major traits can help to optimize these features and enhance plant yield. Flower zygomorphy is a morphological trait that emerged in different independently evolutionary events, normally associated with specific plant-pollinators. In *Antirrhinum majus*, the flower zygomorphy requires the combined activity of four transcription factors: CYCLOIDEA (CYC), DICHOTOMA (DICH), RADIALIS (RAD) and DIVARICATA (DIV) [1-5]. Genetic and molecular studies have revealed that RAD acts downstream of CYC and antagonizes the activity of DIV in the dorsal region of the *Antirrhinum* flower by competing for a DIV-and-RAD-interacting factor (DRIF) [1, 2, 3, 6, 7, 8, 9]. A similar antagonistic action between RAD/DRIF/DIV homologs regulates different developmental processes in other species. Preliminary functional analysis of the DRIF genes in *Arabidopsis thaliana* showed that *DRIF3*, *DRIF4* and *DRIF5* are involved in seed germination, early seedling development in response to light and in the control of flowering time. The main objective of this thesis is to continue the study of the role of the *AtDRIFs*, *AtRADs* and *AtDIVs* in *Arabidopsis*.

Work Plan

During this project the following experiments will be performed:

- Obtain transgenic *Arabidopsis thaliana* plants overexpressing *AtDRIFs*, *AtRADs* and *AtDIVs*.
- Obtain *Arabidopsis thaliana* plants carrying *AtRAD* and *AtDIV* mutations.
- Analyze the phenotype of mutant plants by performing germination assays, apical hook measurements and flowering time assays.
- Analyze the subcellular localization of *AtDRIFs*, *AtRADs* and *AtDIVs* using a reporter gene.
- Analyse the expression of *AtDRIFs*, *AtRADs* and *AtDIVs* during plant development by RT-qPCR and in situ hybridization.
- Obtain new DRIF interaction partners using the yeast two-hybrid technique.

Bibliography:

1. Luo D. et al 1996 Nature 383, 794
2. Almeida J. et al 1997 Development 124, 1387
3. Luo D. et al 1999 Cell 99, 367
4. Galego L. & Almeida J. 2002 Genes Dev. 16, 880
5. Corley S.B. et al 2005 PNAS 102, 5068
6. Costa M.M.R. et al 2005 Development 132, 5093
7. Baxter C.E.L. et al 2007 Plant J. 52, 105
8. Raimundo J. et al 2013 Plant J. 75, 527
9. Raimundo J. et al. 2018 Mol. Biol. Evol. 35, 2873

Students selected for this project, after thesis registration, are eligible to apply to the BioISI Junior Programme (supporting 8 students with a 6-month Scholarship (BII), being the selection criterium the academic merit of the candidates.