Séminaire Biologie des Plantes

Les séminaires ont lieu sur le Campus Montpellier SupAgro/INRA de La Gaillarde (2, place P. Viala Montpellier)

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Linkage and association mapping of *Arabidopsis thaliana* flowering time in nature

Flowering time is a key life-history trait in the plant life cycle. Most studies to unravel the genetics of flowering time in *Arabidopsis thaliana* have been performed under greenhouse conditions. Here, we describe a study about the genetics of flowering time that differs from previous studies in two important ways: first, we measure flowering time in a more complex and ecologically realistic environment; and, second, we combine the advantages of genome-wide association (GWA) and traditional linkage (QTL) mapping. Our experiments involved phenotyping nearly 20,000 plants over 2 winters under field conditions, including 184 worldwide natural accessions genotyped for 216,509 SNPs and 4,366 RILs derived from 13 independent crosses chosen to maximize genetic and phenotypic diversity. Based on a photothermal time model, the flowering time variation scored in our field experiment was poorly correlated with the flowering time variation previously obtained under greenhouse conditions, reinforcing previous demonstrations of the importance of genotype by environment interactions in A. thaliana and the need to study adaptive variation under natural conditions. The use of 4,366 RILs provides great power for dissecting the genetic architecture of flowering time in A. thaliana under our specific field conditions. We describe more than 60 additive QTLs, all with relatively small to medium effects and organized in 5 major clusters. We show that QTL mapping increases our power to distinguish true from false associations in GWA mapping. QTL mapping also permits the identification of false negatives, that is, causative SNPs that are lost when applying GWA methods that control for population structure. Major genes underpinning flowering time in the greenhouse were not associated with flowering time in this study. Instead, we found a prevalence of genes involved in the regulation of the

plant circadian clock. Furthermore, we identified new genomic regions lacking obvious candidate genes.

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