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Oral Communication Abstract – 5.01

VARIATION IN GENOME STRUCTURE AND REPRODUCTIVE TRAITS BETWEEN ANNUAL AND PERENNIAL SPECIES

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The plant life-cycle varies tremendously among species. In many plant families, annual species have evolved from perennial progenitors. Annuals reproduce once in their life time producing high seed yields, whereas perennials live for many years and reproduce each year, but limit the extent of reproduction each year. We study how flowering is controlled by seasonal cues and how this contributes to the limitation of reproductive effort in perennials to ensure that they survive to reproduce in subsequent years. We focus on the Brassicaceae family, in which annual and perennial species have diverged many times. Using the phylogeny of this family, we perform genome comparisons to define changes that occur as annual species arise from their perennial progenitors. We use inter-species crosses, mutagenesis, natural genetic variation and reverse genetics based on CRISPR-cas9 to study the function of genes in the perennial species *Arabis alpina*. We have shown how evolution of orthologues of the MADS box transcription factor FLC can control the duration of flowering and the number of axillary branches that produce inflorescences. In addition, we have identified a regulatory module involving the SPL transcription factor SPL15 and the microRNA156 that plays a crucial role in determining the age at which the plant becomes sensitive to environmental cues that induce flowering. The talk will describe the genomics of divergence of annual and perennial, its application to studying inter-species introgression lines and some of the mechanisms that confer seasonal patterns of flowering in perennials and how these are significant in phenotypic variation among natural European populations.