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FUNCTIONAL CHARACTERISATION OF SHORT VEGETATIVE PHASE BY A CHROMATIN IMMUNO-PRECIPITATION SEQUENCING APPROACH

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In plants organs are formed post-embryonically from populations of undifferentiated cells called meristems. In flowering plants like Arabidopsis thaliana during the vegetative phase the primordia that derive from the shoot apical meristem (SAM) develop into leaves. The change to the subsequent generative phase is called floral transition, which is regulated by multiple flowering pathways that are controlled by environmental and endogenous cues. During the floral transition the SAM is transformed into an inflorescence meristem (IM). The Arabidopsis IM is an indeterminate meristem and develops in a spiral manner multiple determinate floral meristems (FMs) that produce a precise number of floral organs arranged in a whorled pattern.

SVP is a key MADS-box transcription factor for Arabidopsis development since it acts both during vegetative and reproductive phases where it plays different roles probably by interacting with different partners to regulate specific sets of target genes. In fact, whereas SVP functions as a repressor of floral transition during the vegetative phase, it works as floral meristem gene during reproductive phase.

Here we report the identification of genome wide binding sites of SVP using the ChIP-seq technology that consists in ultra-high throughput Solexa (Illumina) sequencing of DNA samples obtained by Chromatin Immune-Precipitation. We studied the binding behavior of SVP during two distinct developmental phases: the vegetative and reproductive phase. Furthermore, by combining the ChIP-seq data with tiling ATH microarray expression analysis and qRT pcr approach, helped us to identify subsets of genes that are directly regulated by SVP during the two distinct phases of development. Finally we compare the genome-wide direct target genes of SVP with that of FLC, a closely related transcription factor that also represses the transition to flowering and with that of AP1, a MADS-box factor which is, together with SVP, a key player during floral meristem development. We detect clear similarities and important differences in the direct target repertoires that are also tissue specific. This analysis allowed us to identify new pathways that are regulated by SVP in vegetative and reproductive tissues and to investigate the dynamics of genome wide interactions of a transcription factor during different phases of development.