

# CHARACTERIZATION OF *REM* GENES INVOLVED IN THE REPRODUCTIVE DEVELOPMENT OF *ARABIDOPSIS THALIANA*

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## Flowering and reproductive development

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## Abstract

The *REproductive Meristem (REM)* gene family encodes for transcription factors belonging to the B3 DNA binding domain superfamily and, even if this family of genes is widespread among both dicotyledons and monocotyledons species, not much it is known about their function.

In *Arabidopsis thaliana* this family is composed of 45 members, preferentially expressed during flower, ovule and seed development. Only a few members of this family have been functionally characterized: *VERNALIZATION1 (VRN1)* regulating flowering time and *VERDANDI (VDD)* together with *VALKYRIE (VAL)* control death of the receptive synergid cell in the female gametophyte.

We focused our attention on three homologous members of this family, *REM34*, *REM35* and *REM36*, which are expressed in the inflorescence meristem and, during flower development, in both female and male reproductive tissues.

To uncover their cryptic role, RNA interference lines for the simultaneously silencing of these three genes were analyzed. At the same time, a CRISPR/Cas9 approach was chosen in order to generate single and multiple mutants.

Both the RNAi lines and the CRISPR/Cas9 mutants showed an aberrant phyllotaxis and a higher rate of flower production. Moreover, the RNAi lines showed defects in both female and male. Both genes involved auxin biosynthesis and transportation were found to be downregulated in the RNAi background, suggesting a novel role for *REM34*, *REM35* and *REM36* in the control of auxin synthesis and/or signaling in *Arabidopsis thaliana*.