RUG8, a novel player in auxin-dependent stem cell specification and meristem patterning in *Arabidopsis* roots

A screen for Plasmodesmata mutants, based on *AtSUC2*p::*GFP* plants, revealed a mutation in a previously unknown gene that was named *REDUCED UNLOADING OF GFP8* (*RUG8*) gene based on the observed phenotype.

RUG8 encodes a putative, plant specific transcription factor, which is involved in stem cell specification and meristem patterning processes in the Arabidopsis root. Loss of this gene leads to an altered appearance of the quiescent center (QC), premature differentiated stem cells and premature elongated meristematic cells, in the *rug8* mutant background.

In line with these phenotypic differences, the mutant plants showed an altered auxin distribution in the root and to ectopic expression of *PINFORMED1* (*PIN1*). Our working hypothesis is that this ectopic *PIN1* expression causes the observed loss of the auxin maximum in the QC, which leads in turn to altered expression of auxin regulated genes like *WUSCHEL-RELATED HOMEOBOX5* (*WOX5*) and the *PLETHORA* (*PLT*) gene family. In addition, *rug8* mutants show patchy expression of *SCARECROW* (*SCR*), which leads to random, mostly periclinal cell divisions or supernumerary cell files in the ground tissue. These results indicate, that *RUG8* is a so far uncharacterized, new key-regulator of the meristem and an important factor for the auxin distribution in the root.

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