MICROSCOPY

Visualizing fate changes

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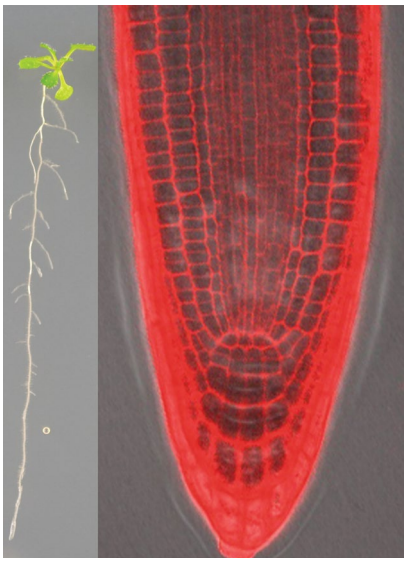

Credit: Ikram Blilou

Cell fate specification in plants largely relies on positional information conferred by cell-to-cell communications. The 'language' of cells involves small RNAs, peptides, hormones, and also mobile transcription factors. The best characterized system to study this process is the root tip system. A recent study from Ikram Blilou's group, Wageningen University and Research Centre, The Netherlands, and her collaborators reported visualization of specific interactions of a mobile transcription factor and its binding partners in different *Arabidopsis* root cells by FRET–FLIM (Förster resonance energy transfer measured by fluorescence lifetime microscopy).

FRET–FLIM allows for direct visualization of protein–protein interactions in live cells. In this study, the researchers used the technology to revisit the interactions between three important transcription factors in *Arabidopsis* root meristem, SHORT-ROOT (SHR), SCARECROW (SCR) and JACKDAW (JKD). FRET-based tagging of SHR, SCR and JKD did not interfere with the functionality of these proteins, and the functional tagged proteins showed distinct association patterns between different pairs in living *Arabidopsis* roots. The cell-specific quantification of in vivo FRET signals confirmed the known interplays between these important cell fate determinants. More importantly, the analysis provides new insights on how conformational changes of interacting transcription factors influence cell fate determination in roots.

Direct visualization of protein–protein interactions in multicellular organisms is challenging. This study showed an unprecedented advantage of implementing lifetime imaging technology to visualize protein–protein interactions in living multicellular organisms.

Lei Lei

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