



Mechanisms of phloem formation in plants

Department of Biological Sciences, Graduate School of Science

Professor Tatsuo Kakimoto

<https://researchmap.jp/read0079052?lang=en>

Assistant Professor Pingping Qian

<https://researchmap.jp/qianpingping2013?lang=en>



Abstract

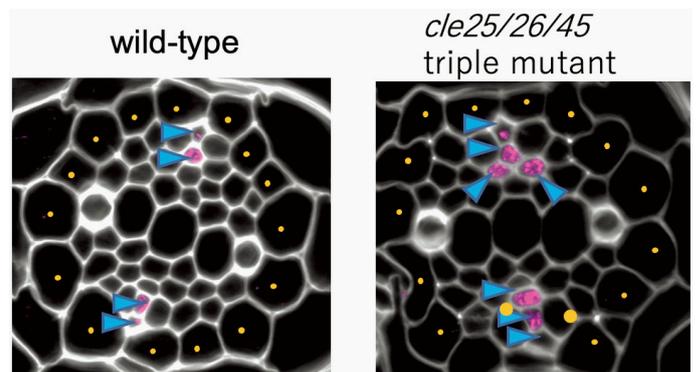
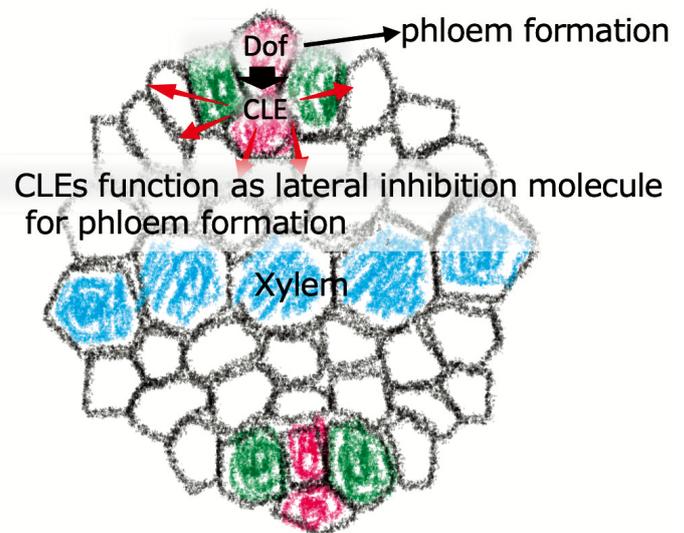
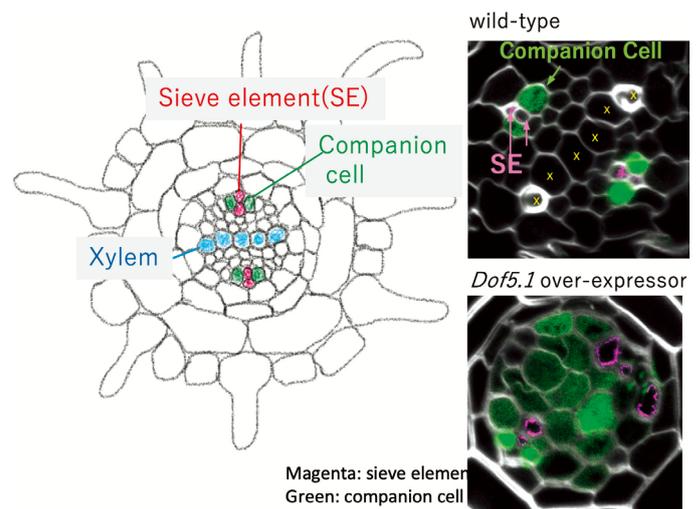
Phloem is an essential tissue for plants, transporting products of photosynthesis and other substances. However, the mechanisms controlling its formation were not well understood. We found that multiple Dof-type transcription factors expressed in phloem precursor cells are necessary and sufficient to form phloem cells. Phloem Dofs not only induce genes necessary for phloem formation, but also induce secretory peptide molecules CLE25, 26, and 45, which inhibit the formation of constituent cells of the phloem. We revealed that CLE25, 26, 45 are perceived by the BAM receptor-CIK co-receptor complex, reducing phloem-Dof and preventing the cells surrounding the intended phloem formation site from becoming phloem.

Background & Results

The phloem consists of a pathway for transporting photosynthetic products called sieve tubes and companion cells, which assist in the metabolic activities of the sieve tubes. The sieve tubes are comprised of cells called sieve elements, which have lost their nuclei and are connected in a row through small pores called sieve pores. Despite lacking nuclei, these cells remain alive and transport nutrients through the sieve pores. Companion cells are attached to the sieve tubes and are involved not only in loading and unloading nutrients but also support the metabolic activities of sieve elements lacking nuclei through small pores known as plasmodesmata. How phloem formation is regulated, including master transcription factor for phloem formation and regulatory mechanisms for phloem pattern formation, were not known well. Initially, we selected candidate transcription factors that were specifically expressed in the phloem. We overexpressed candidate genes and screened for those that could induce phloem ectopically and identified a group of Dof-type transcription factors (phloem-Dof) capable of inducing phloem even in otherwise non-phloem locations. Phloem-Dofs could induce both sieve tubes and companion cells, but the fate determination of whether they become sieve elements or companion cells remains a future challenge. Subsequently, we analyzed the changes in the overall gene expression pattern when phloem-Dof genes were expressed throughout the entire plant using microarray technology. The overexpression not only increased the expression levels of genes known to be involved in phloem formation but also induced peptide signaling molecules CLE25, 26, and 45, which inhibit phloem formation. Disrupting the CLE25, 26, 45 genes or their receptor genes expanded the phloem region. Additionally, it was discovered that the receptor activated by CLE destabilizes the phloem-Dof proteins, exerting lateral inhibition to prevent the surrounding cells from differentiating into phloem.

Significance of the research and Future perspective

This study demonstrated the coordinated action of transcriptional regulation and intercellular communication creates the phloem pattern. This study clarified the regulatory mechanisms of phloem formation, enabling the manipulation of cells to increase or decrease the formation of phloem through mutations or genetic modifications. In the future, this could lead to technologies allowing for the artificial control of phloem formation, potentially influencing the distribution of nutrients in crops and other plants.



Patent

Treatise

URL

Keyword

Qian, Pingping et al. A Dof-CLE circuit controls phloem organization. Nature Plants 2022, 8, 817–827. doi: 10.1038/s41477-022-01176-0

<https://kakimoto0.wixsite.com/kakimoto-lab/en>

phloem, Dof, transcription factor, peptide