

論文内容の要旨

Molecular basis of haustorium development
in Orobanchaceae parasitic plants

(ハマウツボ科寄生植物における吸器発生機構の分子基盤)

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Parasitic plants invade other plants to retrieve nutrients. In particular, genus *Striga* (family: Orobanchaceae) threatens food security through infects food crops such as maize, sorghum, and upland rice. Currently, no efficient countermeasures exist against these noxious weeds because we still lack a clear understanding of the molecular mechanisms underlying plant parasitism. To address this issue, the facultative parasite *Phtheirospermum japonicum* (family: Orobanchaceae) was established as a model plant to study parasite-host interactions at the molecular level. Upon host recognition, parasitic plants, including those in the Orobanchaceae family, develop an invading organ called the haustorium. The haustorium in Orobanchaceae attaches to host roots, penetrates into host cell layers, eventually reaching the vasculature tissue and forming a parasite-host connection via the xylem bridge. During this developmental course, the radial pattern in parasitic root tissues is remarkably reorganized. I successfully developed cell-type-specific markers and observed their expression patterns during tissue reorganization. Interestingly, vascular-meristem-like cell development was observed in the central region of the haustorium. Further clonal analysis showed

that various cell types initiated cell division simultaneously and differentiated into vascular-meristem-like cells, which eventually became the source of xylem cells, thus dictating xylem bridge formation. In addition, I performed tissue-specific transcriptome analysis coupled with laser microdissection and identified the first molecular markers for the parasite-specific intrusive cell that develops at the haustorium interface and has a unique morphological feature. Gene ontology analysis suggested that peroxidase activity may be an important factor at the interface region. Because local auxin gradients can lead to organogenesis and vascular patterning, I investigated whether auxin is a primary factor driving haustorium development. To examine auxin gradient dynamics, I next tracked the expression of synthetic auxin response promoter DR5 throughout haustorium development. Strong DR5 expression was observed on the surface of the haustorium emerging site facing the host root. This strong expression was also maintained at the growing haustorium apex. During the late stage of haustorium development, DR5 expression patterns coincided with the location of xylem bridge formation. To clarify these dynamics, I explored the expression pattern and subcellular localization of PIN and AUX/LAX proteins (respectively auxin efflux and influx carriers). The expression of these proteins and DR5 were similar, suggesting that auxin transport mediators contribute to shaping auxin gradients during haustorium development. Application of auxin transport inhibitors demonstrated that auxin efflux activity is not important for haustorium initiation *per se*, but is crucial for xylem bridge formation. Based on these data, I propose a model of haustorium development regulated by the auxin transport network.