



植物-微生物相互作用の最前線

Frontier in plant-microbe interactions

● 開催概要

会場：筑波大学TARAセンターC棟2階セミナールーム

日時：平成29年3月13日(月) 11:00～12:00

主催：テニュアトラック普及・定着事業

共催：ERATO野村集団微生物制御

講演者：中神弘史 博士（マックス・プランク植物育種学研究所GL/理化学研究所）

● 講演要旨 (Abstract)

Dr Hirofumi Nakagami

“Evolutionary proteomics to understand plant immune system”

“進化プロテオミクスによる植物免疫システムの理解”

Plants activate immune system by recognizing microbe-associated molecular pattern (MAMP) through plasma membrane-located pattern recognition receptors (PRR). While extensive genetic screens successfully identified a number of PRRs and components which affect abundance and maturation of PRRs, signal transduction mechanisms that lead to defense responses is thus far limited. This partly stems from limitations of forward genetics caused by lethality and/or genetic redundancy. Accordingly, we have been taking shotgun phosphoproteomics-based approach to identify the signaling components. By using Arabidopsis as a material, we could successfully identify novel components in plant immunity. Meanwhile, unsophisticated proteomics approaches often resulted in identification of too many potential regulators whose importance are uncertain.

The comparative and evolutionary genomics/proteomics could be efficient approaches to elucidate fundamental components and systems that are broadly conserved across the plant kingdom. Therefore, we started to investigate whether emerging model organism liverworts *Marchantia polymorpha* can be used as new model system to understand plant immunity. Importantly, *Marchantia* genome has been reported to have highly streamlined architecture, with smaller gene families and less redundancy compared to higher plants. Analysis of *Marchantia* with simple gene networks is expected to facilitate exploring the fundamental components of plant immune system. As expected, plant immunity-related genes are found to be less redundant in *Marchantia* compared to higher plants. Interestingly, LysM domain-containing proteins responsible for chitin and peptidoglycan (PGN) perception/signaling in angiosperms are highly conserved in *Marchantia* but not bacterial MAMP receptors such as FLS2 and EFR which belong to the group XII leucine-rich repeat receptor-like protein kinase (LRR-RLK). We have confirmed that *Marchantia* actually recognizes chitin and induces a series of defense responses. Moreover, we have disrupted *LysM* genes in *Marchantia* and revealed that CERK1 homolog is required for chitin and PGN responses in *Marchantia*. These evidences assure that *Marchantia* can be used as new model system to understand basic framework of plant immune system. Based on these findings, we have conducted shotgun phosphoproteomics of chitin responses in *Marchantia*. Scope of proteomics with *Marchantia* to understand signaling pathways will be discussed while referring to our research outcomes.

● 世話人

石賀康博（生命環境系） ishiga.yasuhiro.km@u.tsukuba.ac.jp