

Dynamics, mechanisms, and evolution of a highly resilient plant immune signaling network



講師：片桐 文章 教授

ミネソタ大学 植物生理学科

Prof. Fumiaki Katagiri

Department of Plant and Microbial Biology,
Microbial and Plant Genomics Institute,
University of Minnesota

第5回 ERATO 学術セミナー

ERATO Nomura project : Science Seminar

Microbial pathogens can evolve much faster than plants and compromise the plant immune signaling network. Thus, the immune signaling network needs to be highly resilient against perturbations to its internal components, so that its underlying mechanisms are effectively concealed from pathogen evolution. To overcome the identifiability problem associated with a highly resilient network, we reduced the network to a network of four signaling sectors, the jasmonate (JA), ethylene (ET), PAD4, and salicylate (SA) sectors, in the model plant *Arabidopsis* and simultaneously impaired the four sectors by quadruple mutations (*quad*). Pattern-triggered immunity (PTI) triggered by the bacterial molecular pattern flg22 and effector-triggered immunity (ETI) triggered by the bacterial effector AvrRpt2 were largely abolished in *quad*¹. Then the network functions and the signal flows among the four sectors were analyzed in comprehensive combinatorial states of the sectors. This analysis enabled a conceptual reconstitution of the network at the sector scale, which allowed simpler interpretations of mechanistic relationships among the sectors underlying network resilience^{1,2}. Using network reconstitution, we also demonstrated that transcriptome response during flg22-PTI is highly resilient against loss of some of the sectors³. Furthermore, studying the network with highly impaired resilience in *quad*, we discovered another signaling sector that mediates strong inhibition of ETI signaling by PTI signaling (ETI-Mediating PTI-Inhibited Sector, EMPIS). We speculate that the role of this inhibition is to limit ETI when PTI is not compromised: such a mechanism would limit a negative impact of unnecessary immunity on plant fitness. I will also discuss how such a resilient network may have evolved.

¹ Tsuda *et al.* 2009 PLOS Genet 5, e1000772.

² Kim *et al.* 2014 Cell Host Microbe 15, 84.

³ Hillmer *et al.* PLOS Genet, in press

日時：2017年5月25日(木)

時間：16:00 ~ 17:30

会場：筑波大学総合研究棟 A110 室

参加費無料・事前申し込み不要



お問い合わせ：betsuyaku.shige.ge@u.tsukuba.ac.jp

(研究推進主任：別役重之)

主催：JST ERATO 野村集団微生物制御プロジェクト

<http://www.jst.go.jp/erato/nomura/>

