

植物ゲノム・遺伝子源解析センター

月例セミナー

- とき** 平成22年5月27日(木)
16時～17時15分
- ところ** 農学部 BW106講義室(大講義室)
- 題目** 「Network modeling reveals prevalent negative regulatory relationships between signaling sectors in Arabidopsis immune signaling」
- 講師** 米国ミネソタ大学准教授 Fumiaki Katagiri 博士

概略

With a complex signaling network, in which components are highly interconnected, elucidating structural features of the network that govern its behavior is a challenging task. Here, we demonstrate that use of mRNA profiling to collect and analyze detailed descriptions of changes in the network state resulting from specific network perturbations is a powerful and economical strategy to elucidate regulatory relationships among the components of a complex signaling network. mRNA profiles of 22 Arabidopsis immunity mutants and wild type were collected 6 hours after inoculation with the bacterial pathogen /Pseudomonas syringae/ expressing the effector protein AvrRpt2. This bacterial strain feeds multiple inputs into the signaling network, allowing many parts of the network to be activated at once. Regulatory relationships among the genes corresponding to the mutations were inferred by recursively applying a non-linear dimensionality reduction procedure to the mRNA profile data. The resulting network model accurately predicted 22 of 24 regulatory relationships reported in the literature, suggesting that predictions of novel regulatory relationships are also accurate. The network model revealed two striking features: (i) the components of the network are highly interconnected; (ii) negative regulatory relationships are common between signaling sectors. Complex regulatory relationships, including a novel negative regulatory relationship between the early microbe-associated molecular pattern-triggered signaling sectors and the salicylic acid sector, were validated experimentally. We propose that prevalent negative regulatory relationships among the signaling sectors make the plant immune signaling network a “sector-switching” network, which effectively balances two apparently conflicting demands, robustness against pathogenic perturbations and minimization of negative impacts of immune responses on plant fitness.

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(<http://www.ag.kagawa-u.ac.jp/phytogene/index.html>)