

SEMINAR

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Hosted by Assist. Prof Chae Eunyoung

Paranoid Plants: Genetic Conflict in the Immune System

By **Detlef Weigel ForMemRS**

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Almost two decades ago, we discovered that *Arabidopsis thaliana* is a great model for the study of hybrid necrosis. This widespread syndrome of hybrid failure in plants is caused by plant paranoia – regardless of the presence of enemies, plants “think” they are being attacked by pathogens. The consequence is autoimmunity, which can be extreme enough to kill plants before they set seeds. We have studied in detail the underlying genetics, finding that often only one or two loci are involved, with most of them encoding NLR immune receptors. The NLR gene family is the most variable gene family in plants, and it is thus not surprising that they are often involved in genome-genome conflict, with alleles at one locus greatly changing the activity of alleles at another locus. Similarly, we have found that autoimmunity due to allelic variation at the *ACD6* locus, which probably encodes a channel, is modulated by a slew of extragenic suppressors. I will describe what we have learned and how our unique angle on studying the plant immune system has led to insights that were not obtained with conventional laboratory genetics. Additional information about our work can be found on our website <http://weigeworld.org>.



About the Speaker

*Detlef Weigel, a Director at the Max Planck Institute for Biology Tübingen, is a member of the US National Academy of Sciences and the Royal Society, and a recipient of many scientific awards, such as the recent Novozymes Prize. Detlef has an extensive record of service to the scientific community, and he is strong proponent of open science. Detlef was one of the first to exploit natural genetic variation for understanding how the environment affects plant development. In recent years, this work has come to incorporate questions at the interface of evolution and ecology: How can wild plants adapt to climate change, and how do they manage to keep their pathogens at bay? In this research, he draws on the fruits of a collaborative effort initiated over a decade ago to sequence the genomes of over 1,000 natural *A. thaliana* strains (The 1001 Genomes Project).*