

Constraints on resistance and pathogenicity factors and their consequences on resistance durability

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Molecular co-evolution between pathogens and wild tomatoes Rose L.

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Abstract

Resistance genes typically show evidence of rapid protein evolution in natural host populations. Variability at these loci may be the direct result of a co-evolutionary arms race between host and pathogen. However, the abundance of pseudogenes also segregating in natural populations at well-known resistance genes indicates that the strength of natural selection likely fluctuates and these genes may be subject to bouts of relaxed constraint as well.

In my lab, we investigate the strength and target of natural selection within resistance genes present in natural host plant populations of *Arabidopsis* and wild tomatoes. Using a combination of population genetic studies of well-characterized pathogen resistance genes and functional studies involving protein expression, enzymatic assays, plant transformation and pathogen infection studies, we have determined how naturally occurring protein variation in host populations affects defense to pathogens at the individual level. I will describe the results from these studies and discuss how we can apply what we have learned about natural selection in the wild to discover ways to improve the durability of resistance in our crop species.

Keywords: natural selection resistance genes, Arabidopsis, tomatoes

Constraints on resistance and pathogenicity factors and their consequences on resistance durability

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Abstract

Most recessive resistances to potyviruses in solanaceous crops are controlled by eukaryotic translation initiation factors 4E (*eIF4Es*). Physical interaction between *eIF4E* and the viral protein genome-linked (*VPg*) allows potyviruses to infect the plant. Amino acid substitutions in *eIF4E* can disrupt the molecular interaction with *VPg*, which confers resistance to the plant. Similarly, amino acid substitutions in the *VPg* can restore interaction with the mutated *eIF4E* and confer resistance-breaking properties to the virus. Both *eIF4Es* and *VPgs* are highly constrained proteins and these constraints have important consequences on resistance specificity, resistance durability and the potential efficiency of management strategies.

Keywords: Solanaceae, Potato virus Y, Potyvirus, resistance breakdown

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Sessions

Session 1: Impact of plant disease resistance on the structure and evolution of pathogen populations

Session 3: From plant-pathogen molecular interactions to the durability of resistance

Session 2: Sustainable and integrated breeding and deployment of genetic resistance

Session 4: Socio-economic issues related to the use of resistant varieties and their deployment in agro-systems

Invited Speakers

Sylvain Gandon, CNRS, France - Benoit Moury, INRA, France - Chris Mundt, Oregon State University, USA - Walter Rossing, Wageningen University, The Netherlands - Ravi Prakash Singh, CIMMYT, Mexico - Peter Thrall, CSIRO Plant Industry, Australia

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