CONSERVATION AND DIVERGENCE OF RAR1-MEDIATED NONHOST RESISTANCE DURING LAND PLANT EVOLUTION

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Text
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Over 450 million years of co-evolution, plants and pathogens have developed sophisticated strategies to manipulate one another. In plants, nonhost resistance (NHR) describes a collection of molecular and cellular mechanisms that neutralize non-adapted pathogens. Although NHR has been extensively studied in angiosperms, the origin and evolution of NHR in land plants is largely unknown. Here, we demonstrate the conservation of a NHR mechanism mediated by the RAR1-SGT1-HSP90 chaperone complex and identify lineage-specific divergence in terrestrial ferns. The RAR1-SGT1 interaction is highly conserved among lineages and even occurs between distantly related ortholog pairs. Intriguingly, we identified a single exception in the C-fern, whose homologs were incapable of interactions outside of its lineage. We hypothesize that lineage-specific differences in the SGT1-interacting CHORD2 domain determines this specificity, which is supported by protein-modeling studies. To determine a role for RAR1-mediated NHR in divergent lineages, we generated a liverwort (*Marchantia polymorpha*) *Mprar1* mutant and screened it against 28 diverse *Phytophthora* isolates. Excitingly, the *Mprar1* mutant exhibited significant defects in NHR to candidate pathogens that we are now examining in more detail. Overall, our findings suggest that the core mechanism of RAR1-mediated NHR is conserved in land plants, while plant lineages have fine-tuned the system during their evolutionary histories.

POPULATION STRUCTURE OF CACAO PATHOGEN PHYTOPHTHORA MEGAKARYA

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Text
Phytophthora megakarya is an aggressive and extremely destructive pathogen that causes black pod disease of cacao, significantly limiting yield in the world's leading cacao producing region in West and Central Africa. To effectively use genetic breeding to improve cacao resistance to black pod disease, the genetic diversity of both host and pathogen populations must be considered. We examined genetic diversity and population structure of *P. megakarya* using genomic data from 166 isolates collected from Cameroon, Nigeria, and Ghana. We used reads from genotyping by sequencing of 150 isolates and from published whole genome sequences of 15 isolates to call 2,644 high quality SNPs relative to the reference genome Pm1/GH34 from Ghana. Isolates could be assigned to one of two major clades. One clade contained isolates from Nigeria and Ghana and the other contained isolates collected in all three countries. The two major clades showed differing degrees of genetic variation among isolates and heterozygosity of SNPs. Genomic data will be integrated with isolate phenotypes determined using experimental inoculations of cacao pods to evaluate variation in genetic determinants of virulence in *P. megakarya*.