

Phenotypic resistance diversity underpinned by a diverse repertoire of candidate NLR loci and genotype-specific expression patterns

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Abstract

High levels of phenotypic variation in resistance appears to be nearly ubiquitous across natural host populations. Molecular processes associated with this variation in nature are still poorly known, although theory predicts resistance to evolve at specific loci driven by selection associated with the response to pathogen. Nucleotide-binding leucine-rich repeat (NLR) genes play an important role in pathogen recognition, downstream defense responses and defense signaling. Identifying the natural variation in NLRs has the potential to increase our understanding of how NLR diversity is generated and maintained, and how to manage disease resistance. Here, we sequenced the transcriptomes of five different *Plantago lanceolata* genotypes when inoculated by the same strain of obligate fungal pathogen *Podosphaera plantaginis*. A de novo transcriptome assembly of RNA-sequencing data yielded 24,332 gene models with N50 value of 1,329 base pairs and gene space completeness of 66.5%, suggesting a high-quality assembly. The gene expression data showed highly varying responses where each plant genotype demonstrated a unique expression profile in response to the pathogen, regardless of the resistance phenotype. Analysis on the conserved NB-ARC domain demonstrated a diverse NLR repertoire in *P. lanceolata* consistent with the high phenotypic resistance diversity in this species. We find evidence of selection generating diversity at some of the NLR loci. Jointly, our results demonstrate that phenotypic resistance diversity results from a crosstalk between different defense mechanisms. In conclusion, characterizing the architecture of resistance in natural host populations may shed unprecedented light on the potential of evolution to generate variation.

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