Identification of barley powdery mildew avirulence effectors using association mapping

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Plant pathogens secret small effector proteins into host cells to facilitate host colonization, in turn plants evolve resistance proteins to recognize specific pathogen effectors and trigger host defense response, so called effector-triggered immunity (ETI). Barley resistance protein MLAs are intracellular NLRs and confer race-specific immunity to barley powdery mildew *Blumeria graminis f. sp. hordei* (*Bgh*) by recognizing *Bgh* isolate-specific avirulence effectors. The allelic MLA proteins are highly polymorphic at the C-terminal LRR domains, pointing to a diversifying selection at the effector recognition sites. This indicates a direct recognition and co-evolution between MLAs and avirulence effectors; alternative, MLAs co-evolve with host proteins, leading to an indirect recognition to avirulence effectors. Although 23 MLAs are cloned, their cognate avirulence effectors are ambiguous. Thus, the identification of avirulence effectors from *Bgh* is the key to uncovered the molecular mechanism underlining the recognition and co-evolution between MLAs and effectors. We aimed at identifying MLA-specific avirulence effectors using association mapping with a collection of 20 *Bgh* isolates. First, we determined the pathotype of each isolates on barley near-isogenic lines containing different MLA recognition specificities; then we identified *Bgh* isolate-specific SNPs using their RNAseq data in comparison with the reference genome of isolate DH14. From the association mapping, we successfully identified candidate avirulence effector of MLA7 and MLA13. Expression of the candidate genes into barley leaves by agrobacteria infiltration could trigger a specific cell-death response on the respective MLA containing barley NILs. Further validation of the candidate avirulence effectors is currently in progress.