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Investigating the NHP-dependent SAR pathway in common hexaploid wheat

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Abstract

Plant systemic acquired resistance (SAR) is a phenomenon whereby the recognition of a local microbial invasion in aerial tissue confers a 'whole-plant' immune response against a wide range of pathogens. For the model plant *Arabidopsis thaliana* and various other angiosperms, the key metabolites Pipecolic acid (Pip) and N-hydroxylated pipecolic acid (NHP), synthesized by the reductase SAR-Deficient 4 (AtSARD4) and Flavin-monooxygenase 1 (AtFMO1), respectively, are crucial for proper SAR establishment. However, the extent to which NHP biosynthesis contributes to SAR in common hexaploid wheat (*Triticum aestivum*) remains unclear. Here, we utilized a combination of protein homology, phylogenetic and transcriptomic analyses to elucidate functional orthologs of AtSARD4 and AtFMO1 in wheat. 48 TaFMO1-like and three TaSARD4 candidates were identified, from which representatives were selected for further functional characterization. All three TaSARD4-expressing transgenic $\Delta sard4$ *Arabidopsis* lines generated displayed dwarfism characteristic of autoimmunity, with significant reductions in rosette size (>45%) compared to the *Atsard4* deletion mutant. Two TaFMO1-expressing transgenic $\Delta fmo1$ *Arabidopsis* lines revealed a partial recovery in SAR when infected by the oomycete *Hyaloperonospora arabidopsidis*, indicating possible functional complementation. Furthermore, supplementing 10mM NHP to a local wheat leaf significantly and systemically reduced by 2-fold the proliferation of the biotrophic wheat fungal pathogen, *Puccinia triticina* (Pt); quantification of basal and Pt-induced NHP and Pip levels in wheat by HPLC-MS is currently underway. Altogether, our results suggest that the NHP biosynthetic pathway for pathogen defense is conserved in wheat and illustrate the power of translating knowledge from model to important non-model crop systems.

