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Finding solutions from the wild- Broad resistance to soybean cyst nematodes (SCN) in wild soybean

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Soybean cyst nematode (SCN), *Heterodera glycine*, is globally the most devastating soybean. Applying SCN-resistant soybean varieties is the most efficient and environmentally-friendly strategy for SCN management. However, developing SCN-resistant soybean cultivars has been very challenging due to the rapid evolution of SCN and lack of diverse resistant varieties with broad resistance. Crop wild relatives have demonstrated great potential, harboring exotic and useful genetic resources for crop improvement. In this study, we applied two wild soybean (*Glycine soja*) genotypes with distinct resistance responses (resistant vs. susceptible) to the two different SCN types (HG types 1.2.3.5 and HG type 2.3.5) to dissect the common resistance mechanisms. We identified a core set of differentially expressed genes (DEG) involved in resistance responses to both SCN types based on the RNAseq comparisons between the resistant (S54) and susceptible (S67) genotypes. Further analyses of this core set of DEG revealed that genes involved in phytohormone salicylic acid (SA) biosynthesis were significantly up-regulated in the resistant genotype (S54) after SCN treatment. Consistently, SA levels were significantly induced in S54 compared to those in S67. Our results further indicated that elevated SA was primarily synthesized via the phenylalanine ammonia lyase (*PAL*)-catalyzed biosynthesis branch rather than the isochorismate synthase (*ICS*)-catalyzed branch. These results not only shed light on the molecular mechanisms underlying SCN resistance in wild soybeans, but also facilitate developing novel and diverse soybean cultivars with broad-spectrum resistance to SCN.