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Enhancing legume transformation by altering host immune receptor - Agrobacterium interactions

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While *Agrobacterium tumefaciens* is renowned for its ability to deliver DNA to a wide range of plants, most soybean genotypes are recalcitrant to transformation. Evading the host defense response found in soybean would facilitate a wider range of soybean genotypes suitable for use in transgenic breeding programs. A search for soybean homologs of known plant-immunity-associated pattern recognition receptors (PRRs) identified several candidates in the soybean reference genome, which comes from an *Agrobacterium*-resistant cultivar. Based on re-sequencing data it was found that one of these PRRs is consistently absent in *Agrobacterium*-susceptible soybean genotypes. In addition, *Bradyrhizobium*, a nodulating bacterial symbiont and close relative of *Agrobacterium*, carries a five amino acid insertion within the presumed recognition motif of this soybean PRR. Therefore, we hypothesize that the absence host PRR recognition is associated with successful transformation by *Agrobacterium*.
The *Agrobacterium*-susceptible cultivar is incompatible with the nodule-forming bacterium *Bradyrhizobium*, indicating a related PRR involved in symbiosis may not be present in most genotypes. This *Bradyrhizobium*-specific PRR recognizes a slightly modified recognition motif that may have evolved alongside the *Agrobacterium*-specific PRR. Replacing the recognized *Agrobacterium* protein with its ortholog from *Bradyrhizobium* through homologous recombination may facilitate evasion of host immune recognition, and provide an effective tool to transform resistant varieties for transgenic soybean breeding. Alternatively, the same effect can be achieved by removing the corresponding PRR in the plant genome via mutagenesis or genome editing.