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Harnessing the power of molecular evolutionary analysis to understand strigolactone signaling

Modern DNA sequencing technology has granted unprecedented access to the genetic diversity found in non-model organisms, which has been sifted by evolutionary selection. This wealth of information can be used to investigate hormone signaling mechanisms in a guided manner that is more efficient than random mutagenesis. Parasitic weeds in the Orobanchaceae family use strigolactones as germination stimulants that indicate the presence of a nearby host root. We investigated the basis of host perception in the Orobanchaceae through an evolutionary analysis of karrikin and strigolactone receptor sequences, coupled with homology modeling and cross-species complementation. We found evidence that in parasite genomes, duplication of the karrikin receptor *KAI2* was followed by the evolution of strigolactone perception amongst a clade of fast-evolving *KAI2* paralogs. We extended our analysis to predict which genes found in the basal land plant *Physcomitrella patens* might be involved in strigolactone perception. We are now using several in depth comparisons of functionally diverse *KAI2* paralogs as a basis for reconstructing the evolution of different ligand specificities.