Evolutionary divergence of the plant elicitor peptides (Peps) and their receptors : interfamily incompatibility of perception but compatibility of downstream signalling

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Plant elicitor peptides (Peps) are potent inducers of pattern-triggered immunity and amplify the immune response against diverse pathogens. Peps have been discovered and studied extensively in Arabidopsis and only recently orthologs in maize were also identified and characterized in more detail. Here, the presence of PROPEPs, the Pep precursors, and PEPRs, the Pep receptors, was investigated within the plant kingdom. PROPEPs and PEPRs were identified in most sequenced species of the angiosperms. The conservation and compatibility of the Pep-PEPR-system was analysed by using plants of two distantly related dicot families, Brassicaceae and Solanaceae, and a representative family of monocot plants, the Poaceae. All three plant families contain important crop plants, including maize, rice, tomato, potato, and canola. Peps were not recognized by species outside of their plant family of origin, apparently because of a divergence of the Pep sequences. Three family-specific Pep motifs were defined and the integration of such a motif into the Pep sequence of an unrelated Pep enabled its perception. Transient transformation of Nicotiana benthamiana with the coding sequences of the AtPEPR1 and ZmPEPR1a led to the recognition of Pep peptides of Brassicaceae or Poaceae origin, respectively, and to the proper activation of downstream signalling. It was concluded that signalling machinery downstream of the PEPRs is highly conserved whereas the leucine-rich repeat domains of the PEPRs co-evolved with the Peps, leading to distinct motifs and, with it, interfamily incompatibility.

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