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

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Supplemental Files

Supplementary Table S3: Identity comparison of PROPEP sequences
Full-length amino-acid sequences of published and novel HMMER identified PROPEP sequences were compared for the percentage of identical residues in aligned positions (upper half), and the number of identical residues in aligned positions (lower half). Colours indicate increasing amount of identity from low (blue) via white to high (red).

Supplementary Table S4: Identity comparison of Pep sequences
Pep amino-acid sequences deduced from published and novel HMMER identified PROPEP sequences were compared for the percentage of identical residues in aligned positions (upper half), and the number of identical residues in aligned positions (lower half). Colours indicate increasing amount of identity from low (blue) via white to high (red).

Supplementary Table S5: Identity comparison of PEPR sequences
Full-length amino-acid sequences of PEPR sequences were compared for the percentage of identical residues in aligned positions (upper half), and the number of identical residues in aligned positions (lower half). Colours indicate increasing amount of identity from low (blue) via white to high (red).

Supplementary Table S6: Identity comparison of PEPR LRR domains
The LRR domains of PEPR sequences were compared for the percentage of identical residues in aligned positions (upper half), and the number of identical residues in aligned positions (lower half). Colours indicate increasing amount of identity from low (blue) via white to high (red).

Supplementary Table S7: Identity comparison of PEPR kinase domains
The kinase domains of PEPR sequences were compared for the percentage of identical residues in aligned positions (upper half), and the number of identical residues in aligned positions (lower half). Colours indicate increasing amount of identity from low (blue) via white to high (red).

Supplementary Figure S1: Plasticity of the Pep-PEPR-LRR interaction site
Sequence alignment of the LRR region of the PEPR sequences from Figure 1B. Amino acid residues are coloured based on the conservation and interacting residues of AtPEPR1-LRR (underlined in red) as described by Tang et al., 2015. The LRR sequence of SIPEPR1 and ZmPEPR1a, used in this study, are underlined in grey. Yellow residues: conserved amino acids of AtPEPR1LRR. Magenta residues: AtPep1 interacting amino acids of AtPEPR1LRR. Below the sequence alignment the overall conservation is indicated by pink bars and a sequence logo.