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Exploring the origin and phylogeny of *Cercospora beticola* resistance gene *BvCR4* in geographically diverse populations of wild sea beet (*Beta vulgaris* subsp. *maritima*).

Cercospora beticola is the causal agent of Cercospora leaf spot (CLS), a devastating disease of sugarbeet worldwide. The gene *BvCR4* (CR+) that encodes a plant pattern recognition receptor conferring resistance to CLS was recently introgressed from sea beet into cultivated sugarbeet. To investigate the origin and evolution of this gene, 619 wild and cultivated beet accessions from geographically diverse backgrounds were retrieved from the Germplasm Resource Information Network that contained historic CLS disease phenotypic data. Accessions were screened for *BvCR4* homologs by PCR and the obtained amplicons were sequenced. Phylogenetic relationship between homologs was determined on both coding and amino acid (AA) sequences. A total of 27 accessions produced amplicons, 19 encoded proteins with 79 to 92 % AA sequence identity with BvCR4, while eight were predicted to be non-functional proteins due to premature stop codons. Phylogenetic analyses showed that Italy or Greece is likely the geographic origin of the resistant trait. BvCR4 homolog sequence variation exhibits a high number of AA differences that may impact binding affinity with the corresponding ligand. However, a 25 AA segment was exclusively present in resistant accessions, potentially critical for pathogen pattern recognition and host resistance. Functional variations of BvCR4 in sea beet populations will be valuable for CLS resistance breeding and provide a better understanding of BvCR4 resistance against *Cb* to anticipate how the pathogen may subvert resistance.