

Host differential resistance and pathogenic variability in interactions between *Brassica juncea* and *Albugo candida* isolates from *B. juncea*, *B. rapa* and *B. oleracea*

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White rust, caused by the biotrophic oomycete pathogen *Albugo candida* (AC), is an important disease of *Brassica juncea* (BJ), *B. rapa* (BR) and *B. oleracea* (BO). BJ and BR account for almost one-third of the oilseed crops in India. Severe infection with AC culminates in systemic “staghead” infection of the inflorescence (often in association with *Peronospora parasitica*), which under favourable conditions causes heavy yield losses in susceptible cultivars. For this study, ten isolates of AC were included, five from BJ in India, two from BJ in Canada, two from BR in India and one from BO in the UK. In one set of experiments, fifty-nine accessions of BJ, two of BR and one of BO were screened for their responses at the seedling stage to a mixture of six isolates from BJ, four from India and two from Canada. Forty-six of these accessions were also tested in isolation against the 10 individual isolates. Preliminary results indicated that 52 accessions were uniformly susceptible to the mixture of six isolates. The percentage of plants expressing a resistance response in the remaining seven accessions ranged between only 1% in Pusa Bold and 8% in RESJ-768. All 46 accessions expressed a heterogeneous reaction to at least two isolates, where resistance among the seedling population of individual accessions ranged between 1% in two accessions up to 100% in Cutlass with two Indian isolates of BJ. Cutlass was almost fully susceptible when tested against one Canadian isolate (2v) from BJ, but 4% of the seedling population of this accession were found resistant to the mixture of 6 isolates, which included 2v. The S1 progenies of the selected resistant lines from Cutlass were segregated for resistance to isolate 2v. In the majority of cases, resistance frequency among the seedling population of BJ accessions to isolates from BR was greater than that with isolates from the same host species. All accessions of BJ were resistant to the only isolate from BO used in this study, whereas 76% of the population of one BR accession was susceptible when tested against the isolate from BO and *vice versa*. The response of host accessions to individual and mixed isolates gave strong evidence of distinct pathogenic variability among isolates used in this study. To our knowledge, this is the first report of such evidence among Indian isolates from BJ as well as BR. The results also gave indication of host species specificity in BJ against the isolate from BO. The results of screening against individual isolates could be explained either by a gene-for-gene model or an additive gene model. Interpretation of the results was complicated by the heterogeneous response of the host plant accessions to AC isolates. Selections were made to develop differential lines in a homogeneous genetic background for future studies of the genetics of the host-pathogen interaction and for breeding for disease resistance.