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Prevalence of physiological races of *Phakopsora pachyrhizi* Syd. and molecular variability of its isolates causing Asian Soybean Rust in India

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Morphological variability revealed that the colour of the uredospores ranged from light brown to dark brown, pale yellow to colourless and orange brown. Maximum size (93.9 x 72.2 μm) of uredospore was observed with Ugarkhurd isolate. Three pathotypes were identified based on cultural variability on 13 international set of differentials as Cluster I- Reddish Brown (RB) lesion producing pathotypes, Cluster II- TAN lesion producing pathotypes and Cluster III- Mixed (RB + TAN) producing pathotypes. Race 2 and 3 were recorded in Karnataka while, only race 2 was observed in Maharashtra and north eastern states. The molecular variability study revealed that specific primer sequence (PPa 1 & PPa 2) showed greater variation among the isolates of *Phakopsora pachyrhizi*. Based on phylogenetic analysis two main clades of pathogenic races were identified in India. The rDNA region was amplified with specific primer PPa1 (forward)- 5'-TAAGATCTTTGGGCAATGGT-3' and PPa2 (reverse)- 5'-GCAACACTCAAAA TCCAACAAT-3' primers for all 17 isolates of *P. pachyrhizi*. DNA amplicon was obtained at the region of 332 bp with a concentration of around 150 $\eta\text{g}/\mu\text{g}$. The amplified products were checked on 1.0 per cent Agarose gel electrophoresis. The nucleotide sequences of Dharwad were highly similar with Varur isolate with 99 per cent similarity and least similarity (89.3 per cent) was observed with Imphal isolate when compared to Hukkeri and Ugarkhurd isolates. The Ugarkhurd isolate showed 96.2 per cent similarity to Dharwad isolate.