

HPR P30. Regional characterization of pigeonpea sterility mosaic disease and exploring broad-based resistance

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Pigeonpea sterility mosaic disease (SMD) caused by *Pigeonpea sterility mosaic virus* (PPSMV) is a serious threat to pigeonpea production in the Indian-subcontinent. Recent reports on the possible existence of two different viruses associated with the SMD further complicate the etiology of this difficult to manage viral disease. In this regard, a comprehensive and systematic survey was taken up across several pigeonpea growing areas in southern India to know the disease prevalence and variability in virus isolates. Further, selected pigeonpea elite genotypes were screened in different locations for their broad-based resistance. Results indicate huge variation in SMD incidence among the surveyed states. The highest disease incidence (9.38 percent) was observed in Karnataka, followed by Tamil Nadu state with 8.44 per cent incidence. Andhra Pradesh and Telangana states recorded disease incidences of 4.51 and 2.08 per cent respectively. Samples collected from Patancheru location and tested using viral-specific RNA-3 segment primers were all positive for both the viruses. However, one of the samples collected from Bengaluru location and four samples from Coimbatore location had a positive reaction for PPSMV-2 only. In order to identify broad-based resistance to SMD, 20 pigeonpea genotypes were screened in three different locations (Patancheru, Bengaluru and Coimbatore) in southern-India during rainy seasons of 2017 and 2018. Among them, ICPL- 16078, ICPL-16086 and ICPL-16087 showed resistance reaction (≤ 10 % incidence) in all the three locations, whereas, ICPL-16072, ICPL-16077 and ICPL-16083 showed resistance to Patancheru and Coimbatore isolates but highly susceptible (≥ 40 % incidence) to Bengaluru isolate.