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MOLECULAR MAPPING OF GENE(S) RESISTANCE TO STERLITY MOSAIC DISEASE (SMD) IN PIGEON PEA (CAJANUS CAJAN L.)

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The cultivated pigeon pea (*Cajanus cajan*) is one of the most important source of protein for worlds marginal and vegetarian population. It helps to improve nutritional level, food security and environmental sustainability. Even though India is leading producer of pigeon pea, productivity is very low due to narrow genetic base and susceptibility towards biotic factors i.e. sterlity mosaic disease (SMD) popularly known as "green plague of pigeon pea" and causes severe losses. Keeping in the view, identification of SMD resistant cultivars with better understanding of inheritance of disease along with identification of stable lines with wider adaptability among the resistant lines were key consideration for the present study. For this, SMD screening was conducted at green house, IBT, PJTSAU during *Kharif* 2012 and 2013 seasons and field experiments to study 14 important agronomic traits were carried out at two locations ARS, Tandur and College farm, PJTSAU during *Kharif* 2012 and 2013 at Tandur and *Kharif* 2013 at PJTSAU, respectively. In the present study, 188 recombinant inbred lines (RILs) showed a digenic ratio (9S:7R) for SMD resistance, indicating complementary gene action which showed susceptibility is dominant over resistant. Considerable variability existed among the RILs for most of the characters studied which indicated ample opportunities for the breeder to make effective selections based on desirable characters. Genotyping by sequencing approach which can generate thousands of SNPs in faster and cost effective manner was used to map the QTLs for the traits included in this study. 89,699 SNPs were identified between parental genotypes, keeping stringent criteria for consideration of high-quality SNPs for genetic mapping, construction of the genetic maps was carried out with few hundred loci. These genetic maps contained 484 SNP markers with a map distance of 798.25 cM and with average inter marker distance of 1.65 cM. QTLs identified for SMD was present on CcLG10 and was stable and consistent QTL with a phenotypic variance ranging from 7.41 to 7.61. The present study leads to the identification of SMD resistant lines along with location of QTLs for SMD tolerance. This would greatly aid pigeon pea breeders aiming at development of varieties with resistance to SMD.

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