

Accessing genetic variability in chickpea (*Cicer arietinum* L.) varieties differing in susceptibility to *Fusarium oxysporum* f.sp. *ciceri* using ISSR markers

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Due to *Fusarium* wilt the production of chickpea has been affected in large. Molecular variability encompassed in chickpea offers an efficient means of exploiting disease resistance variety. The DNA-based molecular marker technique, inter simple sequence repeat (ISSR) was used to study the genetic variability for 5 chickpea varieties differing in their susceptibility to wilt disease using a different ISSR primers in present investigation. From the sixteen ISSR primer used, only two primers, primer 6956-022 (sequence of $(GA)_8$ CTC) and 6956-030 ($(AC)_8$ YG) gave three specific amplicon viz., 167, 191, 272 and 196, 249, 408 base pair (bp) respectively, for resistant variety WR-315. Similarly, 6956-029 (146 bp), 6956-022 (311 bp), 6956-038 (1157 bp), 6956-031 (119, 139 bp) and 6956-033 (310 bp) markers associated with the chickpea variety JCP-27. For susceptible variety JG-62, three ISSR primer of a sequence $(GA)_8$ T, $(AG)_8$ YT and $(AC)_8$ CCTA generated unique band for DNA produced 1343, 534 and 231 bp markers, respectively.

Key words : Chickpea, *Fusarium oxysporum* f.sp. *ciceri*, ISSR

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