

Accessing genetic diversity in chickpea (*Cicer arietinum* L.) genotypes using ISSR markers

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Chickpea (*Cicer arietinum* L., $2n=2x=16$) is one of the most important grain legume crops in the world, with the Asia region contributing most of the production. The major chickpea producing countries in Asia are India, Turkey, Pakistan and Iran. Large variations are seen in chickpea yield: from 0.35 t/ha in Iran to 1.60 t/ha in Mexico. In the cereal dominated diets of South-, West- and East-Asia and North Africa, chickpea act as Health food for vegetarians due to its high quality protein. The crop plays a considerable role in farming systems by reducing the need for N fertilization through fixing atmospheric nitrogen. Despite the economic value of chickpea and the relatively long period of traditional breeding, the productivity of the crop has not improved significantly in recent years. This was most probably

due to disease and the effects of poor environmental adaptation. Therefore, chickpea breeding programs are purposeful for improving the genetic potential of the crop by producing various genetic combinations and for this assessment of genetic diversity is the initial step. The ISSR technique uses microsatellites, usually 16-25 bp long, as primers in a single primer PCR reaction targeting multiple genomic loci to amplify mainly the inter-SSR sequences of different sizes. The five ISSR primers were i.e. $(CA)_8AT$, $(CA)_8AC$, $(CA)_8GT$, $(CA)_8GA$ and $GGTC(AC)_7$, were tested for 25 chickpea genotypes which give amplified products in the range 0.3 kb-1.5 kb. The value of cophenetic correlation coefficient (r) comes 0.92 indicating enough diversity among chickpea genotypes under investigation.