Genetic diversity and population ssrs and est-ssrs markers

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xChickpea (Cicer arietinum L.) is an annual self-pollinated legume crop is widely grown worldwide mostly in India, Middle-East, West Asia and North Africa (Hajibarat et al. 2015). Chickpea is the 4th important legume crop as important sources of protein, where it play valuable roles in human diet and animal feeding in poor areas (Jannatabadi et al. 2014). Chickpea originated from Turkey, Iran, Syria and North-Africa, the place that proposed to be Vavilian center of origin most of legume and cereal crops (van der Maesen 1987; Talebi et al. 2008). In most of chickpea growing area, the grain yield is low and instable, which may be contributed to narrow genetic base of chickpea germplasm and extensive use of improved cultivars with close related genomes in breeding programs (Talebi and Karami, 2011). The major constraint for seed yield is genotype × environment (G × E) interactions that affect the quantitative traits that cause the slow genetic improvement for seed yield (Kumar and Ali, 2006; Kumar et al. 2011).

The use of genetically diverse cultivars and breeding lines is an essential and effective strategy in chickpea breeding programs in order to minimize genetic vulnerability (Ghaffari et al. 2014). Utilization of germplasm with diverse genetic base can be useful for allelic richness to create new gene combination in crossing programs and the probability of increasing the different gene combination by different parents (Upadhyaya et al, 2007; Hajibarat et al. 2014). The genetic diversity in crops can be made by different ways such as; morphological markers, biochemical and DNA based molecular markers (Imtiaz et al. 2008). Morphological traits are direct, easy and inexpensive method, however, due to high effect of environments on phenotypes the error can arise and results are not stable and in similar

genotypes it is very difficult to distinguish them (Keneni et al. 2011, Pakseresht et al. 2013). Biochemical markers like as Isozymes are also affected by environmental factors such as temperature or light and also it is influenced from plant phenology like as maturity and growth stages (Imtiaz et al. 2008), therefore, these markers are not amenable for real genetic differentiation in germplasm pools. Genetic diversity analysis in chickpea using different molecular markers such as RAPD (Iruela et al. 2002; Talebi et al. 2008a); AFLP (Singh et al. 2008; Talebi et al. 2008b), ISSR (Iruela et al. 2002; Pakseresht et al. 2013) and SSRs (Saeed et al. 2011; Ghaffari et al. 2014; Hajibarat et al. 2014) has been done.

Recently, EST-based SSR markers using expressed sequenced tags (ESTs) databases have been developed in safflower (Choudhary et al. 2008). EST-SSRs are designed based on conserved gene-rich regions in genome and showed low polymorphism, while genomic SSRs spread throughout genome with higher polymorphism rate (La Rota et al. 2005; Choudhary et al. 2008). Genetic diversity analysis using these molecular markers will help to elucidate the genetic structure of chickpea gene pools and this data can be used for association between markers and important phenotypes like as biotic and abiotic stresses resistance genes (Upadhyaya et al. 2006). Therefore, in the present we aimed to study genetic diversity and population structure of 167 chickpea genotypes using genic SSR and EST-SSR markers and to compare their efficiency in genetic differentiation between chickpea genotypes.