The use of microsatellite markers in the annual and perennial *Cicer* species growing in Turkey

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Abstract: Several types of molecular markers have been used in plant breeding and genetic diversity for a wide range of applications. Generally, single-locus co-dominant markers are preferred, because they make it possible to tag and map the same loci in many different populations and even species. Probably the best markers in this respect are microsatellites. The analysis based on microsatellites in our study has revealed the usefulness of these markers in the identification of polymorphism in chickpea genome, which was earlier thought to be less polymorphic. Such markers will be highly efficient in identifying specific markers linked to the trait of interest. The plant material used in this study included 43 wild and 2 cultivated *Cicer* accessions representing annual and perennial *Cicer* with distribution in Turkey. Ten STMS primers were selected from *Cicer* species depending on their ability to amplify genomic DNA in all species. Separation of the PCR products on agarose gels revealed single bands of the expected size with 10 of the primer pairs. DNA from *C. arietinum*, *C. reticulatum*, *C. echinospermum*, *C. pinnatifidum*, *C. bijugum*, and *C. anatolicum* amplified with the primers GA2, GA24, TA13, GAA47, TA46, TA130, TA72, TA146, TS54, TS72 respectively, were sequenced and compared with the chickpea sequence. The DNA of one accession for each species has been amplified with 45 chickpea-derived STMS primer pairs. Amplification resulted either in the presence or absence of products. For other STMS loci, only three STMS/species combinations were successful which could be used as specific markers (GAA47, TS54 and TA72). We examined whether and to which extent STMS primers designed for the cultigen could also be applied to genome analysis of wild *Cicer* species

Key words: chickpea, DNA isolation, molecular markers, STMS.

Abbreviations: PCR – polymerase chain reaction, RAPD – random amplified polymorphic DNA, SSR – simple sequence repeat, STMS – sequence tagged microsatellite site.

Introduction

The genus *Cicer* belongs to the family *Fabaceae* and the tribe *Cicereae* Alef. It includes 33 perennials, eight annuals, and one unspecified wild species as well as cultivated chickpea. *Cicer* species are predominantly self-pollinating, and the chromosome number of annual species is diploid $2n = 16$ (Van der Maesen, 1987; Ahmad 2000). Chickpea is one of the most important pulse crops in the world. It is grown in South Asia, West Asia, North and East Africa, Southern Europe, Australia, South and North America (Singh, 1997). Chickpea most probably originated from an area of present-day south-eastern Turkey and adjoining areas of Syria. Turkey is one of the largest chickpea exporter providing 31% of the world's export (FAO 2000). Two main types are widely accepted by chickpea breeders: "Kabuli" (white flower, large and cream coloured seeds) and "Desi" (purple flower, small angular and dark seeds). Kabuli types have been grown traditionally in the Mediterranean basin and Central Asia, while Desi types have been mainly produced in the Indian subcontinent. East Africa, Central Asia, and to a limited extent in the Mediterranean basin. It is commonly accepted that Kabuli chickpea originated from the Desi type in the Mediterranean basin (Moreno & Cubero, 1978; Gil & Cubero, 1993). The two main types differ in several important traits. In order to exploit the variation in these two types, Desi × Kabuli crosses were carried out by breeders; however, the transfer of genes between the two major types was slow (Maynez et al., 1993). Resistance to biotic and abiotic stresses was found in wild *Cicer* species (Singh, 1990; Singh et al., 1994). Chickpea breeding aims at high yield combined with resistance to biotic stresses and tolerance to drought and cold. Despite its agronomical importance and the international efforts in conventional breeding, productivity of the crop has not yet been significantly

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