Table S1. Some genetic diversity studies in chickpea

Marker	***Material***	***Outcome***	***Reference***
RAPD			
75 RAPD	9 annual *Cicer* species (1 cultivated, 8 wild- *C. arietinum, C. reticulatum, C. echinospermum, C. bijugum, C. judaicum, C. pinnatifidum, C. chorassanicum, C. yamashitae, C. cuneatum*)	A total of 115 reproducibly scorable RAPD markers were generated, all except 1 polymorphic were utilized to deduce genetic relationships among the annual *Cicer* species. In addition to, species-diagnostic amplification four distinct clusters were observed.	Ahmad, 1999
7 RAPD primers	43 wild and cultivated accession representing ten species of *Cicer* (*C. montbretii, C. isauricum, C. anatolicum, C. incisum, C. pinnatifidum, C. judaicum, C. bijugum, C. echinospermum, C. reticulatum and C. arietinum*)	The dendrogram contained two main clusters, one of which comprised accessions of the four perennial species (*C. montbretii, C. isauricum, C. anatolicum and C. incisum*) together with the accessions of the three annual species (*C. pinnatifidum, C. judaicum and C. bijugum*), and the other cluster included the remaining three annual species (*C. echinospermum, C. reticulatum and C. arietinum*). Analysis of RAPD variation showed that *C. incisum* is the most similar perennial species to annuals, and *C. reticulatum* is the closest annual species to chickpea.	Sudupak *et al.*, 2002
42 RAPD primers	19 wild *Cicer* accessions representing seven annual *Cicer* spp. (*C. echinospermum, C. reticulatum, C. pinnatifidum, C. judacium, C. cuneatum, C. yamashitae, C. arietinum*)	Diversity analysis provided three groups. The Group I included the cultivated species *C. arietinum, C. reticulatum* and *C. echinospermum*. Within this group, *C. reticulatum* accessions were clustered closest to the *C. arietinum, C. yamashitae*. The Group II was separated from the other	Talebi *et al.*, 2009

		clusters. Group III (the annual tertiary group) included *C. judaicum*, *C. pinnatifidum* and *C. cuneatum.*	
16 RAPD	30 genotypes	No significant differences were observed between the mean percentage of the presence of RAPD markers between commercial cultivars and landraces.	Ahmad *et al.*, 2010
ISSR			
15 ISSR markers	6 annual and 7 perennial wild species (*C. acanthophyllum, C. pungens, C. nuristanicum*, *C. anatolicum, C. microphyllum*, *C. oxyodon*)	The clustering pattern was in agreement with the data based on crossability, seed storage protein, isozyme, allozyme and RAPD marker analysis. 39% molecular variance was observed among annual and perennial groups. The results also suggested the monophyletic origin of wild annuals chickpea.	Rajesh *et al.*, 2003
10 ISSR primers	12 chickpea genotypes (released cultivars and breeding lines)	In addition to the diversity analysis, one unique band was produced by the GGAGA primer in the BCP-15 genotype. This band may be linked to temperature tolerance phenotype.	Bhagyawant and Srivastava, 2008
AFLP			
AFLP(*Eco*RI and *Mse*I) 306 positions	47 accessions representing four perennial and six annual species	AFLP-based grouping of species revealed two clusters, Cluster I, includes three perennial species, *C. montbretii, C. isauricum* and *C. anatolicum*, while Cluster II consists of two subclusters, one including one perennial, *C. incisum*, along with three annuals from the second crossability group (*C. pinnatifidum*, *C. judaicum* and *C. bijugum*) and the other	Sudupak *et al.*, 2004

		one comprising three annuals from the first crossability group (*C. echinospermum, C. reticulatum* and *C. arietinum*).	
214 AFLP marker loci	95 accessions that represented 17 species of *Cicer* (*C. arietinum, C. echinospermum, C. reticulatum C. bijugum, C. juidaicum C. pinnatifidum, C. anatolicum C. canariense, C. Cuneatum, C. flexuosum, C. macracanthum C. microphyllum, C. multijugum C. nuristanicum, C. oxyodon C. songaricum, C. yamashitae)*	Three main species groups were identified; Group I included the cultivated species *C. arietinum, C. reticulatum* and *C. echinospermum*. Within this group, *C. reticulatum* accessions were clustered closest to the *C. arietinum* cultivars 'Lasseter', 'Kaniva' and 'Bumper', supporting the hypothesis that *C. reticulatum* is the most probable progenitor of the cultivated species. Group II consists of *C. bijugum, C. judaicum* and *C. pinnatifidum.* While Group III contained all nine perennial species assessed and two annual species *C. yamashitae* and *C. cuneatum.* The genetic variation within a species was highest in *C. pinnatifidum* followed by *C. reticulatum* and lowest in *C. macracanthum.*	Nguyen *et al.*, 2004
455AFLP	146 wild annual *Cicer* accessions (including two accessions of perennial *C. anatolicum* and six cultivars of chickpea)	Maximum genetic diversity of *C. reticulatum, C. echinospermum, C. bijugum* and *C. pinnatifidum* was found in southeastern Turkey, while Palestine was identified as the centre of maximum genetic variation for *C. judaicum*.	Shan *et al.*, 2005

8 AFLP primer pairs	28 chickpea accessions from diverse origin	Greatest genetic diversity was found among accessions from Afghanistan, Iran and Lebanon.	Talebi *et al.*, 2008b
SSR			
12 SSRs	78 genotypes (72 landraces, 4 cultivars, 2 wild species- *C. reticulatum* and *C. echinospermum*)	All the 76 accessions of cultivated chickpea could be readily distinguished with these markers. A significant positive correlation between the average number of repeats (size of the locus) and the amount of variation was observed.	Udupa *et al.*, 1999
90 SSRs	40 accessions (39 annual, 1 perennial)	The degree of conservation of the primer sites varied between species depending on their known phylogenetic relationship to chickpea, ranging from 92.2% in *C. reticulatum*, chickpea's closest relative and potential ancestor, down to 50% for *C. cuneatum*	Choumane *et al.*, 2000
11 SSR	29 accessions	Efficient marker transferability (97%) of the *C. reticulatum* STMS markers across other species of the genus was observed as compared to microsatellite markers from the cultivated species. Phylogenetic analysis clearly distinguished all the accessions	Sethy *et al.*, 2006a
74 STMS	10 accessions (9 cultivated, 1 wild *C. reticulatum*)	The high levels of intra-specific genetic polymorphism in chickpea was clearly evident from dendrogram analysis. Sequence analysis of these amplicons suggested random point mutations followed by the subsequent expansion by replication slippage.	Sethy *et al.*, 2006b

48 SSR markers	3000 accessions of composite collections	This was the most comprehensive genetic diversity studies in chickpea. In total, 1683 alleles were detected in 2915 accessions, of which, 935 were considered rare, 720 common and 28 most frequent. A number of group-specific alleles were detected: 104 in Kabuli, 297 in desi, and 69 in wild *Cicer*; 114 each in Mediterranean and West Asia (WA), 117 in South and South East Asia (SSEA), and 10 in African region accessions. Furthermore, based on comprehensive analysis, a 'reference set' was defined that includes broad-based elite breeding lines/cultivars with superior yield and enhanced adaptation to diverse environments. This is an ideal set of germplasm for allele mining, association genetics, mapping and cloning gene(s), and in applied breeding for the development of environments.	Upadhyaya *et al.*, 2008
10 EST-SSR markers	58 accessions	Crossability-group-specific sequence variations were observed among *Cicer* species that were phylogenetically informative. The neighbor joining dendrogram clearly separated the chickpea cultivars from the wild *Cicer* and validated the proximity of *C. judaicum*	Choudhary *et al.*, 2009
10 SSR markers	47 chickpea (*C. arietinum*) accessions including 21 induced mutation lines, 17 hybrid lines, 5 local cultigens, and 4 non-nodulating lines	UPGMA and ME (minimum evolution) trees classified the accessions into 6 groups and all but 6 accessions could be clearly separated. Grouping was mostly the same in the two phylogenetic trees, but the branching order	Khan *et al.*, 2010

		differed greatly. Recent introgression among the parental lines is suggested for this reason.	
Miscellaneous			
*trn*T-F region in chloroplasts	29 accessions (representing 25 species *C. arietinum, C. bijugum C. cuneatum, C. echinospermum, C. judaicum, C. pinnatifidum, C. reticulatum, C. yamashitae, C. chorassanicum, C. anatolicum, C. canariense, C. flexusoum, C. kermanense, C. microphyllum, C. montbretii, C. multijugum, C. nuristanicum, C. songaricum, C. spiroceras, C. subaphyllum, C. macracanthum, C. pungens, C. stapfianum, C. tragacanthoides, Lens ervoides, Pisum sativum*)	Phylogenetic analysis revealed three major clades in the genus *Cicer*. Inferred phylogenetic relationships supported multiple origins of annual species in the genus *Cicer*. Low variation within the most perennial species in the sequence regions suggests they	Javadi and Yamaguchi, 2004
Repeat unit length variation and internal transcribed spacer (ITS) sequences of nuclear ribosomal DNA	76 accessions of 10 *Cicer* species (*C. reticulatum, C. echinospermum, C. bijugum, C. pinnatifidum, C. judaicum, C. chorassanicum, C. yamashitae, C. cuneatum, C. microphyllum)*	Cladistic analysis of ITS data revealed two major clades, clade I consisting of *C. arietinum*, *C. reticulatum* and *C. echinospermum*, and clade II comprised of *C. judaicum*, *C. chorassanicum*, *C. bijugum* and *C. cuneatum*. *C. microphyllum* grouped with the above four species. *C. pinnatifidum* was present as a separate branch. *C. yamashitae* emerged as the most distinct species.	Singh *et al.*, 2008

12 RAPD, 8 ISSR	75 accessions belonging to 17 species of *Cicer* (*C. arietinum, C. reticulatum, C. echinospermum, C. pinnatifidum, C. judaicum, C. bijugum, C. yamashitae, C. cuneatum, C. anatolicum, C. multijugum, C. macracanthum, C. microphyllum, C. canariense, C. oxyodon*)	The dendrogram showed the variability between species was related to both growth habit and geographical origin	Iruela *et al.*, 2002
17 random genomic and five heterologous probes in 65 probe-enzyme combinations	Five *desi* and five *kabuli* type chickpea cultivars	No polymorphism in chickpea varieties was detected with four RAPD markers studied. However, some degree of polymorphism between *C. arietinum* and its wild relative *C. reticulatum* was detected. The RFLP analysis of chloroplast and mitochondrial genomes showed no polymorphism.	Udupa *et al.*, 2003
Microsatellite derived-RFLP	30 accessions	Greatest genetic diversity was observed in Pakistan, Iraq, Afghanistan, south-east Russia, Turkey and Lebanon. Lower genetic diversity was found in Iran, India, Syria, Jordan and Palestine	Serret *et al.*, 2006

60 RAPD and 10 ISSR primers	19 chickpea cultivars and five accessions of its wild progenitor *C. reticulatum* Ladizinsky	The ISSR analysis clearly indicated that only six polymorphic markers are reliable for estimation of genetic diversity, while nearly 30 RAPD primers are required for the same. Genetic data produced through ISSR can be used to correlate with the relationship measures based on pedigree data and morphological traits to minimize the individual inaccuracies in chickpea.	Rao *et al.*, 2007
33 RAPD and 9 morphological traits	36 genotypes	Correlation between the genetic distances was obtained with RAPD and morphological traits, indicating that there is a strong multi-locus association between molecular and morphological traits in these cultivars.	Talebi *et al.*, 2008a
15 AFLP and 18 STMS primer pairs	21 cultivars of *C. arietinum*	The genetic similarity between cultivars varied from 0.30 to 0.85 for AFLP and 0.22 to 0.83 for STMS markers. Association of varietal type and flower colour was observed as cultivars E 100Ymu and Nabin (both Desi type and pink flower) clustered together in the dendrogram.	Singh *et al.*, 2008