



Research Article

Genetic diversity analysis in chickpea grown under heat stress conditions of Madhya Pradesh

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Abstract

Genetic diversity study was conducted in 100 promising chickpea genotypes sown under late planting using Mahalanobis's D^2 Statistics which was also confirmed by SSR molecular markers. Based on D^2 values, 100 genotypes were grouped into sixteen clusters. The cluster I consisted of maximum 29 genotypes, followed by Cluster II, cluster V and cluster VI, which had 26, 13 and 12 genotypes, respectively. Maximum intra-cluster distance (164.10) was observed in cluster V, followed by cluster VI (150.23), cluster III (123.98) and cluster II (102.52). However, maximum inter cluster distance was noticed between cluster IX and cluster XV (853.43), followed by cluster X and cluster XV (749.13) and cluster VII and cluster XV (742.58). Molecular analysis grouped 100 genotypes into three major clusters. First major cluster consisted of four genotypes (ICCV 93025, ICCV 93024, ICCV 03401 and ICCV 95315) and second cluster consisted of two genotypes (ICCV 03405 and ICCV 01306). Third and last major cluster group contained 94 genotypes. The PIC value among the primers ranged from 0.3245 (TA 78) to 0.4375 (TA 135) and the highest gene diversity were found in TA 135 (0.5378). Among all eleven polymorphic SSR primers, only TA78 (0.0300), H5BO4 (0.0900), ICCAM0123a (0.0500), TA135 (0.0600) and H1G16 (0.1500) were shown heterozygosity. The genotypes conferring diversity at molecular studies (unaffected by environmental variations) can be used in future hybridization programmes and also helpful for plant breeders to screen effective heat tolerance genotypes for the development of high yielding improved lines for diverse environments.

Key words

Chickpea, D^2 statistics, genetic diversity, heat stress, SSR markers

Introduction

Chickpea is one of the most important *Rabi* pulse crop in India. India is the largest chickpea producer accounting a share of about 67% in global chickpea production with about 9.01 m ha area, 7.58 m t production. The total area in Madhya Pradesh reached 3.04 M ha with 3.29 M t of production and productivity of 1082 kg/ha (FAOSTAT, 2013-14). Madhya Pradesh is contributing 40% of India's total chickpea production. In India, chickpea is usually grown in winter-season but during the past three decades, there is significant shift in the growing environment from the cooler, long-season environments of northern India to the warmer, short-season environments of central and southern India. Chickpea area under late-sown conditions is increasing particularly in northern and central India due to inclusion of chickpea in new cropping systems and intense sequential cropping practices leading to a prolonged exposure of chickpea to high temperature. Heat stress is a serious constraint to chickpea production in northern and central India. Reproductive stages (flowering and podding) in chickpea are susceptible to changes in external environment and heat stress (Summerfield *et al.*, 1984; Wang *et al.*, 2006; Krishnamurthy *et al.*, 2011). D^2 analysis by Mahalanobis (1936) is a very important technique of measuring genetic divergence. Now it is reliably and extensively used in plants for measuring genetic divergence <http://ejplantbreeding.com>

(Tripathi *et al.*, 2013; Shinde *et al.*, 2013; Shekhawat *et al.*, 2014). The aim of forming clusters and finding the intra and inter cluster divergence is to provide the base of selecting parents for a planned breeding programme.

The knowledge of genetic diversity has a significant impact on the improvement of crop plants and this information has been successfully used for efficient germplasm management, fingerprinting and genotype selection. Genetic diversity can be estimated using phenotypic identification or molecular markers. However, morphological traits have a number of limitations including low polymorphism, low heritability, late expression, and may be controlled by epistatic and pleiotropic gene effects (Eivazi *et al.*, 2008). Molecular markers are a useful complement to morphological characterization of accessions because they are plentiful, independent of plant tissue or environmental effects, and allow cultivar identification very early in plant development (Manifesto *et al.*, 2001). Simple sequence repeats (SSRs) are common and informative molecular markers used for genetic diversity studies because of their simplicity, high levels of polymorphism, high reproducibility, and co-dominant inheritance patterns (Powell *et al.*, 1996).

Keeping in view the above facts, present investigation was undertaken to determine genetic divergence among 100 genotypes using

morphological and molecular markers to help the breeders in selecting promising and genetically diverse parents for desired improvement in chickpea for late sown conditions.

Materials and methods

Experimental materials: The experimental material comprising 100 genotypes of chickpea (74 Desi and 26 Kabuli, Received from ICRISAT, Hyderabad) were grown during Rabi 2012-2013 under late planting conditions (sown on 26th January, 2013) in a Randomized Complete Block Design with three replications at the Seed Breeding Farm, Department of Plant Breeding and Genetics, JNKVV, Jabalpur. Data were recorded on five randomly tagged plants for days to flower initiation, days to 50% flowering, days to pod initiation, days to maturity, plant height (cm), number of primary branches, number of secondary branches, total number of pods per plant, number of effective pods per plant, 100 seed weight (g), seeds per pod, seed yield per plant (g) and harvest index (%). The D² analysis was done according to Mahalanobis (1936). The clustering of genotypes was done by Tocher's method, as described by Rao (1952). The intra and inter cluster distances were computed as suggested by Singh and Chaudhary (1977).

DNA Isolation and Concentration:

Samples from the youngest leaves (200 mg) were collected from one month old chickpea genotypes for extraction of genomic DNA performed using the modified CTAB method (Saghai-Maroo *et al.*, 1984). Concentrations of DNAs were determined on the spectrophotometer (Nanodrop, model ND-100) after isolation. DNAs were diluted to 50 ng μl^{-1} for equal amounts of the samples from prepared concentration by running on the 0.8% agarose gel (1xTAE buffer) using known λ /HindIII DNA ladder.

DNA amplification using the SSR molecular marker: Eleven SSR primers (Table 1) synthesized by IDT (Promega, USA) and used for DNA amplifications using the PCR reaction mixture containing 2 μl DNA (50 ng μl^{-1}) and 20 μl reaction mixture [2 μl x10 PCR buffer solution (Promega, USA), 1.4 μl of 25 mM MgCl_2 (Promega, USA), 0.2 μl 25 mM dNTP (Promega, USA), 0.2 μl 500 U Taq DNA Polymerase (Promega, USA), 0.5 μl 25 pmol μl^{-1} primer (from each of the forward and reverse primers) and 15.7 μl nuclease free water] were performed in 35 cycles on the Eppendorf PCR device. PCR profile was optimized for amplification by using primers of unique sequence with higher GC ratio at high stringency. The PCR reaction was carried out with a initial denaturation at 94°C for 4 min, final denaturation at 94°C for 30 sec, annealing at above

50-52°C of temperature melting (T_m) for 30 sec, and extension at 72°C for 30 sec, a final extension at 72°C for 5 min and 4°C as holding temperature. The amplified PCR products were size separated by 2.5% (w/v) agarose gel with 1X TAE stained with ethidium bromide and visualized under UV transilluminator and then photographed using Syngene gel documentation system. In order to determine approximated size of bands, 100bp ladder (Promega, USA) was run along with the amplified PCR products. The scoring of SSR amplicons was done for each genotype.

Scoring and cluster analysis for molecular data:

For each SSR locus, sizes of the alleles were estimated for all the thirty eight genotypes and scored in the form of a binary matrix where '1' represented the presence of a band and '0' denoted its absence. Pair-wise genetic similarity (GS) was calculated among 38 chickpea genotypes using Jaccard's similarity coefficient. The values of GS may range from '1' (identical profiles for all marker in the two genotypes) to '0' (no common bands). The binary data generated for all the varieties for the polymorphic markers was entered in the Power Marker version 3.25 software. The similarity matrix was used to generate dendrogram for cluster analysis. Polymorphic information content (PIC) for each SSR locus was calculated based on number of bands per primer using the formula $\text{PIC} = 1 - \sum f_i^2$, where f_i is the frequency of the i^{th} allele in the genotype (Smith *et al.* 1997). A high PIC value establishes the power of SSR as a tool for genetic diversity quantification.

Results and discussion

Analysis of variance for characters under study indicated significant differences among all characters. Among the 13 characters studied, 100-seed weight (24.34%), harvest index (21.84%), number of pods per plant (18.40%) and seed yield per plant (15.25%) contributed maximum in the manifestation of genetic divergence (Table 2). These four traits accounted for 79.83 per cent of total variability. Jethava *et al.* (2000) reported that seed yield per plant, number of pods per plant and 100-seed weight contributed maximum towards genetic diversity. Parashi *et al.*, (2013) reported that seed yield per plant, number of pods per plant contributed maximum to genetic diversity. Prakash and Shekhawat (2012) also reported that 100- seed weight and pods per plant contributed maximum to genetic diversity.

On the basis of Mahalanobis D² statistics and Tocher's method, 100 genotypes used in the present investigation were grouped into 16 clusters. The cluster I was the largest and consisted

of 29 genotypes, followed by cluster II (26 genotypes), cluster V (13 genotypes), cluster VI (12 genotypes) and cluster III (9 genotypes), whereas cluster IV, VII, VIII, IX, X, XI, XII, XIII, XIV, XV and cluster XVI had only one genotype in each (Table 3). Jeena and Arora (2002) found twenty eight genotypes in cluster I, remaining 11 clusters were mono-genotypic. The D^2 analysis established the presence of broad diversity among the inbreds by the formation of 16 clusters. Jethava *et al.* (2000), Raval and Dobariya (2004), Parameshwarappa *et al.* (2011), Parashi *et al.*, (2013) obtained 16, 15, (20, 16, 25 in E1, E2 and E3) and 13 clusters of genotypes, from 70, 52, 103 and 33 genotypes respectively, indicating presence of broad genetic diversity in their materials.

Cluster XV showed highest mean performance for days to flower initiation, days to 50% flowering, days to pod initiation, days to maturity and plant height; cluster XIV for number of primary branches, number of secondary branches, total number of pods per plant and seed yield per plant; cluster XI for number of primary branches and number of seeds per pod and cluster VII for harvest index and number of primary branches. Cluster IX recorded minimum performance for days to flower initiation, days to 50% flowering, days to maturity, plant height and number of primary branches. On the basis of cluster means, the genotypes of cluster XV, XIV, XI, VII and IX were found superior and may be further utilized in breeding programme for yield advancement in chickpea.

The intra cluster distance ranged from 0.00 to 164.10 (Table 4). The cluster V showed maximum intra cluster D^2 value (164.10), followed by cluster VI (150.23), cluster III (123.98), cluster II (102.52) and cluster I (75.35) revealing the inclusion of diversion of diverse genotypes in these clusters. The inter cluster D^2 values ranged from 67.02 to 853.43. Maximum inter cluster distance *i.e.*, 853.43 was reported between cluster IX (ICCV 93014) and XV (ICCV 08102), which indicated that the genotypes included in these different clusters may give high heterotic response and thereby better segregants (Lal *et al.*, 2001). Minimum inter cluster D^2 value was observed between cluster IX and VIII indicating the close relationship among the genotypes included in these two clusters.

Genome analysis tools provide access to thousands of polymorphisms and monitor genetic diversity (Glaszmann *et al.*, 2010). Various molecular markers such as restriction fragment length polymorphism (RFLP) (Udupa *et al.*, 1993) and random amplified polymorphic DNA (RAPD) (Iruela *et al.*, 2002) found to be unsuccessful to <http://ejplantbreeding.com>

detect genetic diversity within chickpea. Among the all markers, simple sequence repeats (SSRs) is widely used to detect genetic variation within chickpea species (Udupa *et al.*, 1999) and construct genomic map (Flandez-Galvez *et al.*, 2003) due to most abundance and co-dominant nature with the highest information content of SSRs in the genome (Gupta and Varshney, 2000). A total of eleven SSR markers were used for estimating genetic diversity in 100 chickpea genotypes.

The polymorphic information content among the primers ranged from 0.3245 (TA 78) to 0.4375 (TA 135) (Table 5). The mean value of polymorphic information content was 0.3629. The marker TA 135 showed highest polymorphic information content (0.4375) as well as highest gene diversity (0.5378). Tiwari *et al.* (2014) found PIC values between 0.049 and 0.550 with mean value of 0.254 and genetic diversity from 0.0512 to 0.622 with a mean value of 0.316. Upadhyaya *et al.* (2008) found values 0.905 of PIC for TA135, respectively and also found 0.70 heterozygosity for TA135, respectively whereas, in this investigation TA135 showed 0.0600 heterozygosity.

Major allele frequency of 11 SSR markers ranged from 0.5400 (TA 135) to 0.7150 (TA 78). The mean value of major allele frequency among the primers was 0.6309. The highest gene diversity was found with TA 135 (0.5378), followed by primer H1B17 (0.5022), ICCM0127 (0.4950), H1G16 (0.4916), TA125 (0.4550), Cam0656 (0.4550) and ICCM0123a (0.4520). Minimum diversity was shown by marker Cam1536 (0.4352). Zakia *et al.* (2012) found 0.69 genetic diversity for primer TA135.

Among all eleven SSR primers, only TA78 (0.0300), H5BO4 (0.0900), ICCAM0123a (0.0500), TA135 (0.0600) and H1G16 (0.1500) have shown heterozygosity (Figure 1, 2 & 3). The heterozygosity in self-pollinating species such as chickpea mainly results from the low level (0 to 1.58%) of out crossing as has been reported earlier (Gowda, 1981) and the number of gene-targeted molecular markers such as SSR of chickpea are limited and show a low level of polymorphism in chickpea (Jafari *et al.*, 2013). Reif *et al.* (2005) observed that modified Euclidian distance is best suited for the estimation of genetic distances under the evolutionary forces that influence the genotypes under consideration is not available and no specific mutation model can be attributed to the allelic variation observed at the SSR loci.

Based on electrophoretic banding pattern, molecular diversity among 100 genotypes of chickpea was estimated and generated genetic



distance-based dendrogram for cluster analysis using neighbor-joining method implemented in Power Marker version 3.25. Cluster analysis revealed that all the genotypes were grouped into three major groups. First major group consisted of four genotypes (ICCV 93025, ICCV 93024, ICCV 03401 and ICCV 95315). Second major group consisted of two genotypes (ICCV 03405 and ICCV 01306). Third and last major cluster contained 94 genotypes. These major groups were further subdivided into several sub groups.

The results of present study revealed that these 100 genotypes, which are morphologically very much distinct from each other are very much similar at molecular level (on the basis of diversity analysis at both levels). This may be due to the genotypic effect (same origin) or the interaction between environments. From this study, it is clearly evident that as molecular markers are independent to environmental fluctuations and also stage or tissue specific, hence more emphasis should be given to the results obtained with molecular studies.

The identified promising lines viz., ICCV 93025, ICCV 93024, ICCV 03401, ICCV 95315, ICCV 03405 and ICCV 01306 could also be potentially utilized by plant breeders for developing elite chickpea lines/cultivars with higher yield and enhanced adaptation to late sown conditions.

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Table 1. SSR primer used for genetic diversity in chickpea genotypes

S.No.	Marker	LG	Forward sequence	Reverse sequence	Reference
1.	H1G16	LG-1	GTTTGCTTCAACACCGAGA	CCCATGAAGGCCTGAATTAT	Spurthi <i>et al.</i> , 2010
2.	TA135	LG-4	TGGTTGGAAATTGATGTTTT	GTGGTGTGAGCATAATTCAA	Winter <i>et al.</i> , 1999
3.	Cam0620	LG-3	ATTCCCAAACATTGGCAAAA	GTTTGGGGTTACTCATGGGA	Shiva, ICRISAT
4.	TA78	LG-5	CGGTAAATAAGTTCCCTCC	CATCGTGAATATTGAAGGGT	Winter <i>et al.</i> , 1999
5.	Cam1536	LG-7	TGATTTGGAGCATCGTCAAC	TTGGAGTAGTTTTTGGGGGA	Shiva, ICRISAT
6.	ICCM0123a	LG-7	GGATGGTCTGCTGGAATCAT	AAAGACAACAAAAAGACAATCATGT	Spurthi <i>et al.</i> , 2010
7.	Cam0656	LG-7	TCACTCTCTCGAAAACCCT	GAGTGAAACCGAGAGCGAAC	Shiva, ICRISAT
8.	TA125	LG-7	TTGAAATTGAACTGTAACAGAACATAAA	TAGATAGGTGATCACAGAAGAGAATG	Winter <i>et al.</i> , 1999
9.	H5B04	LG-8	CATAATTTTAAAAGAGGCACGTTAAAT	ATATAAGCAAAAATAAAGATGAGTTGC	Spurthi <i>et al.</i> , 2010
10.	ICCM0127	LG-6	TGTTGAACGAATTTACTCATCG	GGTGGGCTCCTATTGTTTGA	Spurthi <i>et al.</i> , 2010
11.	H1B17	LG-6	ATTTCGAGGTGGTACCTCTAGTGA	GAGGAACCGACGATGTATCTATT	Spurthi <i>et al.</i> , 2010



Table 2. Proportional contribution of seed yield and its attributing characters to divergence among 100 genotypes of chickpea

Source	Times ranked 1 st	Contribution %
Days to flower initiation	150	3.03%
Days to 50% flowering	11	0.22%
Days to pod initiation	187	3.78%
Days to maturity	215	4.34%
Plant height (cm)	146	2.95%
Number of primary branches	0	0.00%
Number of secondary branches	32	0.65%
Total number of pods per Plant	911	18.40%
Number of effective pods per Plant	219	4.42%
Number of seeds per pod	38	0.77%
100-seed weight (g)	1205	24.34%
Harvest index (%)	1081	21.84%
Seed yield per plant (g)	755	15.25%

**Table 3. Distribution of chickpea genotypes on the basis of D^2 statistic**

Cluster	No. of genotypes	Genotypes
1	29	ICCV 91005, ICCV 96027, JG14, ICCV 6103, ICCV 91006, ICCV 11111, ICCV 91902, ICCV 10115, ICCV 11109, ICCL 84207, ICCV 97318, ICCV 90015, ICCV 91008, ICCL 84228, ICCL 84242, ICCV 91020, ICCV 97024, ICCL 83233, ICCL 86235, ICCV 91021, ICCV 11104, ICCV10114, ICCL 84233, ICCV 10116, JG16, ICCV 10117, ICCV 10104, ICCV 00105, ICCV 10118
2	26	ICCV 96317, ICCV 09314, ICCV 03405, ICCV 05307, ICCV 03410, ICCV 06301, KAK2, ICCV 08104, ICCV 01302, ICCV 03401, ICCV 01306, ICCV 97022, ICCV 05310, ICCV 04306, ICCL 87206, JGK2, ICCV93054, ICCV 93024, ICCV 05113, ICCV 06102, ICCV 05112, ICCV 07118, ICCV 11118, ICCV 11311, ICCV 05303
3	9	ICCV 96001, JAKI 9218, ICCV 91024, JG130, ICCV 04304, ICCV 04307, Vaibhav, ICCV 08108, ICCL 86201
4	1	ICCV 93025
5	13	ICCL 82216, ICCV 11302, ICCV 05107, ICCV 04312, ICCV 04303, ICCV 95332, ICCV 91011, NbeG3, ICCV 93316, ICCV 96316, ICCV 06108, ICCV 90037, ICCL 85207
6	12	ICCV 07111, ICCV 08109, ICCV 07104, ICCV 90005, ICCV 07112, ICCV 93053, ICCV 93005, ICCV 91026, ICCV 91009, ICCV 03211, ICCV 09308, ICCV 03209,
7	1	ICCV 11113
8	1	ICCL 85201
9	1	ICCV 93014
10	1	ICCL89214
11	1	ICCV 03208
12	1	ICCV 00401
13	1	ICCV 95315
14	1	ICCL 84251
15	1	ICCV 08102
16	1	ICCV 91007

**Table 4. Average inter- and- intra cluster distances for 100 genotypes of chickpea**

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI	Cluster XII	Cluster XIII	Cluster XIV	Cluster XV	Cluster XVI
Cluster I	75.35															
Cluster II	196.60	102.52														
Cluster III	247.33	229.07	123.98													
Cluster IV	105.19	138.78	305.46	0.00												
Cluster V	238.10	205.61	323.45	112.90	164.10											
Cluster VI	190.52	340.77	234.63	224.27	287.52	150.23										
Cluster VII	108.01	188.52	383.66	72.84	240.67	318.64	0.00									
Cluster VIII	129.47	163.25	286.06	182.13	352.52	366.02	128.74	0.00								
Cluster IX	150.66	149.78	349.82	135.92	280.89	403.53	106.91	67.02	0.00							
Cluster X	105.86	287.90	330.63	220.81	402.96	298.75	118.35	108.43	118.77	0.00						
Cluster XI	178.61	193.78	212.66	272.95	377.04	350.94	211.38	100.12	108.26	102.71	0.00					
Cluster XII	246.26	159.99	182.37	236.64	243.94	296.74	333.02	271.67	337.77	431.38	323.25	0.00				
Cluster XIII	382.54	236.42	172.30	328.42	296.34	326.43	524.52	432.21	508.59	621.96	456.46	99.93	0.00			
Cluster XIV	373.20	441.89	443.55	232.56	226.70	268.02	455.94	624.90	524.18	610.03	618.66	426.52	416.27	0.00		
Cluster XV	496.47	536.45	265.41	524.50	503.52	285.02	742.58	683.09	853.43	749.13	677.33	319.86	157.08	457.56	0.00	
Cluster XVI	295.59	373.14	433.18	176.29	239.59	262.11	405.98	506.75	507.49	571.14	663.96	271.86	299.86	219.92	354.91	0.00

Table 5: Different parameters used for molecular diversity analysis in chickpea

Marker	Major Allele Frquency	Gene Diversity	Heterozygosity	PIC
TA125	0.6500	0.4550	0.0000	0.3515
TA78	0.7150	0.4076	0.0300	0.3245
H5BO4	0.6650	0.4456	0.0900	0.3463
H1B17	0.6000	0.5022	0.0000	0.4027
Cam0620	0.6700	0.4422	0.0000	0.3444
ICCM0127	0.5500	0.4950	0.0000	0.3725
Cam0656	0.6500	0.4550	0.0000	0.3515
ICCAM0123a	0.6550	0.4520	0.0500	0.3498
Cam1536	0.6800	0.4352	0.0000	0.3405
TA135	0.5400	0.5378	0.0600	0.4375
H1G16	0.5650	0.4916	0.1500	0.3707
Mean	0.6309	0.4654	0.0345	0.3629

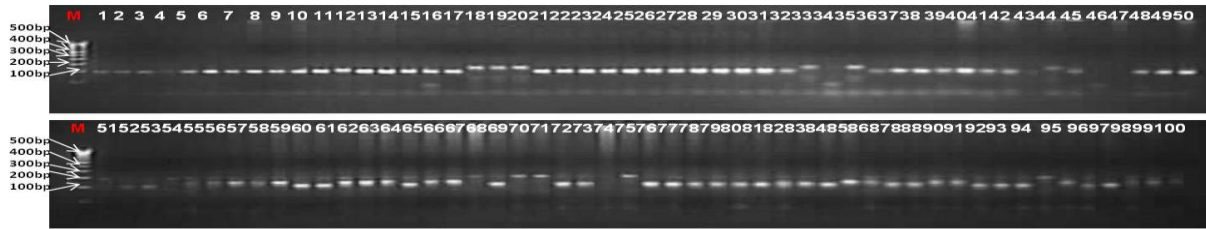


Fig.5 The banding pattern of SSR TA 78 marker among chickpea genotypes on 2.5% agarose gel

Figure 1. The banding pattern of TA 78 SSR markers among genotypes on 2.5 % agarose gel



Figure 2. The banding pattern of H5B04 SSR markers among genotypes on 2.5 % agarose gel

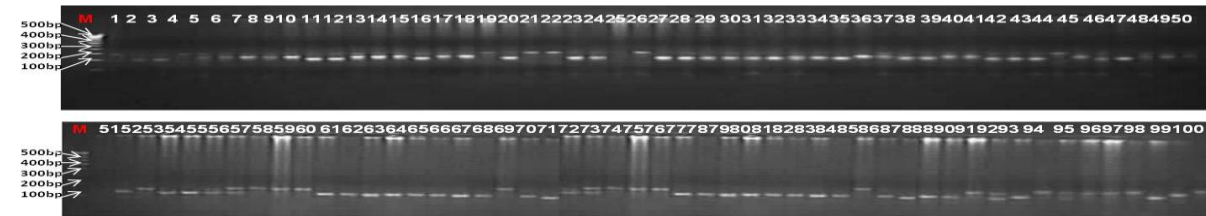


Figure 3. The banding pattern of TA 135 SSR markers among genotypes on 2.5 % agarose gel

M-100bp Ladder	Lane 21-ICCV 91008	Lane 41-ICCV 97022	Lane 61-ICCV 00105	Lane 81-ICCV 10115
Lane 1-ICCL82216	Lane 22-ICCV 91009	Lane 42-ICCV 97318	Lane 62-ICCV 03208	Lane 82-ICCV 10116
Lane 2-ICCL83233	Lane 23-ICCV 91011	Lane 43-ICCV 00401	Lane 63-ICCV 03209	Lane 83-ICCV 10117
Lane 3-ICCL84207	Lane 24-ICCV 91020	Lane 44-ICCV 01302	Lane 64-ICCV 03211	Lane 84-ICCV 10118
Lane 4-ICCL84248	Lane 25-ICCV 91021	Lane 45-ICCV 01306	Lane 65-ICCV 05107	Lane 85-ICCV 97024
Lane 5-ICCL84233	Lane 26-ICCV 91024	Lane 46-ICCV 03401	Lane 66-ICCV 05112	Lane 86-ICCV 11104
Lane 6-ICCL84242	Lane 27-ICCV 91026	Lane 47-ICCV 03405	Lane 67-ICCV 05113	Lane 87-ICCV 11109
Lane 7-ICCL84251	Lane 28-ICCV 91902	Lane 48-ICCV 03410	Lane 68-ICCV 06102	Lane 88-ICCV 11111
Lane 8-ICCL85201	Lane 29-ICCV 93005	Lane 49-ICCV 04303	Lane 69-ICCV 06103	Lane 89-ICCV 11113
Lane 9-ICCL85207	Lane 30-ICCV 93014	Lane 50-ICCV 04304	Lane 70-ICCV 06108	Lane 90-ICCV 11118
Lane 10-ICCL86201	Lane 31-ICCV 93024	Lane 51-ICCV 04306	Lane 71-ICCV 07104	Lane 91-ICCV 11302
Lane 11-ICCL86235	Lane 32-ICCV 93025	Lane 52-ICCV 04307	Lane 72-ICCV 07111	Lane 92-ICCV 11311
Lane 12-ICCL87206	Lane 33-ICCV 93053	Lane 53-ICCV 04312	Lane 73-ICCV 07112	Lane 93-JG14
Lane 13-ICCL87207	Lane 34-ICCV 93054	Lane 54-ICCV 05303	Lane 74-ICCV 07118	Lane 94-JG14
Lane 14-ICCL89214	Lane 35-ICCV 93316	Lane 55-ICCV 05307	Lane 75-ICCV 08102	Lane 95-JG130
Lane 15-ICCV 90005	Lane 36-ICCV 95315	Lane 56-ICCV 05310	Lane 76-ICCV 08104	Lane 96-JAK19218
Lane 16-ICCV 90015	Lane 37-ICCV 96001	Lane 57-ICCV 06301	Lane 77-ICCV 08108	Lane 97-NBeG3
Lane 17-ICCV 90037	Lane 38-ICCV 96027	Lane 58-ICCV 09308	Lane 78-ICCV 08109	Lane 98-Vaibhav
Lane 18-ICCV 91005	Lane 39-ICCV 96316	Lane 59-ICCV 09314	Lane 79-ICCV 10104	Lane 99-JGK2
Lane 19-ICCV 91006	Lane 40-ICCV 96317	Lane 60-ICCV 95332	Lane 80-ICCV 10114	Lane 100-KAK2