

## Assessing biochemical and molecular diversity in Ker (*Capparis decidua*): A multipurpose shrub of Thar Desert

S. Ali<sup>1</sup>, S. Kumar<sup>1,2</sup>, S.N. Saxena<sup>1,3</sup>, R. Sharma<sup>1,4,\*</sup>, P.K.Singh<sup>1,5</sup>, G. Singh<sup>1</sup>

<sup>1</sup>Plant Biotechnology Center, SK Rajasthan Agricultural University, Bikaner- 334006

<sup>2</sup>Anand Agricultural University, Anand - 388 110

<sup>3</sup>National Research Centre on Seed Spices Tabiji, Ajmer- 305 206

<sup>4</sup>Central Arid Zone Research Institute, Jodhpur- 342 003

<sup>5</sup>Indian Institute of Vegetable Research, Varanasi- 221 305

### Abstract

*Capparis decidua* (Forssk.) Edgew., commonly known as ker, is a highly exploited rangeland perennial bushy shrub in the Thar Desert. No management or conservation efforts have been established for this species. The present study was carried out with the aim to examine the targeted location specific biochemical and molecular variability present in 19 plants of *Capparis decidua* from Bikaner and Kodemdesar region of Rajasthan. Thirteen biochemical parameters and eight minerals (a total 21 parameters) on fruit and bud were estimated. The Manhattan's dissimilarity coefficient obtained on the basis of 21 biochemical parameters showed range of similarity from 63% to 97.7% with 88.8% average similarity for fruits. Comparable range of 70 to 97.8% with 90.5% average similarity was obtained for buds also. A total of 15 RAPD primers produced 43 band positions, of which 88.37% were polymorphic. Jaccard's similarity coefficients ranged from 33.4 to 93.1%. The biochemical and RAPD based phylogenetic dendrograms were not correlated. Nevertheless, RAPD was found to be more efficient in estimating the diversity as compared to biochemical and chemical parameters. However, combined knowledge of biochemical- and molecular-based diversity will assist in selection of diverse plants to promote conservation for future use.

**Key words :** Biochemical parameters, *Capparis spp*, diversity, RAPD

### Introduction

The western Thar desert represents a characteristic environment where several plants species have adapted to rid hostile conditions. It has the richest diversity of plants as compared to other deserts of the world. *Capparis decidua* or Ker is a rangeland multipurpose woody plant of the Thar desert belongs to *Capparaceae*. Ker is a small much branched shrub of arid regions. Dry heat and intense sunlight is preferred environment for caper plants. Plants are productive in zones having 350 mm annual precipitation (falling mostly in winter and spring months) and easily survive summertime temperatures higher than 48°C. However, caper is a cold tender plant and has a temperature hardiness (-8°C) range similar to the olive tree (Vyas *et al.*, 17). *C. decidua* is used as vegetable, pickle and condiment. The fruits of this species are rich in proteins, carbohydrates, fibre and minerals. Beside this, it has medicinal value; stem and root bark extracts contain isocodonocarpine, alcoholic extract have sedative and anticonvulsant effect (Goyal *et al.*, 8) and other alkaloids

which are effective in treating asthma, inflammation, cough etc.

Among numerous techniques available for assessing the genetic diversity and relatedness among plant germplasm, DNA-based markers are very effective and reliable tools. The information recorded for various morphological traits in *C. decidua* has been generated by various workers sporadically but no systematic information is available for its nutritional value (Kumar *et al.*, 12). Documenting the genetic variations at biochemical, nutritive and molecular level will provide an efficient tool for identifying useful genotypes that could be used as cultivars for extraction of standard drugs or for food purpose. However, biochemical and nutrition based studies may be misleading as most of these traits are multigenic in inheritance and are influenced by the environment, so the variability was also studied at molecular level using RAPD markers.

Very limited studies on genetic diversity analysis have been conducted for efficient utilization of ker (Abdel-Mawgood *et al.*, 2; Vyas *et al.*, 17; Kumar *et al.*, 12). Similarly, inadequate studies have been done in *C. decidua* for its biochemical and nutritive value (Vyas

*et al.*, 17; Kumar *et al.*, 12). While species like *C. spinosa* has been widely studied for its nutritive value and for diversity analysis with AFLP (Inocencio *et al.*, 11). Still little effort has been made to study comprehensively the chemical and genetic diversity on the same accessions. This investigation deals with estimating the extent of genetic variability using RAPD analysis in relation to biochemo-variation observed among accessions from two different locations.

## **Material and methods**

### ***Plant material***

Fruits and buds from 10 randomly tagged wild plants from barren land of village Kodamdesar and nine plants from uncultivated land of Agricultural Research Station (ARS) Bikaner were collected during April to May separately in paper bags. Scanty rainfall (250mm), high temperature, deep water table combined with sandy soil makes harsher environment of area studied. Similar sized buds and fruits were picked on visual basis for chemical study to eliminate morphological variation.

### ***Biochemical and RAPD analysis***

Moisture content was obtained by heating the samples to a constant weight in a thermostatically controlled oven at 100°C (ICMR, 10). The ash, dietary fiber (hemicellulose, cellulose and lignin), crude fiber, crude protein, crude fat, total carbohydrate, vitamin C content and calcium contents were obtained using the methods described by Association of Official Analytical Chemists (AOAC, 1). Phosphorus was determined by calorimetric method of AOAC (1). Protein was determined using the micro-Kjeldhal method ( $N \times 6.25$ ). The soluble sugar and starch was estimated by anthrone method described by Dubios *et al.* (7). Magnesium, iron, zinc, manganese, copper and cobalt was determined by using Atomic Absorption Spectrophotometer (Bishnoi and Brar, 5) while sodium and potassium were estimated using flame photometer (AOAC, 1). Proline was estimated by method given by Bates *et al.* (4).

For random amplified polymorphic DNA (RAPD) analysis total genomic DNA was extracted using the method of Doyle and Doyle (6) from leaves. The PCR reactions were accomplished in a 25  $\mu$ l reaction mixture containing 1 $\times$  assay buffer, one unit of Taq DNA polymerase (Bangalore Genei Pvt. Ltd., India), 200  $\mu$ M of each dNTPs (Bangalore Genei Pvt. Ltd., India), 0.2  $\mu$ M primers and 50 ng of template DNA. The PCR reactions were carried out in DNA thermal cycler (Model-CGI-96, Corbett Research, Australia) and reiterated thrice for each primer to ensure the repeatability of RAPD results. Only highly repeatable primers were included in the study. PCR amplification was performed in following steps: initial denaturation at 94°C for 4 min, 43 cycles of denaturation at 94°C for 1 min, primer annealing at 37°C for 1 min,

extension at 72°C for 2 min and final step of extension at 72°C for 4 min. Amplified products were electrophoresed in 1.5% agarose in 1 $\times$ TBE buffer. The gels were stained with ethidium bromide and documented using gel documentation system.

### ***Statistical analysis***

The RAPD bands were scored for the presence (1) or absence (0) and each band was regarded as a locus. All calculations were done using computer program NTSYSpc v 2.02 (Rohlf, 15). Similarity matrix was constructed using the Jaccard's similarity coefficients and subjected to UPGMA (unweighted pair-group method with arithmetic averages) analysis to generate dendrogram. The matrices derived from RAPD and biochemical data were correlated using MxCOMP module of NTSYSpc. The discriminatory power of included primers was analyzed using the standard statistical package of Tessier *et al.* (16). Polymorphism information content (PIC) was also calculated according to Anderson *et al.* (3). In case of biochemical parameters, Manhattan distance coefficients were used. Dissimilarity matrix constructed using Manhattan coefficients were subjected to UPGMA analysis to generate dendrogram, using computer program NTSYSpc after the standardization of quantitative data. Pairwise population comparisons were analyzed with an analysis of molecular variance (AMOVA) using Genalex 6.5 (Peakall and Smouse, 14).

Nei's measurements of genetic diversity among natural populations were also calculated, including the total genetic diversity (HT that is, expected heterozygosity), mean genetic diversity within populations (HS), and the proportion of genetic diversity occurring among populations, GST (inter-population genetic differentiation) = (HT-HS)/HT. All of these genetic diversity parameters were estimated using POPGENE (Yeh *et al.*, 19) version 1.32 assuming all loci to be dominant and in Hardy-Weinberg equilibrium. Gene flow (Nm, number of migrants) was estimated from the  $Nm = 0.5 \times (1 - G_{st})/s_{t}$ . Gene flow (Nm) is a major factor impacting genetic structure and genetic differentiation among populations.

## **Results and discussion**

### ***Phenotypic diversity***

The analysis was conducted for thirteen biochemical parameters and eight minerals (a total 21 parameters) on fruit and bud for 19 different samples from two populations. During biochemical analysis, vitamin C was present in non-detectable quantities in dried fruits while in mineral analysis, manganese and cobalt were not detected in any of the samples.

The similarity matrix indices were estimated considering all individual traits and converted into a cluster tree

(Fig 1). The pair wise genetic relationships based on fruits and buds biochemical parameters were calculated using method of Manhattan dissimilarity coefficient analysis (Table 1). The Manhattan dissimilarity values for fruits ranged from 0.023 (K8 and K12) to 0.370 (IABM4 AND K7) with an average of 0.112 (11.2%) for biochemical parameters. Vyas *et al.* (2009) have also reported the similar results in ker from Thar. The similarity within Bikaner genotypes was higher (89.4%) compared to the genotypes between Bikaner and Kodamdesar (88.8%) and within Kodamdesar (88.5%) (Table 2).

For buds, the Manhattan dissimilarity coefficient values ranged from 0.022 (K8 and IABM) to 0.300 (IABM4 and K7) with an average of 0.095 (9.5%) which is in congruence with Kumar *et al.* (12). The similarity within Bikaner genotypes was higher (90.9%) compared to the genotypes within Kodamdesar (90.1%). However the similarity (90.5%) between Bikaner and Kodamdesar was lying between the within-group mean.

The dendrogram based on fruit and bud biochemical data has put all the genotypes in three major groups (group A, B and C) comprising of same entries, at 76.5% and 83% between group similarities, respectively. Group A consists K2, K8, K12, K14, S1M, K16, BIABM1, IABM and K7, total 9 genotype having 94.9% (fruits) within group similarity and group B consists, K23, SBF, BIABM2, R10, IABM1, S2M, K26, and K25, total 8 genotypes, with 94.4% (fruits) within group similarity and Group C consists K28 and IABM4 having 91% (fruits) within group similarity. Similar pattern of within group similarities was observed for buds, it was A and B 95% and 93.7% for group C. The similarity between group A and B was found to be 89.4% (fruits) 90% (buds). The similarity of group C with rest of group B and C for fruits was 76.5% whereas for buds it was 83%. In contrast to present investigation, Vyas *et al.* (17) generated two groups in dendrogram for biochemical parameters. This may be due to collection of material from Fatehpur region of Thar desert lying nearly 200km apart from present collection region.

#### **RAPD based Diversity**

DNA amplification of 19 ker accessions was studied using 15 decamer RAPD primers. Out of 15, seven primers failed to show any amplification while other eight primers generated fragments ranging from 3 (OPF-7) to 7 (OPF-5 and OPG-4). A total of 43 amplified fragments (5.37 bands per primers) were obtained, of which 38 (88.3%) were polymorphic. The size of amplicons generated varied from 300-4000bp. Though, none of the single primers produced unique patterns for all the nineteen genotypes, they could distinguish all the genotypes collectively. Similar results were detected by Vyas *et al.* (17) and Kumar *et al.* (12) in RAPD marker whereas Inocencio *et al.* (11) could found only 2% unique bands while working with AFLP. PIC values

ranged from 0.199 (OPF-7) to 0.345 (OPG-11) with an average of 0.29 for all eight primers which is little less than Vyas *et al.* (17). The single numerical index of discrimination value (D) ranged from 0.520 (OPF-7) to 0.959 (OPG-4) for single primer based RAPD patterns which is congruence with Vyas *et al.*, (2009) and Kumar *et al.* (2013). However, both of these primers had 66.6% and 100% polymorphism level respectively (Table 3). The PIC and Discriminatory values had a correlation coefficient of  $r = 0.87$ . This correlation was considerably higher than previously reported (Vyas *et al.*, 17).

Pairwise similarities between the accessions calculated on the basis of Jaccard's coefficient ranged between 0.344 (IABM1 and K14) and 0.931 (BIABM1 and S1M), with a mean of 0.60 (Table 4). The average dissimilarity observed through biochemical parameters (11.2%) was lower than the RAPD (60%) suggesting better efficiency of the RAPD profile to analyze diversity that exploits sites from unexpressed genome sequences as well as from genes contributing structurally and functionally and not confounded by environmental factors (Vyas *et al.*, 17; Henry, 9). But the diversity analysed through biochemical parameters reflects expressed genetic composition obviously limiting the range of diversification beyond functional integrity. A greater diversity range (34.4% to 93.1%) is the direct indication of good adaptability of this wild plant in the region studied. The concluded diversity was much higher than the earlier reported (Abdel-Mawgood *et al.*, 2). Within-group mean Jaccard's pairwise similarity was higher in Bikaner genotypes (66.1%) than Kodamdesar (56.6%), while the similarity between Bikaner and Kodamdesar (60.1%) fell between the within-group mean. The Pairwise population comparisons were examined using Analysis of Molecular Variance (AMOVA). The AMOVA indicated that most (96%) of the molecular variation in ker populations exists among individuals within populations, with lesser amounts among populations (4%).

The dendrogram divided 19 accessions into two clusters i.e. A and B at 46% between group similarities. First group formed by a total of 15 accessions (K2, IABM, IABM4, K23, SBF, K16, BIABM2, R10, K26, K25, IABM1, K7, K12, S1M and BIABM1) having 68.96% within group similarity and group B consists of 4 genotypes (K8, K14, K28 and S2M) with 55.76% within group similarity (Fig 2).

#### **Gene diversity and frequency**

The analysis of gene diversity is an alternative method to measure the variation present in a population (Weir, 18). It is a proportion of individual heterozygous at a locus and a measurement unit for population heterozygosity. Highest level of Nei's gene diversity value (0.4998) was observed at OPG11 locus. Population Bikaner with the higher mean  $I$  (0.4348+ 2775) value was exhibited lower

percentage of polymorphic loci (74.32%). The average total genetic diversity (Ht), genetic diversity within population (Hs) and coefficient of genetic differentiation (Gst) across all loci were  $0.3158 \pm 0.0332$ ,  $0.2925 \pm 0.0298$  and  $0.0738$ , respectively. The Gst are used to predict gene flow which is a fundamental micro evolutionary force that can determine the potential for genetic differentiation among populations and for local adaptation and also influences the geographical spread of novel adaptations (Musa *et al.*, 13). In this study the gene flow was 6.2782. Both the populations vary for allelic frequencies for most of the markers. Two of the bands (OPF9-1270 bp and OPF2-1250bp) were present only in Kodamdesar genotypes (K2 and K14). One null marker (OPF2-830bp) was present only in Bikaner genotype R10. This clearly indicates separation of two population led by genetic drift. The highest level of gene frequency value (1.000) was observed in allele 1 with the 4 primers (OPF5, OPF2, OPF7 and OPF9) and the lowest frequency value (0.0270) was obtained in allele 1 using same 2 primers (OPF1 and OPF2).

Comparing the gene frequency with corresponding loci in the kodemdesar, the gene frequency of the Bikaner population was unchanged at 11.62% of all loci, decreased at 30.23% and increased at 58.13%. The variation of gene frequency represents the changes occurring in genetic structure among both populations. Thus, compared with the Kodemdesar population, the genetic structure has changed in the Bikaner population. The lesser amount of geographical distance and the limited numbers of parents could have led to this situation.

Weak correlation between biochemical and genetic matrices can be explained, because for a biochemical synthesis usually a pathway consisting of several enzymes plays their role. The low correlation between the genetic and biochemical parameter is expected because all the loci, which are actually responsible for biochemical gene expression, are not being covered by the RAPD markers (Kumar *et al.*, 12).

In conclusion, the percentage of polymorphic loci in Kodemdesar and Bikaner populations was 83%. Compared with those in the Kodemdesar population, the percentage of polymorphic loci in Bikaner population was differed, showing that the genetic diversity difference in both populations under the same natural conditions. The efficacy of biochemical parameters is better than RAPD, as marker shows only the diversity of DNA while the results of biochemical parameters can be used for the diversity as well as for the drug, and medicinal values and present true picture of plant's biochemical composition. Nevertheless, RAPD was found to be more efficient in estimating the diversity as compared to biochemical and chemical parameters. However, collective knowledge of

biochemical- and molecular-based diversity will assist in selection of nutritionally rich samples for medicinal purpose, while genetic diversity to face natural challenges and find sustainable ways to promote conservation for future use.

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Table 1. Manhattan dissimilarity coefficients of 19 *C. decidua* (fruits and buds) samples based on biochemical/minerals parameters

| Samples | K2    | K7    | K8    | K12   | K14   | K16   | K23   | K25   | K26   | K28   | SIM   | SBF   | BIABM1 | BIABM2 | IABM  | IABM4 | R10   | S2M   | IABM1 |  |
|---------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--------|-------|-------|-------|-------|-------|--|
| K2      | 0     |       |       |       |       |       |       |       |       |       |       |       |        |        |       |       |       |       |       |  |
| buds    | 0     |       |       |       |       |       |       |       |       |       |       |       |        |        |       |       |       |       |       |  |
| K7      | 0.060 | 0     |       |       |       |       |       |       |       |       |       |       |        |        |       |       |       |       |       |  |
| fruits  | 0.061 | 0     |       |       |       |       |       |       |       |       |       |       |        |        |       |       |       |       |       |  |
| buds    | 0.027 | 0.066 | 0     |       |       |       |       |       |       |       |       |       |        |        |       |       |       |       |       |  |
| K8      | 0.049 | 0.082 | 0     |       |       |       |       |       |       |       |       |       |        |        |       |       |       |       |       |  |
| fruits  | 0.027 | 0.065 | 0.023 | 0     |       |       |       |       |       |       |       |       |        |        |       |       |       |       |       |  |
| buds    | 0.032 | 0.072 | 0.034 | 0     |       |       |       |       |       |       |       |       |        |        |       |       |       |       |       |  |
| K12     | 0.034 | 0.081 | 0.037 | 0.035 | 0     |       |       |       |       |       |       |       |        |        |       |       |       |       |       |  |
| fruits  | 0.053 | 0.099 | 0.038 | 0.040 | 0     |       |       |       |       |       |       |       |        |        |       |       |       |       |       |  |
| buds    | 0.053 | 0.099 | 0.056 | 0.054 | 0.039 | 0     |       |       |       |       |       |       |        |        |       |       |       |       |       |  |
| K14     | 0.043 | 0.087 | 0.029 | 0.040 | 0.028 | 0     |       |       |       |       |       |       |        |        |       |       |       |       |       |  |
| fruits  | 0.096 | 0.148 | 0.088 | 0.084 | 0.092 | 0.075 | 0     |       |       |       |       |       |        |        |       |       |       |       |       |  |
| buds    | 0.121 | 0.158 | 0.083 | 0.099 | 0.081 | 0.083 | 0     |       |       |       |       |       |        |        |       |       |       |       |       |  |
| K23     | 0.143 | 0.194 | 0.133 | 0.146 | 0.132 | 0.121 | 0.082 | 0     |       |       |       |       |        |        |       |       |       |       |       |  |
| fruits  | 0.119 | 0.159 | 0.087 | 0.107 | 0.089 | 0.085 | 0.054 | 0     |       |       |       |       |        |        |       |       |       |       |       |  |
| buds    | 0.129 | 0.177 | 0.116 | 0.117 | 0.120 | 0.102 | 0.065 | 0.073 | 0     |       |       |       |        |        |       |       |       |       |       |  |
| K25     | 0.152 | 0.190 | 0.112 | 0.128 | 0.101 | 0.115 | 0.043 | 0.05  | 0     |       |       |       |        |        |       |       |       |       |       |  |
| fruits  | 0.252 | 0.307 | 0.248 | 0.255 | 0.234 | 0.221 | 0.176 | 0.148 | 0.158 | 0     |       |       |        |        |       |       |       |       |       |  |
| buds    | 0.203 | 0.253 | 0.176 | 0.189 | 0.176 | 0.168 | 0.115 | 0.101 | 0.103 | 0     |       |       |        |        |       |       |       |       |       |  |
| K28     | 0.045 | 0.088 | 0.036 | 0.026 | 0.051 | 0.056 | 0.073 | 0.130 | 0.108 | 0.24  | 0     |       |        |        |       |       |       |       |       |  |
| fruits  | 0.037 | 0.075 | 0.046 | 0.028 | 0.046 | 0.047 | 0.102 | 0.104 | 0.132 | 0.185 | 0     |       |        |        |       |       |       |       |       |  |
| buds    | 0.091 | 0.146 | 0.082 | 0.082 | 0.083 | 0.064 | 0.026 | 0.075 | 0.065 | 0.183 | 0.068 | 0     |        |        |       |       |       |       |       |  |
| SIM     | 0.107 | 0.154 | 0.082 | 0.094 | 0.060 | 0.068 | 0.037 | 0.057 | 0.065 | 0.131 | 0.094 | 0     |        |        |       |       |       |       |       |  |
| fruits  | 0.054 | 0.095 | 0.042 | 0.047 | 0.049 | 0.038 | 0.072 | 0.115 | 0.085 | 0.220 | 0.053 | 0.069 | 0      |        |       |       |       |       |       |  |
| buds    | 0.069 | 0.109 | 0.028 | 0.044 | 0.045 | 0.041 | 0.065 | 0.071 | 0.094 | 0.153 | 0.052 | 0.066 | 0      |        |       |       |       |       |       |  |
| BIABM1  | 0.103 | 0.160 | 0.096 | 0.105 | 0.099 | 0.077 | 0.045 | 0.059 | 0.064 | 0.168 | 0.095 | 0.033 | 0.078  | 0      |       |       |       |       |       |  |
| fruits  | 0.084 | 0.135 | 0.064 | 0.089 | 0.069 | 0.052 | 0.053 | 0.051 | 0.075 | 0.129 | 0.087 | 0.050 | 0.055  | 0      |       |       |       |       |       |  |
| buds    | 0.046 | 0.101 | 0.048 | 0.049 | 0.046 | 0.042 | 0.070 | 0.103 | 0.096 | 0.174 | 0.048 | 0.057 | 0.040  | 0.065  | 0     |       |       |       |       |  |
| IABM    | 0.060 | 0.095 | 0.022 | 0.041 | 0.051 | 0.041 | 0.093 | 0.096 | 0.124 | 0.174 | 0.048 | 0.093 | 0.031  | 0.075  | 0     |       |       |       |       |  |
| fruits  | 0.317 | 0.370 | 0.312 | 0.310 | 0.306 | 0.282 | 0.230 | 0.201 | 0.219 | 0.093 | 0.293 | 0.235 | 0.281  | 0.232  | 0.278 | 0     |       |       |       |  |
| IABM4   | 0.248 | 0.300 | 0.223 | 0.231 | 0.207 | 0.217 | 0.154 | 0.146 | 0.127 | 0.063 | 0.226 | 0.165 | 0.197  | 0.180  | 0.218 | 0     |       |       |       |  |
| buds    | 0.120 | 0.174 | 0.115 | 0.120 | 0.106 | 0.094 | 0.058 | 0.056 | 0.044 | 0.145 | 0.104 | 0.059 | 0.085  | 0.052  | 0.083 | 0.212 | 0     |       |       |  |
| R10     | 0.127 | 0.168 | 0.096 | 0.109 | 0.076 | 0.088 | 0.054 | 0.048 | 0.047 | 0.118 | 0.103 | 0.047 | 0.075  | 0.069  | 0.102 | 0.137 | 0     |       |       |  |
| fruits  | 0.128 | 0.180 | 0.121 | 0.122 | 0.121 | 0.093 | 0.054 | 0.066 | 0.055 | 0.155 | 0.110 | 0.061 | 0.086  | 0.059  | 0.090 | 0.212 | 0.052 | 0     |       |  |
| S2M     | 0.116 | 0.155 | 0.082 | 0.096 | 0.073 | 0.076 | 0.048 | 0.045 | 0.056 | 0.112 | 0.095 | 0.043 | 0.060  | 0.058  | 0.086 | 0.145 | 0.031 | 0     |       |  |
| buds    | 0.113 | 0.165 | 0.109 | 0.117 | 0.097 | 0.088 | 0.058 | 0.052 | 0.073 | 0.158 | 0.107 | 0.056 | 0.078  | 0.049  | 0.075 | 0.216 | 0.040 | 0.042 | 0     |  |
| IABM1   | 0.134 | 0.173 | 0.096 | 0.109 | 0.099 | 0.096 | 0.035 | 0.041 | 0.045 | 0.093 | 0.104 | 0.058 | 0.073  | 0.058  | 0.100 | 0.131 | 0.048 | 0.036 | 0     |  |
| buds    |       |       |       |       |       |       |       |       |       |       |       |       |        |        |       |       |       |       |       |  |

**Table 2.** Percent Similarity among various groups for RAPD and Biochemical analysis in Buds and Fruits of *C. decidua*

| Groups                         | RAPD   | Buds   | Fruits |
|--------------------------------|--------|--------|--------|
| Within Bikaner                 | 66.10% | 90.90% | 89.40% |
| Within Kodamdesar              | 56.60% | 90.10% | 88.50% |
| Between Bikaner and Kodamdesar | 60.10% | 90.50% | 88.80% |
| Average                        | 60.70% | 90.50% | 88.80% |

**Table 3.** List of RAPD primers showing total and polymorphic amplicons along with PIC and discrimination power for *Capparis decidua*

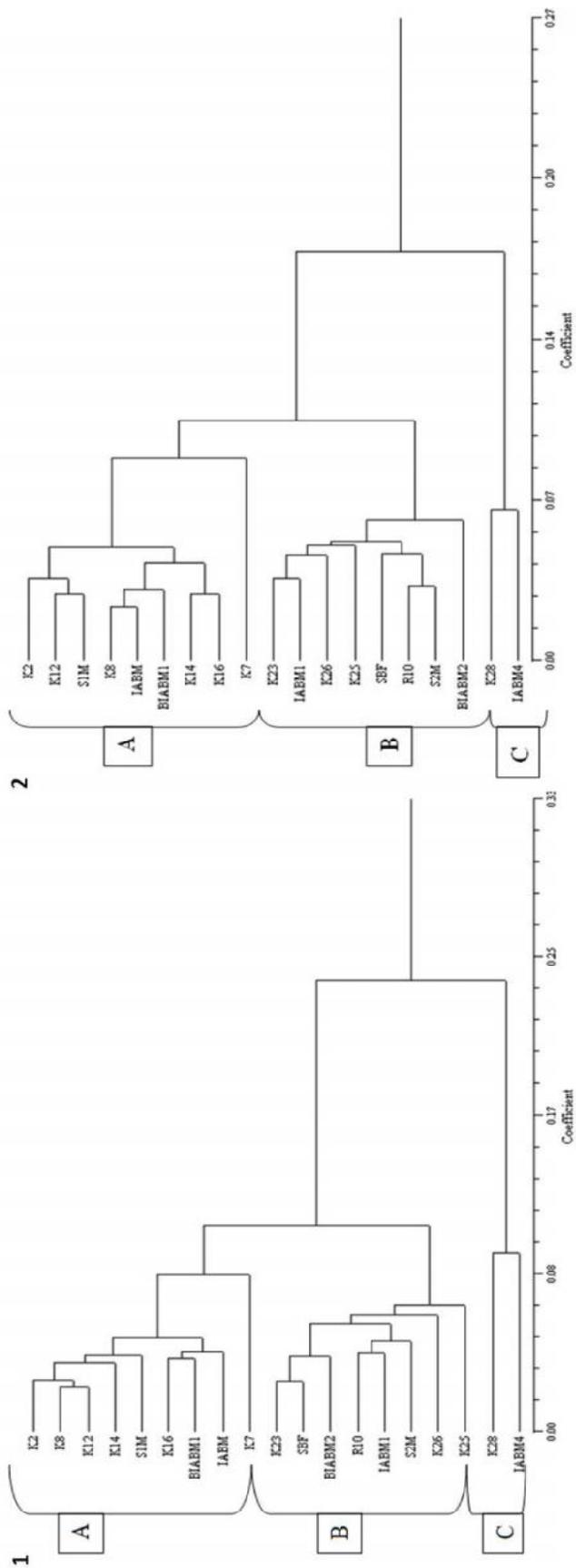
| Primers | Sequences<br>(5' Æ 3') | Total<br>bands | Polymorphic<br>bands | Polymorphism<br>(%) | PIC   | Discrimination<br>index<br>(D) |
|---------|------------------------|----------------|----------------------|---------------------|-------|--------------------------------|
| OPF-1   | ACGGATCCTG             | 5              | 5                    | 100                 | 0.321 | 0.865                          |
| OPF-2   | GAGGATCCCT             | 5              | 4                    | 80                  | 0.219 | 0.777                          |
| OPF-5   | CCGAATTCCC             | 7              | 6                    | 85.71               | 0.292 | 0.912                          |
| OPF-7   | CCGATATCCC             | 3              | 2                    | 66.6                | 0.199 | 0.520                          |
| OPF-9   | CCAAGCTTCC             | 6              | 4                    | 66.6                | 0.203 | 0.696                          |
| OPG-4   | AGCGTGTCTG             | 7              | 7                    | 100                 | 0.344 | 0.959                          |
| OPG-8   | TCACGTCCAC             | 5              | 5                    | 100                 | 0.332 | 0.883                          |
| OPG-11  | TGCCCGTCGT             | 5              | 5                    | 100                 | 0.345 | 0.900                          |
| Total   |                        | 43             | 38                   | -                   | -     | -                              |
| Average |                        | -              | -                    | 88.37               | 0.281 | 0.814                          |

PIC Polymorphism information content

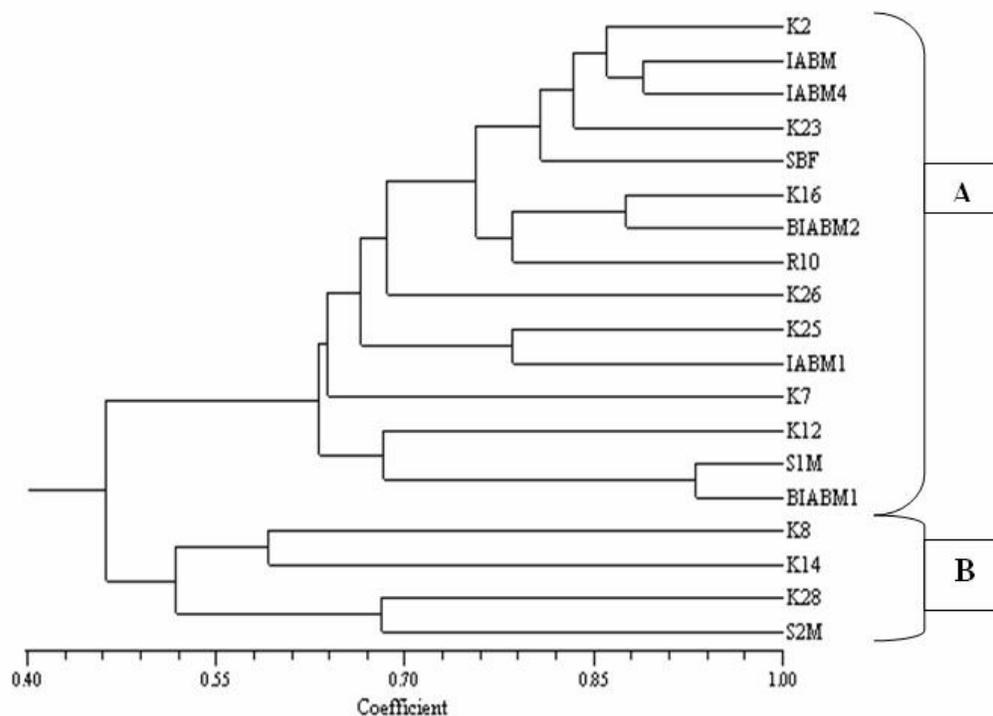
Table 4. Jaccard's similarity coefficients of 19 *C. deciddua* samples based on RAPD markers

| Samples | K2    | K7    | K8    | K12   | K14   | K16   | K23   | K25   | K26   | K28   | SIM   | SBF   | BIABM1 | BIABM2 | IABM  | IABM4 | R10   | S2M   | IABM1 |  |
|---------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--------|-------|-------|-------|-------|-------|--|
| K2      | 1.000 |       |       |       |       |       |       |       |       |       |       |       |        |        |       |       |       |       |       |  |
| K7      | 0.649 | 1.000 |       |       |       |       |       |       |       |       |       |       |        |        |       |       |       |       |       |  |
| K8      | 0.429 | 0.567 | 1.000 |       |       |       |       |       |       |       |       |       |        |        |       |       |       |       |       |  |
| K12     | 0.629 | 0.588 | 0.536 | 1.000 |       |       |       |       |       |       |       |       |        |        |       |       |       |       |       |  |
| K14     | 0.400 | 0.484 | 0.591 | 0.448 | 1.000 |       |       |       |       |       |       |       |        |        |       |       |       |       |       |  |
| K16     | 0.722 | 0.686 | 0.548 | 0.667 | 0.469 | 1.000 |       |       |       |       |       |       |        |        |       |       |       |       |       |  |
| K23     | 0.848 | 0.568 | 0.469 | 0.636 | 0.394 | 0.735 | 1.000 |       |       |       |       |       |        |        |       |       |       |       |       |  |
| K25     | 0.697 | 0.606 | 0.500 | 0.581 | 0.414 | 0.636 | 0.710 | 1.000 |       |       |       |       |        |        |       |       |       |       |       |  |
| K26     | 0.781 | 0.588 | 0.483 | 0.613 | 0.448 | 0.571 | 0.742 | 0.633 | 1.000 |       |       |       |        |        |       |       |       |       |       |  |
| K28     | 0.471 | 0.424 | 0.500 | 0.536 | 0.591 | 0.455 | 0.469 | 0.400 | 0.593 | 1.000 |       |       |        |        |       |       |       |       |       |  |
| SIM     | 0.667 | 0.629 | 0.484 | 0.710 | 0.452 | 0.657 | 0.629 | 0.486 | 0.559 | 0.533 | 1.000 |       |        |        |       |       |       |       |       |  |
| SBF     | 0.853 | 0.622 | 0.400 | 0.647 | 0.371 | 0.694 | 0.765 | 0.667 | 0.697 | 0.400 | 0.686 | 1.000 |        |        |       |       |       |       |       |  |
| BIABM1  | 0.667 | 0.629 | 0.484 | 0.656 | 0.452 | 0.657 | 0.629 | 0.486 | 0.606 | 0.533 | 0.931 | 0.686 | 1.000  |        |       |       |       |       |       |  |
| BIABM2  | 0.771 | 0.735 | 0.500 | 0.618 | 0.469 | 0.875 | 0.686 | 0.636 | 0.618 | 0.455 | 0.657 | 0.794 | 0.657  | 1.000  |       |       |       |       |       |  |
| IABM    | 0.886 | 0.615 | 0.444 | 0.686 | 0.378 | 0.730 | 0.853 | 0.706 | 0.735 | 0.444 | 0.676 | 0.857 | 0.676  | 0.730  | 1.000 |       |       |       |       |  |
| IABM4   | 0.833 | 0.615 | 0.444 | 0.686 | 0.417 | 0.829 | 0.800 | 0.657 | 0.686 | 0.486 | 0.676 | 0.757 | 0.676  | 0.778  | 0.889 | 1.000 |       |       |       |  |
| R10     | 0.818 | 0.676 | 0.438 | 0.606 | 0.452 | 0.738 | 0.727 | 0.625 | 0.656 | 0.484 | 0.647 | 0.733 | 0.647  | 0.813  | 0.771 | 0.824 | 1.000 |       |       |  |
| S2M     | 0.500 | 0.500 | 0.512 | 0.517 | 0.410 | 0.485 | 0.500 | 0.387 | 0.571 | 0.682 | 0.516 | 0.429 | 0.469  | 0.485  | 0.472 | 0.472 | 0.469 | 1.000 |       |  |
| IABM1   | 0.706 | 0.667 | 0.419 | 0.594 | 0.344 | 0.647 | 0.667 | 0.786 | 0.594 | 0.375 | 0.588 | 0.676 | 0.588  | 0.647  | 0.714 | 0.667 | 0.688 | 0.364 | 1.000 |  |

Fig. 1. Dendrogram derived from Manhattan dissimilarity coefficient of biochemical parameters in 1) fruits and 2) Buds of *C. decidua*



**Fig. 2.** Dendrogram derived from UPGMA cluster analysis using a Jaccard's similarity coefficient of RAPD based markers in *C. decidua*



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