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Research Article**Genetic diversity for yield and its component traits in chickpea (*Cicer arietinum* L.)****A.G. Vijayakumar¹, Ishwar Boodi^{2*}, P.M. Gaur³ and H.D. Upadhyaya⁴**^{1,2}NFSM Project, AICRP for Dryland Agriculture, RARS, Vijayapura, Karnataka, India.^{3,4}International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India.**E-mail:** ishwarhb.uasdagri@gmail.com

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Abstract

An investigation was carried out among the 169 germplasm, including indigenous and exotic collections, of chickpea to study the nature and magnitude of genetic divergence using Mahalanobis's D^2 Statistics. The experiment was carried out during *rabi* season of 2015 at RARS, Vijayapura. Based on D^2 analysis, the 169 germplasm lines were grouped into eight different clusters indicating diverse nature of material studied. Cluster I was the largest with 53 genotypes followed by cluster III (44 genotypes) and cluster II (34 genotypes), while clusters VI, VII and VIII were solitary indicating the grouping of exotic collections in definite groups. Among the seed yield components, seed yield followed by number of days to maturity and days to 50% flowering contributed maximum towards the divergence. Cluster V showed the maximum mean value for seed yield. The intra and inter cluster divergence among the genotypes was varying in magnitude. The intra-cluster distance was maximum in cluster IV followed by clusters III and V. The widest inter cluster distance was noted between cluster IV and V followed by V and VIII, II and IV. Cluster VI, VII and VIII were solitary giving scope for hybridization programme for improvement of chickpea genotypes. The grouping of genotypes was irrespective of desi or kabuli types used in the study.

Key wordsChickpea, D^2 statistics, genetic variability, inter cluster distance and intra cluster distance**Introduction**

The genus *Cicer* comprises 34 wild perennial, eight annual wild and one annual cultivated species. Chickpea (*Cicer arietinum*) is the third most important food legumes in the world in terms of area (11.55 million hectares) and production (10.46 million tons) (FAOSTAT 2014). India is the largest producer of chickpea in the world sharing about 70% of area and production (FAOSTAT 2014). In India, chickpea is cultivated in an area of 9.39 million ha with the production of 9.53 million tons (Dixit 2015) with productivity of 960 kg/ha. In India, productivity is low as compared to other chickpea producing countries like Mexico (1809 kg/ha), Australia (1268 kg/ha), Ethiopia (1265 kg/ha) Hence, utilization of diverse germplasm is the key to develop high yielding varieties to bridge this yield gap.

In chickpea, there are reports available on the evaluation of genetic stock in agro-morphological traits (Singh *et al.* 1990, Farshadfar and Farshadfar 2008, Ali *et al.* 2010, Wadikar *et al.* 2010). These reports suggest that pod/plant, 100 seed weight (g), plant height and number of primary branches/plant are the major yield contributing traits (Singh *et al.* 1990). To strengthen ongoing breeding program, study of the available natural genetic variation is of immense importance. It is imperative to collect and evaluate germplasm precisely to draw valid conclusions.

Limited or lack of genetic variability is important factor for the limited progress achieved in increasing the productivity of grain legumes including chickpea (Sachin *et al.*, 2014). When the parents utilized in a cross are genetically similar, it is quite likely that the different lines derived reveal low diversity. On the contrary, when diverse parents are used in obtaining a segregating population, the derived lines reveal greater diversity (Borate *et al.*, 2010).

In any program aimed at genetic amelioration of yield, genetic diversity is the basic requirement. Effective hybridization program between genetically diverse parents will lead to considerable amount of heterotic response in F_1 hybrids and broad spectrum of variability in segregating generations. Mahalanobis's D^2 statistics is a powerful tool in quantifying the degree of variability at the genotype level (Mahalanobis, 1936). So, the present experiment was formulated to study the genetic divergence and clustering pattern of the chickpea genotypes for selection of suitable parents for utilizing in hybridization programme and to study the genetic parameters attributing to yield.

Materials and methods

The experimental material comprising of 169 genotypes of Chickpea, collected from ICRISAT, Hyderabad, was grown during *Rabi*-2015 in an augmented design at Regional Agricultural Research Station, Vijayapura, University of agricultural sciences, Dharwad. Data were

recorded on five randomly tagged plants for *viz.*, days to 50% flowering, days maturity, plant height (cm), height of the first pod, number of pods per plant, angle of branch (degree), number of branches per plant, plant count at harvest, 100 seed weight(g) and seed yield(g). The experimental data was analyzed statistically to find out the significance of mean difference between varieties and different genetic parameters were estimated. Analysis of variance was performed to test the significance of difference among the genotypes for the characters studied. Mahalanobis D^2 technique (Mahalanobis, 1936) was used to analyze genetic diversity.

Results and discussion

One hundred and sixty nine genotypes of Chickpea showed significant differences among all characters under study. Seed yield(g) contributed maximum towards divergence followed by days to maturity, days to 50% flowering, the same characters are positively associated with yield and are the main yield components in chick pea.

The parameters of genetic variability revealed high PCV and GCV values for seed yield followed by number of pods per plant and 100 seed weight and days to 50% flowering, respectively, (Table 1) indicating that these traits could be used as selection indices for yield improvement. Similar findings were reported by Sachin *et al.*, 2014 and Borate *et al.*, 2010. High heritability (> 60%) was observed in all characters studied. The high heritability with high genetic advance was recorded for seed yield (100%, 126.953%) followed by days to maturity (100%, 23.600%) and (100%, 16.206%). The estimates of GA ranged from 0.2087 and 0.7911 with the highest estimate in case of seed yield (g). The highest genetic advance as per cent of mean was observed for seed yield (124.208%) followed by number of branches/plant (76.653%), 100 seed weight (62.154%), number of pods per plant (61.651%) and days to 50% flowering (42.646%). It indicates that most likely the heritability is due to additive gene effects and selection for these traits may be rewarding. Similar findings have been reported by Sachin *et al.*, 2014 Syed *et al.*, 2012 and Zakia *et al.*, 2012 in chick pea.

The one hundred and sixty nine genotypes studied were grouped into ten clusters (Table 2 & Fig. 1.) by using Tocher's methods, cluster I with 53 genotypes, cluster III with 44 genotypes, cluster II with 34 genotypes, cluster IV with 22 genotypes and clusters VI, VII and VIII were solitary indicating the grouping of indigenous and exotic collections in definite groups.

The intra-cluster distance was maximum in cluster IV (1497.95) followed by clusters III (1326.77) and V (1260.51) (Table 3). The widest inter cluster

distance was noted between cluster IV and V (41690.04) followed by V and VIII (27674.59), II and IV (22420.28) indicating wide divergence among the clusters. This also suggests that genetic architecture of the lines in one cluster differs entirely from those included in the other cluster giving scope for hybridization programme for improvement of chickpea genotypes. The distance between clusters V and VII (2017.74) was minimal indicating close relationship between those clusters suggesting that the genotypes in this cluster may be used as parents in hybridization programme to obtain desirable recombinants. These results are in agreement with the findings by Rajkumar *et al.*, 2015, Sachin *et al.*, 2014, Syed *et al.*, 2012 and Zakia *et al.*, 2012.

Cluster means were found highest for different characters (Table 4) *viz.*, Cluster V showed highest mean performance for seed yield (227.38). Cluster VI showed highest mean performance for days to 50% flowering (69.00) and days to maturity (97.00). Cluster VIII showed higher mean performance for plant height (40.60), height of the pod (24.40) and number of pods per plant (57.60), number of branches per plant (3.80). Cluster I for angle of branch (78.87) and cluster VII showed highest mean performance for (29.50). Based upon D^2 values, per cent contribution of different characters towards divergence was obtained. Among the ten characters studied the most important characters contributing to the divergence were seed yield (82.01%), days to maturity (6.79%), days to 50% flowering (4.83%), number of pods per plant (2.09%) and 100 seed weight (1.91%). These results are in agreement to the earlier findings by Rajkumar *et al.*, 2015, Sachin *et al.*, 2014, Syed *et al.*, 2012 and Zakia *et al.*, 2012.

Genotypes belonging to clusters separated by high genetic distance may be used in hybridization program to obtain a wide spectrum of variation among the segregates in the present study and similar suggestion had been made by Sachin *et al.*, 2014, Syed *et al.*, 2012 and Zakia *et al.*, 2012. The genotypes included in the diverse clusters namely, V, VI, VII and VIII hold good promise as parents for obtaining potential hybrids and thereby creating greater variability of these characters to improve the yield.

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Table 1. Estimates of variability parameters for different characters of Chickpea

| Characters/ Var. Parameters | DFE | DM | PH (cm) | HFP (cm) | NPP | AB° | NBP | PCH | HSW (g) | SY (g) |
|--------------------------------|--------|---------|---------|-------------|--------|--------|--------|--------|---------|-----------|
| σ^2_g | 90.103 | 131.250 | 27.589 | 13.978 | 61.893 | 14.786 | 1.1690 | 37.854 | 54.211 | 3797.960 |
| GCV | 20.702 | 13.932 | 15.558 | 18.023 | 29.928 | 4.914 | 37.210 | 30.421 | 30.172 | 60.295 |
| σ^2_p | 90.103 | 131.250 | 27.589 | 13.978 | 61.893 | 14.786 | 1.169 | 37.854 | 54.211 | 3797.960 |
| PCV | 20.702 | 13.932 | 15.558 | 18.023 | 29.928 | 4.914 | 37.210 | 30.421 | 30.172 | 60.295 |
| h ² (Broad Sense) % | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 |
| G A (5%) | 19.554 | 23.600 | 10.820 | 7.702 | 16.206 | 7.921 | 2.227 | 12.674 | 15.167 | 126.953 |
| GA as % of Mean 5% | 42.646 | 28.700 | 32.050 | 37.126 | 61.651 | 10.122 | 76.653 | 62.667 | 62.154 | 124.208 |
| General Mean | 45.852 | 82.231 | 33.761 | 20.744 | 26.288 | 78.254 | 2.905 | 20.225 | 24.403 | 102.210 |

σ^2_g : Genotypic variation; **GCV**: Genotypic coefficient of variation; **σ^2_p** : Phenotypic variation; **PCV**: Phenotypic coefficient of variation; **h²**: Heritability; **G.A**: Genetic advance. **DFE**: Days to 50% Flowering; **DM**: Days to Maturity; **PH**: Plant height; **HFP**: Height of the 1st pod; **NPP**: No. of pods/plant; **AB°**: Angle of Branch; **NBP**: No. of branches/ plant; **PCH**: Plant count @ Harvest; **HSW**: 100 seed weight; **SY**: Seed yield.



Table 2. Distribution of 169 genotypes of Chickpea in different clusters

| Cluster No. | No. of genotypes | Genotype included |
|-------------|------------------|---|
| I | 53 | ICCX-070163- F4-P7-BP, ICCX-060119-F3-BP-P30-BP, ICCX-080063-F4-P1-BP, H 1128, ICC 4302, ICC 6874, 17 PAO 30/1281, 47 PAO 31/310, 83/5352, 83/6060, 83/5181, 83/5936, ICC 13124, ICC 10546(RG 1403), ICC 10127(RG 3096), ICC 8114(RG 1338), ICC 6874, ICC 3325, ICC 1194(RG 2296), ICC 506, 13 PAO 30/1205, 125 PAO 30/1215, 194 PAO 30/1012, 97 PAO 30/1105, 176 PAO 30/1287, 60 PAO 30/1238, PAO 1414 R Plot-1013(89), PAO 1414 R Plot-1016(70), ICC 15868, ICC 15950, ICC 14402, ICC 14346, 3/260, 3/1120, 53 PAO 30/1381, 190 PAO 30/1140, 54 PAO 30/1002, 18 PAO 30/1019, 3/667, 3/636, 3/626, 3/281, 3/943, 83/6065, 83/5416, 83/5005, 3/886, 3/811, 3/1155, 3/1045, 83/5014, 83/5502 and 83/5960 |
| II | 34 | ICCX-060156- F3-BP-P22-BP, ICCX-060119- F3-BP-P2-BP, ICCX-060119- F3-BP-P6-BP, ICCX-080026- F4-P3-BP, ICCX-060119-F3-BP-P19-BP, ICCX-060121-F3-BP-P4-BP, ICCX-060150- F3-BP-P13-BP, ICCX-080026- F4-P5-BP, ICCX-070011-F2-P120-P2-P1-BP-BP, ICCMABCA-12, ICCMABCA-22, ICCMABCA-23, ICCMABCA-28, ICCMABCA-42, ICCX-080058-F4-P2-BP, ICCX-080058-F4-P4-BP, ICCX-080058-F4-P12-BP, ICCX-090021-F4-P7-BP, ICCX-090031-F4-P7-BP, ICCX-070157- F4-P4-BP, ICCX-080062-F4-P18-BP, ICCX-080066-F4-P10-BP, ICCRIL01-0246, ICCRIL01-0266, ICCRIL01-0410, ICCRIL05-0089, ICCV 88202, ICCV 96029, F3WF x 16BR, NEC1153,PI360347, ICC 13124, ICC 14402, ICC 14877 (BG 256) and ICCX-070163- F4-P8-BP |
| III | 44 | ICC 3825, ICC 8933, ICC 12267, ICC 1205, ICCMABCA-34, ICCX-080058-F4-P1-BP, ICCX-070007-F2-BP-P40-BP-P1-BP-BP, ICCX-060119-F3-BP-P4-BP, ICCMABCA-24, 58/2069, ICC 14648, ICCX-060157-F3(Early) BP-P1-BP, ICCX-060155-F3-BP-P10-BP, 95/11014, ICCX-070157- F4-P6-BP, ICCMABCA-8, 14 PAO 30/1218, ICC 2580, JG-11, ICCX-060119- F3-BP-P17-BP, 105 PAO 30/1266, ICC 7441, 83/5922, 83/5999, 83/5605, ICCV 96030, 129 PAO 30/1004, 175 PAO 30/1257, ICC 14395, NEC 2303, WP 2793 C, ICCX-060152- F3-BP-P11-BP, ICCX-080058-F4-P17-BP, ICCX-090019-F4-P12-BP, Shimbera, ICCX-060119-F3-BP-P19-BP, ICCX-080026-F4-P2-BP, 25 PAO 31/303, ICC 2580, ICCX-070010-F2-BP-P108-BP-P1-BP, T 70 B, ICCX-070163- F4-P2-BP, ICCX-090031-F4-P8-BP and ICCX-080062-F4-P6-BP |
| IV | 22 | PAO 1414 R Plot-1010(101), 83/5021, 83/5318, 3/656, ICC 5319(RG 1330), ICC 1231(RG 2299), 28 PAO 34/129, ICC 16796 ICCX-060156- F3-BP-P12-BP, ICC 9826(RG 3065), 58/2033, 3/1322, 58/2014, ICC 5818(RG 2634), ICC 4664, ICCX-090036-F4-P23-BP, ICC 1161, ICCRIL05-0088, 58/1016, ICCX-060122-F3-BP-P13(Pea type)-BP, ICCRIL01-0334 and ICCX-060119-F3-BP-P7-BP |
| V | 13 | ICCX-060119- F3-BP-P12-BP, ICCX-090038-F4-P15-BP, ICCX-090040-F4-P6-BP, ICCX-070011-F2-BP-P87-BP-P1-BP-BP, ICCX-080062-F4-P19-BP, ICCX-080026- F4-P9-BP, ICC 14648, ICCX-070011-F2-BP-P68-BP-P1-BP-BP, ICCX-090039-F4-P1-BP, ICCV 11603, ICCRIL01-0246ICCRIL01-0250, ICCX-090035- F4-P12-BP and ICCRIL01-0306 |
| VI | 1 | P3046,PI 450953 |
| VII | 1 | 83/5314 |
| VIII | 1 | ICC 12506 (RG 3254) |

Table 3. Intra cluster and inter cluster distances of eight clusters of Chickpea

| Cluster | I | II | III | IV | V | VI | VII | VIII |
|---------|---------------|---------------|----------------|----------------|----------------|-------------|-------------|-------------|
| I | 926.05 | 14518.75 | 3223.93 | 2322.49 | 30318.60 | 7441.17 | 5976.11 | 2542.11 |
| II | | 819.14 | 6196.68 | 22420.28 | 4053.68 | 2446.11 | 2991.46 | 12986.81 |
| III | | | 1326.77 | 6888.55 | 17300.83 | 2198.94 | 2107.39 | 3382.06 |
| IV | | | | 1497.95 | 41690.04 | 12467.63 | 12061.74 | 4134.82 |
| V | | | | | 1260.51 | 10292.64 | 10601.63 | 27674.59 |
| VI | | | | | | 0.00 | 2017.74 | 6544.61 |
| VII | | | | | | | 0.00 | 6024.93 |
| VIII | | | | | | | | 0.00 |

Table 4. Cluster means for different traits in Chickpea

| Characters/C luster | DFE | DM | PH | HFP | NPP | AB° | NBP | PCH | HSW | SY |
|-----------------------|-------|-------|-------|-------|-------|-------|------|-------|-------|--------|
| I | 38.53 | 73.09 | 30.95 | 19.37 | 22.36 | 78.87 | 2.89 | 19.74 | 24.62 | 58.04 |
| II | 51.03 | 91.74 | 37.13 | 21.76 | 31.47 | 78.62 | 2.84 | 23.00 | 27.46 | 172.13 |
| III | 48.45 | 84.59 | 33.80 | 20.84 | 26.72 | 78.20 | 2.83 | 20.43 | 23.63 | 101.16 |
| IV | 47.45 | 80.95 | 33.01 | 21.66 | 21.03 | 76.95 | 3.19 | 15.23 | 17.59 | 27.59 |
| V | 48.38 | 90.15 | 37.02 | 21.55 | 34.11 | 77.54 | 2.85 | 23.15 | 29.42 | 227.38 |
| VI | 69.00 | 97.00 | 32.60 | 21.40 | 23.60 | 78.00 | 3.20 | 21.00 | 27.00 | 132.00 |
| VII | 37.00 | 66.00 | 34.80 | 19.60 | 24.60 | 74.00 | 2.80 | 22.00 | 29.50 | 131.50 |
| VIII | 61.00 | 66.00 | 40.60 | 24.40 | 57.60 | 78.00 | 3.80 | 12.00 | 20.00 | 67.50 |
| % contribution | 4.83 | 6.79 | 0.67 | 0.13 | 2.09 | 0.42 | 0.00 | 1.16 | 1.91 | 82.01 |

DFE: Days to 50% Flowering; **DM:** Days to Maturity; **PH:** Plant height; **HFP:** Height of the 1st pod; **NPP:** No. of pods/plant; **AB°:** Angle of Brach; **NBP:** No. of branches/ plant; **PCH:** Plant count at Harvest; **HSW:** 100 seed weight; **SY:** Seed yield.

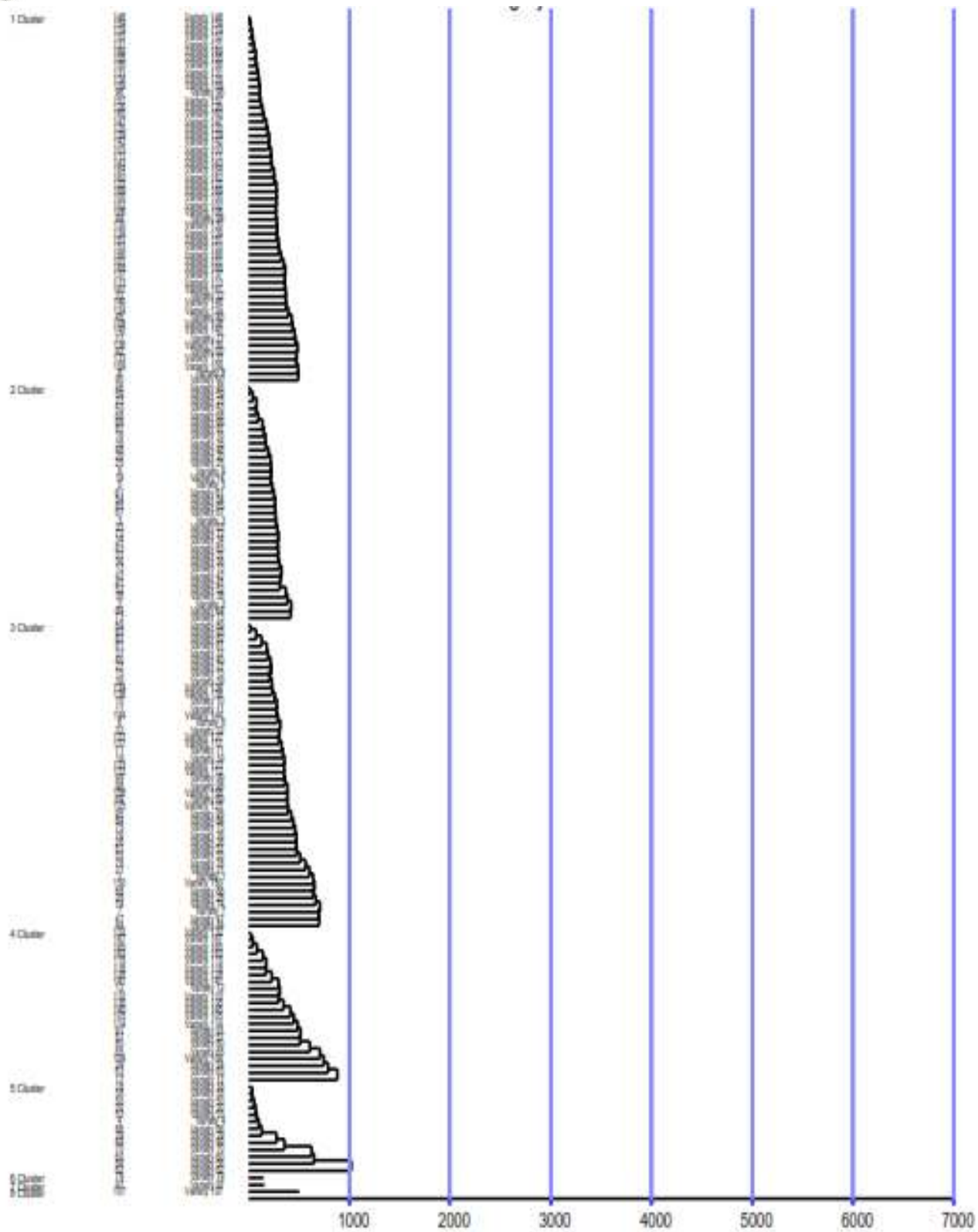


Fig. 1. Clustering by Tocher's method