

CHARACTERIZATION AND PRELIMINARY EVALUATION OF DEKOKO (*Pisum Sativum* Var. *Abyssinicum*) ACCESSIONS USING QUANTITATIVE TRAITS IN SOUTHERN TIGRAY, ETHIOPIA

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ABSTRACT: Cultivated *Pisum* is dominated with *Pisum sativum* subgroup, but *Pisum sativum* var. *abyssinicum* (Dekoko) is a unique subgroup developed and cultivated in Ethiopia. The objectives of the study were characterization of Dekoko accessions using 17 quantitative traits and study the genetic variability present in the population. Twenty-four accessions of Dekoko (*Pisum sativum* var. *abyssinicum*) collected from North Ethiopia (South Tigray and North Wello) by Alamata Agricultural Research Center, were planted in 3 replications of the RCBD design at Mekhan farmers' Training Centre in Endamekhoni in 2010. Considerable extent of genetic variability was available for days to flowering, leaf area index and crude protein content while the remaining quantitative traits did not show statistically significant variation in the population of Dekoko studied. Protein content ranged between 17.9% (T-018/08 Ko) to 38.4% (T-010/08 K). Traits such as days to flowering and maturity and leaf width had low Phenotypic Coefficient of Variation, Genotypic Coefficient of Variation and low genetic advance (<20%). Clustering of the accessions using quantitative traits indicated that the number of accessions in each cluster varied from 1 in cluster IV to 11 in cluster I.

Key words: Characterization, Dekoko, *Pisum sativum* var. *abyssinicum*, accession, crude protein

1. INTRODUCTION

Worldwide field pea (*Pisum sativum* L.), with a global production of 10,485,464 t and a harvested area of 7,238,123 ha, is the fourth annual legume after soybean (*Glycine max* (L.) Merr), faba bean (*Phaseolus vulgaris* L.) and ground nut (*Arachis hypogea* L. [10], [12], [21]). Field pea (*Pisum sativum* L.) is the fourth most important legume crop in Ethiopia after faba bean, haricot bean and chick pea in terms of both area and total amount of production. Field pea covers over 203,990.64 ha with a total production of 257,031.41 tons which accounts for 13 percent of the total grain legume production [5]. The origin of field pea is controversial. Ethiopia is undoubtedly the centre of diversity for this crop since wild and primitive forms are known to exist in the high elevations of the country. Ethiopia is one of the major Vavilovian centers of diversity for several grain legume crops including lupine, field pea and wild ancestors of cow pea [1]. Cultivated *Pisum* is dominated by *P. sativum*, but *P. sativum* ssp *abyssinicum* (or simply *P. abyssinicum*) is a unique sub-species independently developed and cultivated in Ethiopia. The existing germplasm in the country shows tolerance/resistance to disease [13], [22]. *Pisum sativum* is widespread across the Middle East and has affinity with the wild *P. elatius* while *P. abyssinicum* is restricted to highland regions of Ethiopia (South Tigray and North Wello) and Southern Yemen and shows a greater affinity to *P. fulvum* [13], [25]. However, *P. fulvum* is found around the eastern edge (Syria, Lebanon, Israel, Palestine and Jordan) and not common in Ethiopia, Macted and Ambrose [16]. *P.s. abyssinicum* is locally known as Dekoko (minute seeded) in Tigray and Yagere Ater (pea of my country) or Tinishu Ater (the smallest pea) in Amharic. Dekoko is capable of producing seed yield of up

to 1.95 t/ha under phosphorus fertilization and is known for its high market price (more than double of other pulses) and for its food preference [25]. Farmers and consumers call it as the "Dero-Wot of the poor" (chicken stew of the poor) probably to express its high nutritional value. Most often, the dry seeds of Dekoko are decorticated and split ('split peas') before boiling. Sometimes they are boiled without decortications and consumed as soup (personal observation). In Ethiopia the annual consumption per person of field pea including Dekoko seed is estimated at 6-7 kg, Messiaen *et al.* [17], [22]. A large genetic diversity has been found in *Pisum sativum* collections from both Africa (e.g. Ethiopia) and Asia. High to medium field pea genetic diversity in Ethiopia was observed in collections from Shoa, Gojam, Gondar, Wello, and Tigray while low to trace genetic diversity was observed in collections from Arsi, Gamo-gofa, Wellega, Illubabur and Kafa [1]. Morphological characterization or description of germplasm is the first step in the description and classification of the germplasm Smith & Smith [22]. An understanding of morphological characters facilitates the identification, selection of desirable traits, designing new populations, in transferring their desirable genes into widely grown food legumes through biotechnological means, resistance to biotic and abiotic stresses that are known to individual accessions increase the importance of the germplasm, [14], [19], [24]. In Ethiopia, more than 15 cultivars of field pea, with superior yield potential, seed size, seed color and disease resistance, have been released for different agro-ecological conditions MoARD [18]. Some of these varieties were obtained from local collections while others were obtained through hybridization of landraces with introduced germplasm. Land races are the genetic wealth that a crop acquires over many years of its existence and have

considerable breeding values as they contain valuable adaptive genes to different circumstances [1], [17]. Even though Dekoko (*Pisum sativum* var. *abyssinicum*) is important both for the local farmers and consumers, the existing germplasm was not characterized; neither was there any improvement work on this crop so far. The current study was, therefore, conducted with the objectives of characterizing Dekoko accessions using quantitative traits and studying the genetic variability present in the population.

2. MATERIALS AND METHODS

2.1 Description of the Study Area

The research was conducted in Southern zone of Tigray regional state, Wereda Endamekhoni at tabia Mekhan farmers' training center which is one of the mandate areas of Alamata Agricultural Research Center (AIARC). Mekhan is only five kilo-meters south of Maichew. It is located about 660 kilo-meters north of Addis Ababa and about 120 kilo-meters south of Mekelle. The soil of the experimental site is black clay loam. The Wereda has a temperature range of 9 -18 °c with a mean annual rain fall of 600-700 mm. Farmers in the study area practice mixed farming systems in which crop production is assisted with animal production [9]. The site is considered as conducive for the production of Dekoko and other pulse crops.

2.2. Accessions Evaluated

Twenty four accessions collected from two regions; South-Tigray and North-Wello were tested at Mekhan farmers training center (FTC) at an elevation of 2100 meters above sea level. The accessions were collected in 2008 by Alamata Agricultural Research Center from weredas: Alamata, Oflla, Endamekhoni, Alaje, and Hintalo-Wejerat in South Tigray, and Kobo, Guba-lafto, Srinka and Habru in North-Wello.

Table1. Accessions of Dekoko Included in the Study and Their Sources

| No | Accession name | accessions | | Source | of |
|----|----------------|------------|-----------------|--------------------|---------------------------|
| | | Region | Wereda | Major Agro-ecology | Altitude of wereda (masl) |
| 1 | T-001/08 Of | Tigray | Oflla | High land | 2457 |
| 2 | T-002/08 Of | Tigray | Oflla | High land | 2457 |
| 3 | T-003/08 Of | Tigray | Oflla | High land | 2457 |
| 4 | TK-004/08 AI | Tigray | Alamata | Low land | 1178-3148 |
| 5 | TK-005/08 AI | Tigray | Alamata | Low land | 1178-3148 |
| 6 | TK-006/08 AI | Tigray | Alamata | Low land | 1178-3148 |
| 7 | TK-008/08 AI | Tigray | Alamata | Low land | 1178-3148 |
| 8 | T-023/08 Mw | Tigray | Endamekhoni | High land | 2100 |
| 9 | T-022/08 E/A | Tigray | Emba-Alaje | High land | 2116 |
| 10 | T-024/08 E/A | Tigray | Emba-Alaje | High land | 2116 |
| 11 | T-021/08 H/W | Tigray | Hintalo-Wejerat | Mid-altitude | 1400-3050 |
| 12 | T-007/08 Ko | Amhara | Kobo | Low land | 1100-3000 |
| 13 | T-009/08 Ko | Amhara | Kobo | Low land | 1100-3000 |
| 14 | T-010/08 Ko | Amhara | Kobo | Low land | 1100-3000 |
| 15 | T-017/08 Ko | Amhara | Kobo | Low land | 1100-3000 |
| 16 | T-018/08 Ko | Amhara | Kobo | Low land | 1100-3000 |
| 17 | T-019/08 Ko | Amhara | Kobo | Low land | 1100-3000 |
| 18 | T-020/08 Ko | Amhara | Kobo | Low land | 1100-3000 |
| 19 | T-012/08 G/L | Amhara | Guba-lafto | High land | 2061 |
| 20 | TA-013/08 Sr | Amhara | Srinka | Mid-altitude | 1868 |
| 21 | TA-014/08 Sr | Amhara | Srinka | Mid-altitude | 1868 |
| 22 | TA-015/08 Sr | Amhara | Srinka | Mid-altitude | 1868 |
| 23 | T-011/08 Hb | Amhara | Habru | Low land | 700-1900 |
| 24 | T-016/08 Hb | Amhara | Habru | Low land | 700-1900 |

2.3 Experimental Design and Trial Management

The trial was conducted using Randomized Complete Block Design with three replications and the plot size for each accession was 1.5 m² with inter- and intra-row spacing of 25 and 5 cm, respectively. Accessions were sown in six rows each 1m long. Phosphorus and Nitrogen fertilizers with normal recommendation rates to other pulse crops (46 kg P₂O₅ and 18 kg N ha⁻¹, i.e., 100 Kg DAP (Di-Ammonium Phosphate ha⁻¹) and seed rate of 150 kg ha⁻¹ were applied.

2.4. Statistical Analysis

2.5.1 Analysis of Quantitative Data

2.5.1.1. ANOVA and Estimation of Variability Parameters

For the estimation of variance components of the various sources of variation, RCBD ANOVA was used. The SAS computer software SAS (1994) was employed for the analysis of variance (Table 2). The difference among accession means was compared using Duncan's Multiple Range Test, DMRT as mentioned by [8]. Variance components were computed only for traits where significant difference coefficient existed between the accessions.

Table2. Form of analysis of variance of table for each quantitative character

| Source of variation | Df | MS |
|----------------------------|------------|-----|
| | EMS‡ | |
| Replication | r-1 | MSr |
| Accessions | a-1 | MSa |
| $\sigma^2_e + r\sigma^2_g$ | | |
| Error | (r-1)(a-1) | MSe |
| σ^2_e | | |

Genotypic variance (σ^2_g) = (MSa - MSe)/r
‡EMS - Expected Mean Square

Error variance (MSe) = σ^2_e

Where r = number of replications; a = number of accessions; MSr = mean square of replication; MSa = mean square of accessions; MSe = mean square of error; σ^2_g = genotypic variance; σ^2_e = error variance and σ^2_p = phenotypic variance = $\sigma^2_g + \sigma^2_e / r$

Phenotypic and Genotypic Coefficients of Variation

Phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were estimated according to [4] as

$$PCV = \frac{\sqrt{\sigma^2_p}}{\bar{X}} * 100$$

$$GCV = \frac{\sqrt{\sigma^2_g}}{\bar{X}} * 100$$

Where \bar{X} = Mean value of the trait

σ^2_p = Phenotypic variance of the character

σ^2_g = Genotypic variance of the character

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

Heritability in broad sense (h^2): was calculated according to [3] as:

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p} * 100$$

3. RESULT AND DISCUSSION

3.1 Quantitative Traits

3.1.1 ANOVA of Quantitative Traits

Result of the Analysis of Variance of 17 quantitative traits is presented in Table 3. The difference between the 24 Dekoko accessions included in this study was statistically non-significant for all traits except in number of days to flowering, leaf area index and protein content. Although the range was wide in traits such as above ground biomass yield, harvest index and seed yield, the large experimental error on these traits might have masked the differences between the accessions. CVs of these traits were 28%, 37.7%, and 42.0% respectively. For example above ground biomass yield varied between 1.57 (acc. 24) to 3.37 t ha⁻¹ (acc. 16), harvest index varied between 0.13 (acc. 22) to 0.35 (acc. 4) and grain yield varied between 0.35 (acc. 23) to 0.85 (acc.22) t ha⁻¹. Such wide range was also observed in thousand seed weight and plant height. In general it seems that the main emphasis has been in the selection of the protein content of this crop rather than the improvement of seed yield.

Days to Flowering (DF)

Days to flowering ranged between 38.7 days (Acc. 8) to 45.3 days (Acc. 7), a range of about seven days. Accessions 3, 4, 11, 15 and 24 were the earliest to flower (38.7 to 41.7 days), while accessions 5, 6, 12, 14, 17, 21 and 22 were the latest to flower (44.0 to 45.3 days).

Leaf Area Index

Leaf area index ranged from 1.300 (acc.5) to 2.733 (acc.19) and was statistically significant at 0.05 probability level (Table 3). The mean value was in agreement with findings of [25] in which the value was 1.80 in their finding and 2.03 in the current finding.

Crude Protein Content (PROT)

The effect due to accessions was highly significant for crude protein content (Table 3). Accession T-010/08 Ko (Acc. 14) had the highest mean protein content (38.4%) while accession T-018/08 Ko (Acc. 16) was with lowest mean protein content (17.9%). Accessions 6, 8, 9, 10, 14, 18 & 19 had the highest protein content (> 34%), while accessions 1, 2, 3, 7, 15, 16, 17, 21 and 22 had the lowest protein content (<27%). Two of the accessions with the highest protein content were from Alamata, two from Emba-Alaje, two from Kobo and one accession from Guba-lafto. Most of the accessions that had high protein content gave low seed yield. The top five accessions with the highest seed yields were, 13, 8, 16, 15 and 22 which gave from 0.838 to 0.851 tons per hectare. Accessions 14, 10 and 9 which contained high protein content were among the low yielding genotypes by seed yield, producing from 0.40 - 0.59 t ha⁻¹. Accessions 6 (T-009/08 Ko) and 8 (T-023/08 Mw), which were collected from Alamata and Endamekhoni, can therefore, be recommended for production since they contain reasonably high protein content (>34.4%) and also gave good seed yield (> 0.82 t ha⁻¹). Hence future breeding

work can concentrate on improving the seed yield of these high-protein accessions. Yemane and Skjelvåg [25] found crude protein content of 25.6 % and 24.8 % for Dekoko and field pea respectively. In a similar study for protein content of field pea the range was found to be between 18 - 35 % [15]. In another study of 506 field pea accessions the mean protein value was 22-32% [2]. Similarly, field pea variety, Tullushenen, was found to be with higher protein content (25.6%) at Sinnana Agricultural Research Centre, Getachew [11]. The protein percent in dry beans was also found to be from 17% - 35%, [7]. In the current study, the mean crude protein content of Dekoko was found to be 29.1 %. Thus, this finding was in agreement to the reports above on field pea and faba bean. The nearness of Dekoko crude protein content to the maximum range of protein content in field pea may show the superiority of Dekoko in its protein content and may suggest the name "Dero-Wot of the poor" (chicken stew of the poor) given by the community. However, further investigation and research is needed to confirm this assumption.

Table3. ANOVA results of 17 Quantitative Traits of Dekoko Grown at Mekhan, Endamekhoni, in 2010 G.C.

| Source of variation | Df | Mean Square | | | | | | | | |
|---------------------|----|--------------|--------------|---------------------|---------------------|---------------------|----------------------|---------------------|---------------------|---------------------|
| | | DE | DF | DM | LL | LW | LN | LAI | PPP | SPP |
| Replication | 2 | 13.431** | 11.347 ** | 71.264 ** | 0.018 _{ns} | 0.095 _{ns} | 7.277 _{ns} | 0.199 _{ns} | 8.880 *** | 0.003 _{ns} |
| Accession | 23 | 2.173 | 9.295 *** | 8.947 _{ns} | 0.035 | 0.065 _{ns} | 33.424 _{ns} | 0.397* | 0.704 _{ns} | 0.464 _{ns} |
| Error | 46 | 1.315 | 2.840 | 9.394 | 0.050 | 0.050 | 37.125 | 0.219 | 0.919 | 0.421 |
| CV (%) | | 12.19 | 3.95 | 4.07 | 6.07 | 11.49 | 13.25 | 23.06 | 19.87 | 13.44 |
| DMRT | | 2.049 | 2.616 | 6.868 | 0.845 | 0.531 | 22.039 | 0.96 | 2.134 | 1.27 |

Continued...

| Source of variation | DF | Mean Square | | | | | | | |
|---------------------|----|----------------------|---------------------|-----------------------|----------------------|-----------------------|---------------------|---------------------|--------------|
| | | BIO | YL | TSW | PH | HI | DIS | PES | PROT |
| Replication | 2 | 562.059*** | 0.423 ** | 2252.375 ** | 596.187** | 0.00012 _{ns} | 0.264 _{ns} | 0.097 _{ns} | 47.388 *** |
| Accession | 23 | 49.418 _{ns} | 0.064 _{ns} | 274.415 _{ns} | 28.690 _{ns} | 0.00089 _{ns} | 0.280 _{ns} | 0.048 _{ns} | 87.525 *** |
| Error | 46 | 56.123 | 0.079 | 435.361 | 27.500 | 0.0008 | 0.510 | 0.054 | 8.323 |
| CV (%) | | 27.98 | 42.09 | 13.35 | 12.65 | 34.98 | 40.18 | 21.96 | 9.90 |
| DMRT | | 16.05 | 0.72 | 49.50 | 8.83 | 0.023 | 3.119 | 0.671 | 3.409 |

* = significant at $\alpha = 0.05$, ** = highly significant at $\alpha = 0.01$ probability level

NB: - DE=days to emergence, DF= days to flowering, DM=days to maturity, LL=leaf length, LW=leaf width, LN=leaf number, LAI=leaf area index, PPP=pods per plant, SPP= seeds per pod, BIO=biomass, YLD=grain yield, TSW=1000 seed weight, PH= plant height, HI=harvest index, DIS=disease, PEST=pest, and PROT=Protein content.

3.2. Genotypic and Phenotypic Variances

Estimates of genetic variances of the quantitative traits were smaller than their respective phenotypic variances for all the traits evaluated. However, estimates of genetic variances were higher than those of environmental variances for all the traits evaluated. Genotypic variances ranged from 0.00001-605.7 (Table 4). The genotypic variance was the highest for thousand seed weight (605.7), followed by plant height (189.6) and biomass yield (168.6) indicating the greater magnitude of genetic variability for these traits. Phenotypic variance values ranged from 0.00004 – 750.792. The highest phenotypic variance was that of thousand seed weight (750.792). Minimum phenotypic variance was observed for harvest index (0.00004). Higher environmental variance was observed in thousand seed weight (145.1) and biomass (18.7) while the minimum was obtained for harvest index (0.00003). This indicates that both 1000-seed weight and biomass are highly influenced by environment while harvest index is less affected.

3.3. Genotypic and Phenotypic Coefficient of Variations

Genotypic coefficient of variation ranged from 3.952 - 50.578 % (Table 4). The highest genotypic coefficient of variation was obtained for grain yield (50.578%) followed by biomass (48.500) while lowest genotypic coefficient variation (3.952) was observed for days to flowering. Phenotypic coefficient of variation (PCV) ranged from 4.564 - 56.113 %. Highest phenotypic coefficient of variation was obtained for grain yield (56.113%) followed by biomass (308.218) whereas lowest phenotypic coefficient of variation was observed for days to flowering (4.564).

3.4. Estimates of Heritability and Genetic Advance of the Quantitative Traits

Heritability is defined as the ratio of genotypic variance to the phenotypic variance. Broad sense heritability (h^2) expressed as the percentage of the ratio of the genotypic variance (V_g) to the phenotypic variance (V_p) and Genetic advance (GA) on genotypic mean basis were estimated as described by Allard [3]. Accordingly, maximum value of heritability was recorded for plant height (95.40%) followed by days to emergence (90.2) and biomass (90.0). In spite of the ANOVA results, many characters including days to emergence and maturity, number of pods per plant, biomass, grain yield, 1000 seed weight, and plant height have expressed heritability values of greater than 75% (Table 4). These traits were expected to remain stable under varied environmental conditions, since environment has less influence on highly heritable traits and could easily be improved by applying selection pressure. Coulibaly *et al.* [6] suggested that high variability was an indication to the scope of improvement through simple selection suggested for various Legumes. Biomass (94.791) showed maximum genetic advance of mean followed by grain yield (93.915) (Table 4). The expected genetic advance was highest for 1000 seed weight (45.535) followed by plant height (27.701) while smaller value (0.0004) was obtained for harvest index. High heritability and high genetic advance

were indications that those traits were controlled by additive genes.

Table 4. Values of Variance Components & Coefficients, with Broad Sense Heritability, Genetic advance, Mean & Genetic Advance of the Mean for Dekoko Accessions.

| Traits | s ² _g | s ² _p | s ² _e | GCV (%) | PCV (%) | h ² (%) | GA | Mean | GAM |
|--------|-----------------------------|-----------------------------|-----------------------------|---------|---------|--------------------|--------|--------|---------|
| DTE | 4.039 | 4.477 | 0.438 | 21.373 | 22.502 | 90.2 | 3.932 | 9.40 | 41.818 |
| DTF | 2.836 | 3.782 | 0.947 | 3.952 | 4.564 | 74.9 | 3.004 | 42.61 | 7.049 |
| DTM | 20.623 | 23.755 | 3.131 | 6.033 | 6.475 | 86.8 | 8.717 | 75.28 | 11.579 |
| LW | 0.015 | 0.032 | 0.017 | 6.289 | 9.143 | 47.3 | 0.173 | 1.95 | 8.913 |
| PPP | 2.654 | 2.960 | 0.306 | 33.761 | 35.657 | 89.6 | 3.177 | 4.83 | 65.848 |
| BIO | 168.645 | 187.353 | 18.708 | 48.500 | 51.119 | 90.0 | 2.538 | 2.68 | 94.791 |
| YLD | 0.115 | 0.141 | 0.026 | 50.578 | 56.113 | 81.2 | 0.629 | 0.669 | 93.915 |
| SW | 605.672 | 750.792 | 145.120 | 15.746 | 17.532 | 80.67 | 45.535 | 156.29 | 29.135 |
| PH | 189.562 | 198.729 | 9.167 | 33.213 | 34.007 | 95.4 | 27.701 | 41.45 | 66.823 |
| HI | 0.00001 | 0.00004 | 0.00003 | 1s.961 | 3.922 | 34.1 | 0.0004 | 0.26 | 17.459 |
| Pest | 0.014 | 0.032 | 0.014 | 11.405 | 17.055 | 44.7 | 0.166 | 1.06 | 15.711 |
| PROT | 13.021 | 15.796 | 2.774 | 12.381 | 15.796 | 82.4 | 6.749 | 29.145 | 23.1569 |

N.B: s²_g = Genotypic variance, s²_p = phenotypic variance, s²_e = Environmental variance, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, h² = Heritability, GA = Genetic Advance, and GAM = Genetic Advance of the Mean.

3.6 Divergence Analysis

Cluster and divergent analyses were undertaken in the present study in order to constitute homogeneous groups of accessions and measure the distance between the clusters based on quantitative traits.

3.7.1 Cluster Analysis Using Quantitative Traits

Cluster means of 18 quantitative traits used for clustering are presented in table 6 and Dendrograms summarizing similarity among 24 accessions of Dekoko based on quantitative traits is given in Fig 1. The clustering pattern indicated that the number of accessions in each cluster varied from 1 in cluster IV to 11 in cluster I. Cluster I that comprised 11 accessions (45.83 %) is composed of one accession from Ofla, four accessions from Alamata, three accessions from Kobo, one accession from Endamekhoni, and two accessions from Srinka. Accessions in this cluster were predominantly characterized by relatively higher values of 1000 seed weight, late flowering and maturity, and higher yield (0.76 t/ha) and low protein (Table 6). Cluster II (33.33 %) are relatively better in yield next to cluster I than the others (0.67 t/ha). Cluster III that comprises 16.67 % of the accessions are characterized by lower seed yield and high protein content.

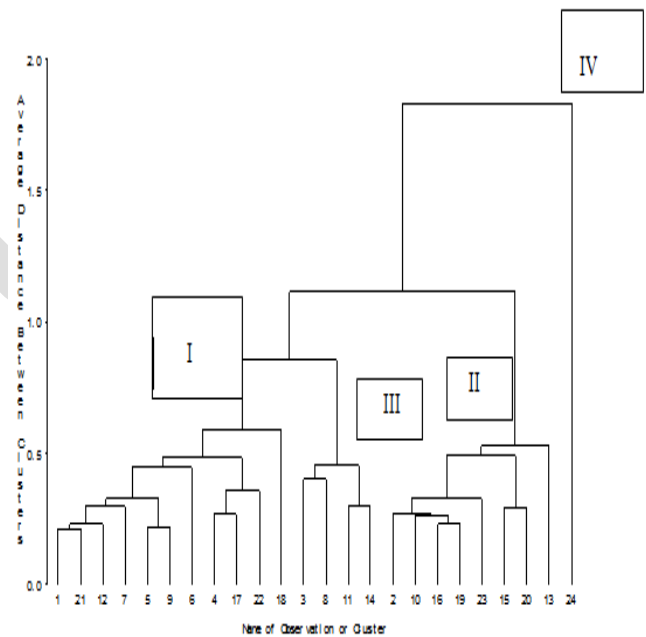


Figure 1 Clustering of the Accessions by Quantitative Traits

Table5. Distribution of Dekoko Accessions based on quantitative traits in to Four Clusters

| Cluster | No. of accessions | Serial number | Name of the accessions in cluster |
|---------|-------------------|-------------------------------------|--|
| I | 11 | 1, 4, 5, 6, 7, 9,12, 17, 18, 21, 22 | T-001/08Of, TK-004/08 Al, TK-005/08 Al, TK-006/08 Al, TK-008/08 Al, T-023/08 Mw, T-007/08Ko, T-019/08Ko, T-020/08Ko, TA-014/08 |
| II | 8 | 2, 10, 13, 15, 16, 19, 20, 23 | T-002/08Of, T-021/08 H/W, T-009/08 Ko, T-017/08 Ko, T-018/08 Ko, T-012/08 G/L, TA-013/08 Sr, T-011/08 Hb |
| III | 4 | 3, 8, 11, 14 | T-003/08Of, T-023/08 Mw, T-021/08 H/W, T-010/08 Ko |
| IV | 1 | 24 | T-016/08 Hb |

Table 6. Means of 17 Quantitative Traits Used for Clustering

| Quantitative Traits | Clusters | | | |
|---------------------|----------|--------|--------|--------|
| | I | II | III | IV |
| DE | 9.29 | 9.83 | 9.39 | 8.67 |
| DF | 42.54 | 42.08 | 42.82 | 43.67 |
| DM | 75.96 | 74.75 | 75.12 | 73.67 |
| LL | 3.76 | 3.67 | 3.67 | 3.67 |
| LW | 2.00 | 1.77 | 1.93 | 2.33 |
| LN | 48.12 | 42.93 | 45.41 | 47.67 |
| LAI | 1.59 | 1.97 | 1.97 | 2.33 |
| PPP | 4.80 | 4.87 | 4.83 | 4.13 |
| SPP | 4.9 | 5.02 | 4.73 | 4.47 |
| BM | 2.73 | 2.61 | 2.62 | 2.77 |
| YLD | 0.76 | 0.67 | 0.66 | 0.58 |
| TSW | 157.88 | 151.67 | 159.00 | 160.00 |
| PH | 40.83 | 39.47 | 41.30 | 42.22 |
| HI | 0.28 | 0.26 | 0.26 | 0.21 |
| PDNS | 75.62 | 74.42 | 75.48 | 78.67 |
| DIS | 1.88 | 1.75 | 1.76 | 2.00 |
| PEST | 1.21 | 1.08 | 1.06 | 1.00 |
| PROT | 26.44 | 27.11 | 30.22 | 34.45 |

NB: - DE=days to emergence, DF= days to flowering, DM=days to maturity, LL=leaf length, LW=leaf width, LN = leaf number, LAI=leaf area index, PPP=pods per plant, SPP=seeds per pod, BIO=biomass, YLD=grain yield, TSW=1000 seed weight, PH= plant height, HI=harvest index, DIS=disease, PEST=pest, and PROT=Protein content.

Distance Analysis between Clusters Based on Quantitative Traits

The pair wise generalized distance (D^2) between the clusters is given below.

Table 7. Distance between Different Clusters of Dekoko accessions

| Cluster | I | II | III | IV |
|---------|---------|--------|---------|-------|
| I | 0.000 | | | |
| II | 42.075 | 0.000 | | |
| III | 41.059 | 82.704 | 0.000 | |
| IV | 101.271 | 59.545 | 141.838 | 0.000 |

As seen from the above table the minimum cluster distance was between clusters I and III (41.059) and the maximum inter cluster distance was observed between clusters III and IV (141.838).

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