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# GENETIC DIVERGENCE IN TARAMIRA (*ERUCA SATIVA* L.) GERMPLASM BASED ON QUANTITATIVE AND QUALITATIVE CHARACTERS

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**Abstract**

The breeding potential of the *Eruca sativa* (Taramira) genotypes held in IABGR gene-bank has not been exploited to date. A total of 100 *Eruca sativa* genotypes collected from various eco-geographical regions of Pakistan were assessed to estimate the phenotypic diversity for 20 quantitative and 5 qualitative characters. A significant level of morphological diversity was recorded among quantitative and qualitative traits. The correlation coefficient analysis suggested that many traits had significant positive correlation with seed yield. Cluster analysis recognized four major clusters. Cluster analysis suggested that genotypes were mainly grouped due to their morphological dissimilarities. These results point out a number of valuable traits in the gene pool and a huge phenotypic variation that offers a fine basis of diversity for the selections of best Taramira accessions. Our findings have an important application for *Eruca sativa* germplasm evaluation, improvement, classification and preservation in Pakistan.

## Introduction

Taramira (*Eruca sativa* Mill) is an important oilseed crop that belongs to rapeseed-mustard group and family Brassicaceae. The genus *Eruca* includes three species, i.e., *E. sativa, E. vesicaria and E. pinnatifida.* The circulation of these species founds in Central Asia, Mediterranean countries and Europe (Warwick *et al*., 2007). The crop is grown on soil with reduced fertility and is preferred over other relative species due to its stress nature and adaptability to unfavorable environmental conditions (Gupta *et al*., 1998). Its original cultivation dates back to the early on Greeks and Romans. *Eruca sativa* is important leafy vegetables are used in several ways, such as salads, cooked vegetables, and functional plants (Kim *et al*., 2006). In addition its accepted uses as vegetables, it is also believed an important medicinal plant in many countries of the world. Besides that Taramira is an important oil seed crop, it was given minor weight and so, the yielding capability is very much restricted (Gupta *et al*., 1998). Although a lot of researches has been conducted the assessment, genetic improvement and connection between agronomic characters in Brassica species there is no comprehensive scientific assessment in *Eruca* spp. germplasm.

As a general rules the achievement in genetic enhancement of the crop and the growth of a species wants the ease of access of genetic diversity (Sultan *et al*., 2012). Detection of replica, organization of core set of a specific population and the selection of assortment of parents for the breeding activities are directly connected to the genetic variability (Jan *et al*., 2012). The germplasm evaluation association for identifying the relationships amongst agronomic characters in genetically assorted population at genotypic rank also would attend as a useful means for making growth in crop enhancement (Bello *et al*., 2006, Akbar *et al*., 2011). A number of ways have been designed to evaluate diversity by means of morphological biochemical and physiological categorization (Greene *et al*., 2004; Geleta *et al*., 2005, Mumtaz *et al*., 2011). Morphological characterization is the easiest way for the assessment of genetic diversity and useful as a point to follow up categorization and assessment studies. Evaluation of a large amount of morphological characters needs for the improvement of any crop breeding program. Conventionally genetic diversity investigations depend upon on quantitative and morphological traits (Zeb *et al*., 2011). Undoubtedly the genetic diversity there in the Pakistani Taramira genotypes wants safety from the constant genetic erosions. Therefore, this investigation was carried out to identify and classify genetic variation of 100 Taramira germplasm bring together from varied environmental conditions all over the country and to select Taramira accessions with best morphological and agronomic characters.

## Materials and Methods

Field research work was conducted in the field area of Institute of Agri-Biotechnology & Genetic Resources, (NARC) Islamabad, Pakistan during 2012. Yearly average rainfall in this area varies from 500-900mm with 31% in winter and 69% in summer. Hundred different Taramira genotypes collected from different areas of Pakistan were investigated (Table 1). The experiment was carried out in a distended plan. Taramira seeds were sown in a loamy soil with a pH 7.6, in plots each of 1.4 x 3.2m$^2$ keeping the row length of 3.4m and maintaining the distance between two beds of 2.3m with a path of 0.73m between the rows. Pre-sowing irrigation was done for seed bed preparation. Hand drill machine was used for planting. Weeds were removed by hand once 20 days after plant germination. A doze of 50 kg/ha potassium and nitrogen was added as merged fertilizer at the time of sowing.

Total 25 traits were recorded i.e. 20 quantitative and 5 qualitative traits (Table 2). Quantitative traits were recorded for plant height, days to maturity, days to flower initiation, days to 50% flower completion, days to complete flower completion, leaf petiole length, leaf length, leaf width, silique per plant, primary and secondary branches per plant main raceme length, silique per main raceme, silique length, silique width, seeds per silique, 1000-seed weight, seed yield per plant, seed yield per raceme.

**Table 1. List of Taramira accessions used in present study.**

| No. | Accession | Collection area | No. | Accession | Collection area | No. | Accession | Collection area |
|---|---|---|---|---|---|---|---|---|
| 1. | 1759 | Badin | 35 | 3675 | Attock | 69 | 3709 | - |
| 2. | 1760 | D.G. Khan | 36 | 3676 | Attock | 70 | 3710 | - |
| 3. | 1767 | Khushab | 37 | 3677 | Haripur | 71 | 3711 | - |
| 4. | 3644 | Attock | 38 | 3678 | Rawalpindi | 72 | 3712 | - |
| 5. | 3645 | Chakwal | 39 | 3679 | Rawalpindi | 73 | 17381 | Chakwal |
| 6. | 3646 | Chakwal | 40 | 3680 | Rawalpindi | 74 | 17382 | Jhelum |
| 7. | 3647 | Chakwal | 41 | 3681 | Chakwal | 75 | 17385 | Khushab |
| 8. | 3648 | Chakwal | 42 | 3682 | Chakwal | 76 | 17386 | Bhakkar |
| 9. | 3649 | Bhakkar | 43 | 3683 | Chakwal | 77 | 17387 | Layyah |
| 10. | 3650 | Khushab | 44 | 3684 | Chakwal | 78 | 17388 | D.G. Khan |
| 11. | 3651 | Vihari | 45 | 3685 | Chakwal | 79 | 17389 | Lakki Marwat |
| 12. | 3652 | Bahawalpur | 46 | 3686 | Chakwal | 80 | 17390 | Attock |
| 13. | 3653 | Bahawalpur | 47 | 3687 | Chakwal | 81 | 17391 | Attock |
| 14. | 3654 | Rajanpur | 48 | 3688 | Chakwal | 82 | 17392 | Attock |
| 15. | 3655 | Rajanpur | 49 | 3689 | Khushab | 83 | 17393 | Attock |
| 16. | 3656 | Rajanpur | 50 | 3690 | Sargodha | 84 | 17394 | Chakwal |
| 17. | 3657 | Rajanpur | 51 | 3691 | Sargodha | 85 | 17395 | Chakwal |
| 18. | 3658 | Rajanpur | 52 | 3692 | Hafizabad | 86 | 17396 | Chakwal |
| 19. | 3659 | Rajanpur | 53 | 3693 | Jhelum | 87 | 17397 | Chakwal |
| 20. | 3660 | Rajanpur | 54 | 3694 | Jhelum | 88 | 17398 | Chakwal |
| 21. | 3661 | D.G. Khan | 55 | 3695 | Jhelum | 89 | 17399 | Chakwal |
| 22. | 3662 | D.G. Khan | 56 | 3696 | Rawalpindi | 90 | 17400 | Chakwal |
| 23. | 3663 | D.G. Khan | 57 | 3697 | Sargodha | 91 | 17402 | Chakwal |
| 24. | 3664 | D.G. Khan | 58 | 3698 | Sargodha | 92 | 17403 | Chakwal |
| 25. | 3665 | D.G. Khan | 59 | 3699 | T.T Singh | 93 | 17405 | Chakwal |
| 26. | 3666 | D.I. Khan | 60 | 3700 | Faisalabad | 94 | 17406 | Chakwal |
| 27. | 3667 | D.I. Khan | 61 | 3701 | Okara | 95 | 17407 | Mianwali |
| 28. | 3668 | D.I. Khan | 62 | 3702 | Sahiwal | 96 | 17408 | Chakwal |
| 29. | 3669 | D.I. Khan | 63 | 3703 | Pakpattan | 97 | 17409 | Hangu |
| 30. | 3670 | D.I. Khan | 64 | 3704 | Kasur | 98 | 17410 | Kohat |
| 31. | 3671 | Lakki Marwat | 65 | 3705 | Kasur | 99 | 17411 | Attock |
| 32. | 3672 | Karak | 66 | 3706 | Sheikhupura | 100 | 17412 | D.I. Khan |
| 33. | 3673 | Karak | 67 | 3707 | Rawalpindi | Ch1 | 26187 | - |
| 34. | 3674 | Attock | 68 | 3708 | Umarkot | Ch2 | 27460 | - |

Trait assortment and measurement procedures were based on IPGRI descriptors of Taramira. Investigation of variance was based on mean values of accessions detected in each block. The formulae recommended by Kwon & Torrie, (1964) were used for the correlation coefficient investigations. Cluster analysis was used to assess the level of dissimilarity among the Taramira genotypes.

**Results and Discussion**

A significant level of phenotypic variation was noticed among the 100 Taramira Germpasm for most of the quantitative characters considered (Table 3). Sample of deviation among the genotypes was diverse for different characters. The largest variation was recorded for seed yield per plant, silique per plant, plant height and days to flower completion. The variances for the above characters were 6982.6, 6462.9, 466.9 and 184.9, respectively. Relatively, a low level of variability was distinguished in thousand seed weight, siliqua width and leaf length to leaf width ratio, etc. The mean values of the Taramira genotypes for days to 50% flowering, days to maturity and days to flower initiation, were 75.9, 175.8 and 64.6 with a range of 57 to 99, 172 to 182 and 47.0 to 87.0 days, respectively. These characters could be evaluated to know for both early and delayed maturity. The Taramira cultivar 26187 showed high values in this regard, while a lot of other Taramira accessions demonstrated earliness in our observations. Both early and delayed maturity are vital for breeding programs trying for variation of plant germplasms to a variety of ecological areas on photoperiod and thermo-sensitivity (Suddihiyam *et al*., 1992; Rehman *et al*., 2009). Rest of the other traits demonstrated wide genetic deviation and accessions with such a huge level of genetic assortment often used for the identification of best germplasm for varied ecological circumstances.

**Table 2. Morphological and seed traits recorded for Taramira germplasm.**

| Trait | Scale | Description of the trait |
|---|---|---|
| **Quantitative traits** | | |
| Days to flower initiation (DFI) | Days | Number of days from seed sowing until 50% of plants have first flower in each accession |
| Days to 50% flowering (50% DF) | Days | Numbers of days from seed sowing until 50% plants have at least one flower in each accession |
| Days to flower completion (DFC) | Days | Numbers of days from seed sowing until flowers completed |
| Days to maturity (DM) | Days | Number of days from seed sowing until 75% of plants reaching physiological maturity |
| Leaf petiole length (LPL) | cm | It is measured where blade intercepts with petiole |
| Leaf length (LL) | cm | Measured largest leaf including petiole |
| Leaf width (LW) | cm | Measured at the widest point of largest leaf, just before harvest maturity |
| Leaf length/ Leaf width (LL/LW) | cm | Both petiole length / width ratio were computed |
| Plant height | cm | Mean height of five random plants from ground level to the apex of the main stem. |
| Primary branches per plant (PB/P) | No. | Total number of branches originating from main stem which gives rise to other silique -bearing branches. |
| Silique/Plant (S/P) | No. | Total number of silique on both primary and secondary branches. Mean of five randomly selected plants |
| Main raceme length (MRL) | cm | |
| Silique/Main raceme (S/MR) | No. | |
| Silique length (SL) | cm | Distance from the tip of pedicle to the tip of siliqua |
| Silique width (SW) | cm | Distance across the widest point of the same silique used for length |
| Silique length/ Silique width (SL/SW) | cm | Both siliqua length / width ratio were computed |
| Seeds/Silique (S/S) | No. | Mean number of seeds from five randomly selected silique from five different plants |
| 1000- seed weight (1000-SW) | g | Weight of 100 random dried seeds was calculated and then converted to 1000-seed weight by multiplying 10 |
| Seed yield/Plant (SY/P) | g | Average seed weight of five randomly selected plants for each accession was recorded at 13% moisture content |
| Seed yield/Raceme (SY/R) | g | |
| **Qualitative traits** | | |
| Leaf shape (LS) | - | 1 = Lanceolate; 2 = Elliptic; 3 = Spatulate; 4 = Ovate; 5 = Obovate; 6 = Oblong; 7 = Broad-elliptic; 9= Broad-circular |
| Leaf margin (LM) | - | 1 = Entire; 2 = crenate; 3 = Lobbed ; 4 = serrate; 5 = Cleft |
| Leaf colour (LC) | - | 1 = White green; 2 = yellow green; 3 = light green; 4 = green; 5 = dark green; 6 = purple green; 7 = purple |
| Leaf incision (LI) | - | 0 =entire; 1=crenate; 2 =dentate; 3 =serrate; 4 =undulate; 5 =doubly dentate |
| Flower colour (FC) | - | 1 =white; 2 =cream; 3 =yellow |

**Table 3. Variation in quantitative traits of 105 local Taramira accessions from Pakistan.**

| Descriptive Statistics | | | | | | |
|---|---|---|---|---|---|---|
| **Trait** | **Mean** | **Minimum** | **Maximum** | **SD** | **CV%** | **Variance** |
| DFI | 64.6 | 47.0 | 87.0 | 8.3 | 12.9 | 69.2 |
| DF50% | 75.9 | 57.0 | 99.0 | 11.2 | 14.8 | 126.1 |
| DFC | 87.0 | 62.0 | 106.0 | 13.6 | 15.6 | 184.9 |
| DM | 175.8 | 172.0 | 182.0 | 2.7 | 1.5 | 7.3 |
| LPL | 3.7 | 1.2 | 8.3 | 1.2 | 33.1 | 1.5 |
| LL | 23.1 | 10.9 | 48.3 | 5.9 | 25.4 | 34.3 |
| LW | 8.7 | 3.5 | 12.8 | 1.9 | 22.4 | 3.8 |
| LL/LW | 2.7 | 1.7 | 4.7 | 0.5 | 20.2 | 0.3 |
| PH | 113.3 | 45.0 | 263.7 | 21.6 | 19.1 | 466.9 |
| PB/P | 7.0 | 4.2 | 11.6 | 1.6 | 22.4 | 2.4 |
| S/P | 207.6 | 49.8 | 539.0 | 80.4 | 38.7 | 6462.9 |
| MRL | 58.8 | 18.0 | 85.7 | 12.8 | 21.7 | 162.8 |
| S/MR | 19.7 | 8.4 | 39.2 | 5.2 | 26.4 | 26.9 |
| SL | 55.2 | 33.7 | 74.7 | 12.2 | 22.1 | 149.6 |
| SW | 4.5 | 2.9 | 6.2 | 0.8 | 16.9 | 0.6 |
| SL/SW | 12.3 | 8.4 | 16.6 | 1.6 | 13.2 | 2.6 |
| S/S | 18.4 | 11.7 | 28.1 | 3.0 | 16.0 | 8.7 |
| TSW | 2.9 | 1.4 | 7.5 | 1.0 | 35.4 | 1.1 |
| SY/P | 7.9 | 2.3 | 18.1 | 3.2 | 40.2 | 10.1 |
| SY/R | 199.1 | 45.0 | 400.0 | 83.6 | 42.0 | 6982.6 |

**Table 5. Correlation coefficients among 20 quantitative traits in Taramira germplasm.**

| Trait | DFI | DF50% | DFC | DM | LPL | LL | LW | LL/LW | PH | PB/P | S/P | MRL | S/MR | SL | SW | SL/SW | S/S | TSW | SY/P | SY/R |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DFI | 1.00 | | | | | | | | | | | | | | | | | | | |
| DF50% | 0.84** | 1.00 | | | | | | | | | | | | | | | | | | |
| DFC | 0.82** | 0.82** | 1.00 | | | | | | | | | | | | | | | | | |
| DM | 0.19 | 0.17 | 0.29** | 1.00 | | | | | | | | | | | | | | | | |
| LPL | 0.37** | 0.36** | 0.37** | 0.02 | 1.00 | | | | | | | | | | | | | | | |
| LL | 0.64** | 0.62** | 0.64** | 0.32** | 0.48** | 1.00 | | | | | | | | | | | | | | |
| LW | 0.56 | 0.47** | 0.48** | 0.35** | 0.15 | 0.70** | 1.00 | | | | | | | | | | | | | |
| LL/LW | 0.22* | 0.32** | 0.34** | 0.00 | 0.45** | 0.50** | -0.24 | 1.00 | | | | | | | | | | | | |
| PH | 0.25* | 0.24* | 0.23* | 0.20* | 0.35** | 0.42** | 0.31** | 0.20* | 1.00 | | | | | | | | | | | |
| PB/P | 0.16 | 0.10 | 0.09 | 0.25* | 0.04 | 0.31** | 0.40** | -0.08 | 0.10 | 1.00 | | | | | | | | | | |
| S/P | 0.17 | 0.17 | 0.32** | 0.17 | 0.08 | 0.41** | 0.31** | 0.19 | 0.17 | 0.34** | 1.00 | | | | | | | | | |
| MRL | 0.43** | 0.35** | 0.36** | -0.02 | 0.27** | 0.43** | 0.49** | 0.04 | 0.34** | 0.11 | 0.30** | 1.00 | | | | | | | | |
| S/MR | 0.41** | 0.40** | 0.35** | 0.21 | 0.28** | 0.59** | 0.59** | 0.12 | 0.34** | 0.39** | 0.38** | 0.63* | 1.00 | | | | | | | |
| SL | 0.01 | 0.11 | 0.07 | -0.14 | 0.10 | 0.25* | 0.11 | 0.24* | 0.06 | 0.03 | 0.19 | 0.04 | -0.01 | 1.00 | | | | | | |
| SW | -0.08 | -0.04 | -0.07 | -0.15 | 0.05 | 0.16 | 0.08 | 0.14 | 0.04 | 0.00 | 0.13 | 0.14 | 0.01 | 0.82** | 1.00 | | | | | |
| SL/SW | 0.13 | 0.24* | 0.22* | -0.05 | 0.10 | 0.24* | 0.09 | 0.23* | 0.06 | 0.06 | 0.15 | -0.11 | -0.03 | 0.66** | 0.11 | 1.00 | | | | |
| S/S | 0.33** | 0.22* | 0.23* | 0.30** | -0.01 | 0.29** | 0.39** | -0.09 | 0.06 | 0.31** | 0.19 | 0.10 | 0.28** | -0.32 | -0.47 | 0.07 | 1.00 | | | |
| TSW | -0.06 | 0.02 | 0.16 | 0.49** | -0.06 | 0.09** | 0.07 | 0.03 | -0.07 | -0.05 | 0.12 | -0.15 | -0.20 | 0.15 | 0.20* | -0.02 | -0.22 | 1.00 | | |
| SY/P | 0.10 | 0.05 | 0.21* | 0.19 | 0.05 | 0.35** | 0.27* | 0.16 | 0.21* | 0.40** | 0.56** | 0.16 | 0.29** | 0.28** | 0.26* | 0.13 | 0.09 | 0.21* | 1.00 | |
| SY/R | 0.58** | 0.59** | 0.56** | 0.18 | 0.41** | 0.66** | 0.61** | 0.19 | 0.30** | 0.22* | 0.23* | 0.55* | 0.60** | 0.10 | 0.04 | 0.11 | 0.30** | -0.11 | 0.18 | 1.00 |

0.27 & above (**Highly significant at 0.01 probability level)

0.20 to 0.26 (*Significant at 0.05 probability level)

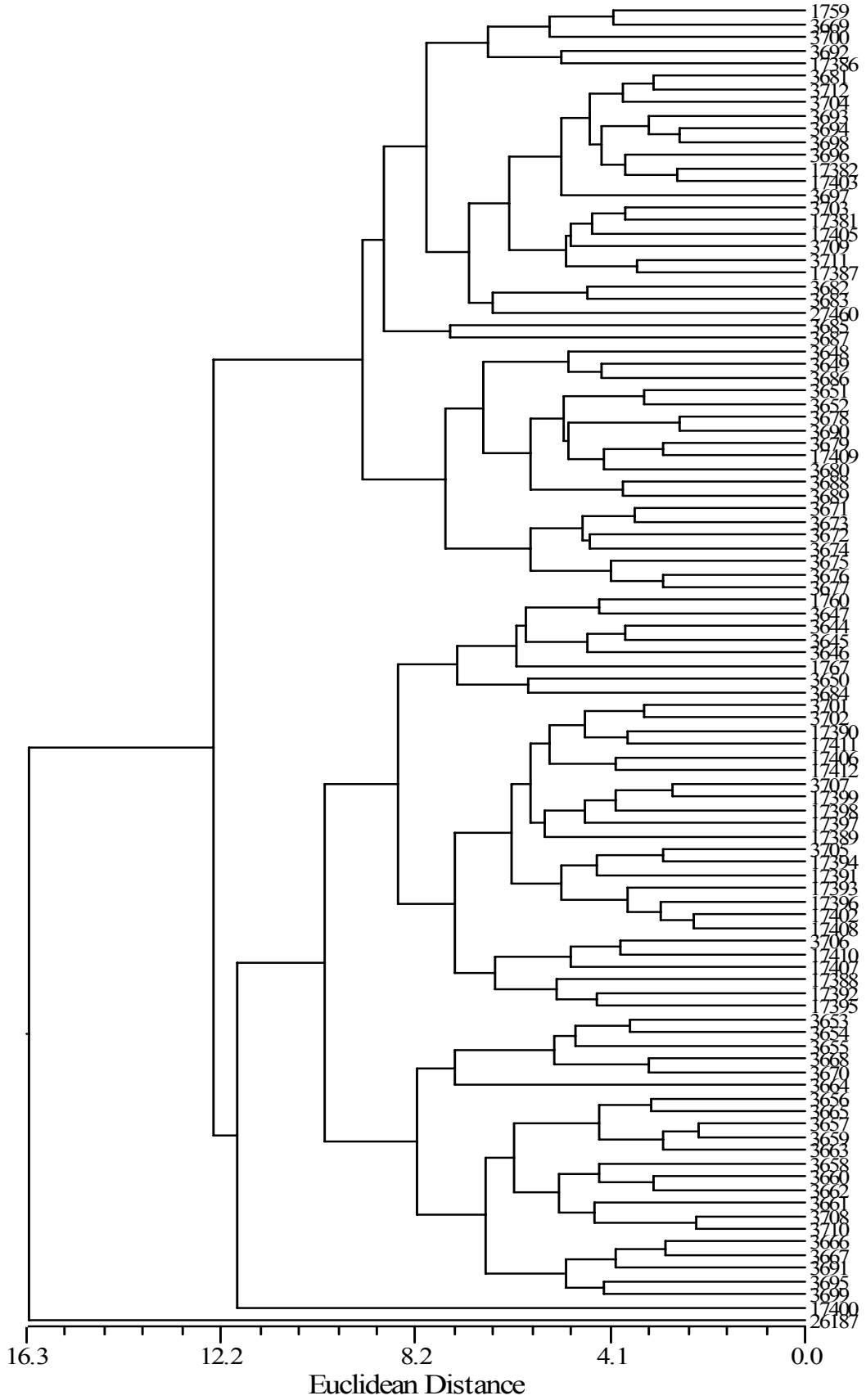


Fig. 1. Scatter diagram of quantitative traits in 100 accessions of Taramira germplasm.

Correlation coefficients of seed yield and yield components are given in (Table 5). Data exposed that number of silique per plant, primary branches per plant, siliqua per main raceme, and silique length had the significant positive contribution with seed yield plant per plant. Positive but not statistically significant correlation was observed in thousand seed weight, silique width, leaf width, and days to flower completion. While no one trait showed negative and significant correlation with seed yield per plant. Our results disagreed with the finding of Gnanasekaran *et al*., (2008) and Yol *et al*., (2010) who noticed negative and significance correlation of these traits with seed yield per plant.

Generally Principal components analysis, often conducted to builds a new set of orthogonal coordinate axes and to find out the relative significance of classification variables. There are no dealings to discover the worth of a coefficient but that is eigenvector (Düzyaman, 2005). According to Sneath & Sokal, (1973) top coefficients for some characters designated the relatedness of that trait to relevant PC axes. In our assessments, the first PC contributed 30.68% of the overall variance of the agronomic data, the second 13.20%, the third 10.12%, the fourth 8.26%, the fifth 6.67% and the sixth 6.25% (Table 4). Principal component analysis revealed that primary branches per plant, silique per plant, seed per silique, thousand seed weight, days to 50% flowering etc, were the most vital characters which accounted for a considerable level of phenotypic variation recorded in this Taramira genotypes. It is suggested that work on these character would be very helpful screening and classification of elite Taramira genotypes in Pakistan.

**Table 4. Eigenvalues, proportion of variability and quantitative traits that contributed to the first six principal components of Taramira germplasm from Pakistan.**

| PCA Table | | | | | | |
|---|---|---|---|---|---|---|
| | **PC1** | **PC2** | **PC3** | **PC4** | **PC5** | **PC6** |
| Eigenvalue | 6.14 | 2.64 | 2.02 | 1.65 | 1.33 | 1.25 |
| Cumulative Eigenvalue | 6.14 | 8.78 | 10.80 | 12.45 | 13.79 | 15.04 |
| % Total variance | 30.68 | 13.20 | 10.12 | 8.26 | 6.67 | 6.25 |
| Cumulative % | 30.68 | 43.88 | 54.00 | 62.26 | 68.93 | 75.18 |

Cluster analysis based on both quantitative and qualitative characters divided all the Taramira genotypes into 4 main clusters (Fig 1). Grave evaluation of clusters showed that clusters were diverse within themselves and between each other based on main trait associations. The cluster analysis executed with 20 quantitative and 5 qualitative traits divided 100 accession lines and 2 checks into 4 different clusters. Over all most of the variations observed in the quantitative characters. First cluster was the largest one that included 47 Taramira genotypes gathered from diverse area of Pakistan characterized by maximum days of flowering completion and tall in height. In this cluster, leaf width was 3.5cm and the length was 10.9cm, these being the smallest leaf values amongst the all germplasm. Siliqua width was shorter in this cluster in contrast to other clusters, while the siliqua per plant was small in number and the lowest 1000-seed weight was recorded in this group of Taramira genotypes. The second cluster composed of 32 genotypes and signified the second largest cluster. This cluster had accessions characterized by high 1000-seed weight (4.0) and lowest seed yield per plant (15.7g). The third cluster included 22 Taramira genotypes and represented by small number of siliqua per main raceme greater leaf length and leaf width as compare to other clusters. The fourth and final cluster comprised of only one accession 26157 (from CGN, Netherlands), characterized by large siliqua per main rename, longer leaf petiole length and high leaf length to leaf width ratio. This accession was also used as a check and had distinguished characters as compare to other accessions used in our study. Clustering of different genotype was not allied with the geographical allocation instead Taramira genotypes were mostly clustered owing to their morphological distinctions. Our results are in agreement with investigations of Gupta *et al*., (2001). This may be the movement of different Taramira accessions from one region to another in collection positions. According to Baydar & Gurel, (1999) a few environmental factors could also induce the gene flow among populations from various geographical sources.

## Conclusions

A considerable level of phenotypic variation genetic variation based on quantitative and qualitative characters was recorded in our research work. Our agro-morphological research work would be very helpful in screening and classification and conservation of elite Taramira genotypes in Pakistan.

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