

GENETIC DIVERSITY IN HYBRID PEA LINES ON THE BASIS OF MORPHOLOGY

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ABSTRACT

24 genotypes were grown in the glass house of the university of Malakand for determination of morphological traits analysis. Out of these 7 genotypes shown tallest range up to 68 cm, while their root length reaches up to 15 cm. 10 genotypes were dwarf and reach up to 30 cm while the root length were below than 12cm.

Remain 7 genotypes were shown moderate growth. Plant length, stem length and mass, Root length and mass and root hairs were noted. These all findings were taken in 3 data and data were taken every 15 days. Morphological, cluster analysis and genetic variation were observed during statistical analysis and Dendrogram were divided into two major linkages e. g. L1 and L2.

KEYWORDS: Pisum Sativum, Glass House, Linkages, Morphological Traits & Variation

INTRODUCTION

Pea belongs to the Fabaceae family (Genus: Pisum, subfamily: Faboideae tribe: Fabeae), which has a significant ecological benefit because it have ability to fix atmospheric free nitrogen into the soil by symbiotic living with bacteria of Rhizobium species and sustaining of soil fertility (Albayrak et al., 2004). Economically, legumes represent the second most important family of crop plants after Poaceae (grass family), accounting for approximately 27% of the world's crop production (Gregoir and Aubert, 2012). Dry pea currently ranks second only to common bean as the most widely grown grain legumes in the world with primary production in temperate regions and global production of 10.4 M tons in 2009 (Judith and Burstin, 2011).

Pea seeds are rich in protein (23–25%), slowly digestible starch (50%), Agronomy 2012, 2 soluble sugars (5%), fiber, minerals and vitamins (Clarice Coyne, 2012). On a worldwide basis, legumes contribute about one-third of humankind's direct protein intake, while also serving as an important source of fodder and forage for animals and of edible and industrial oils. One of the most important attributes of legumes is their capacity for symbiotic nitrogen fixation, underscoring their importance as a source of nitrogen in both natural and agricultural ecosystems (Ellis, 2012)

Resent year, biochemical and molecular genetics techniques have emerged as a complementary strategy in conjunction with traditional approaches in the management of plant Genetic resources (Nisar et al., 2009, Ayad, 1995 and Bretting 1995).

Genetic marker provides an attractive alternative to desirable trait selection, making the breeding process more efficient and less resource demanding. Once a genetic marker that is closely linked to the desirable traits has been identified, marker assisted (MAS) can be practiced at an early stage of plant development, thus avoiding selection through traits exposure (Rakshit et al., 2001). MAS can be useful not only for qualitative traits controlled by a single gene, but also for quantitative traits (Land and Thompson, 1990). Little attention has been given to varieties improvement of peas and is

used as a marginal crop for cultivation in Pakistan (Bashir and Arshad, 2002). The present work is objected to estimate genetic diversity and morphological traits correlation and association.

MATERIALS AND METHODS

A total of 24 genotype combinations was sown in three replicates in the glass house of the Department of the Botany, University of Malakand, at Randomize complete Block (RCB) Design. Pea glasses were irrigated according to the need of the plant. The soil was dried and prepared for sowing and the 33 glass was prepared by having two separate parts.

Seed was sown in glasses at the depth of 2cm. All the seed was sown parallel to sunshine. The germination rate of different pea glasses was noted. The germination rates were noted in the percentage of all varieties. Morphological characters were split into two categories. i.e. Qualitative and Quantitative.

Different qualitative traits were selected for studies such as (1) stem length (2) stem weight (3) root length (4) root weight (5) root hairs.

Cluster and Data Analysis

Scored data were analysis through statistical software STATISTICA which give us the result of cluster analysis. Cluster analysis a statistical process which estimating the relationship among variables and analyzing several variables When the focus on the relationship between on independent variables.

RESULTS

A total of 24 genotypes was grown in the glass house at University of Malakand in three replicate sets, during the growing season of 2013 in order to determine the genetic linkage in the pre-developed pea lines (Nisar and Ghafoor, 2009). Total five morphological traits, i.e. Stem length, stem mass, root length, root mass and root hair were considered to explore and to evaluate the genetic diversity in 24 hybrid pea lines. Details of morphological traits are represented in table 1. The morphological traits were subjected to statistical software "STATISTICA" to find out the genetic diversity. Dendrogram was constructed by using Wards method and is represented in fig. 1. The Dendrogram divided 24 hybrid pea lines into two linkages i.e. Linkage-1 and linkage-2. Linkage 1 is further divided into two clusters i.e. Cluster-1 and cluster-2. The cluster-1 consist of 8 pea line i.e. Pea line 18, 22, 06, 15, 16, 21, 9 and 1. Cluster-2 consist of 7 genotypes i.e. Pea line 5, 17, 4, 3, 7, 12 and 23. Linkage-2 consists of one cluster i.e. Cluster-3. The cluster 3 comprises of 9 genotypes i.e. Pea line 24, 19, 10, 14, 2, 20, 13, 8 and 1

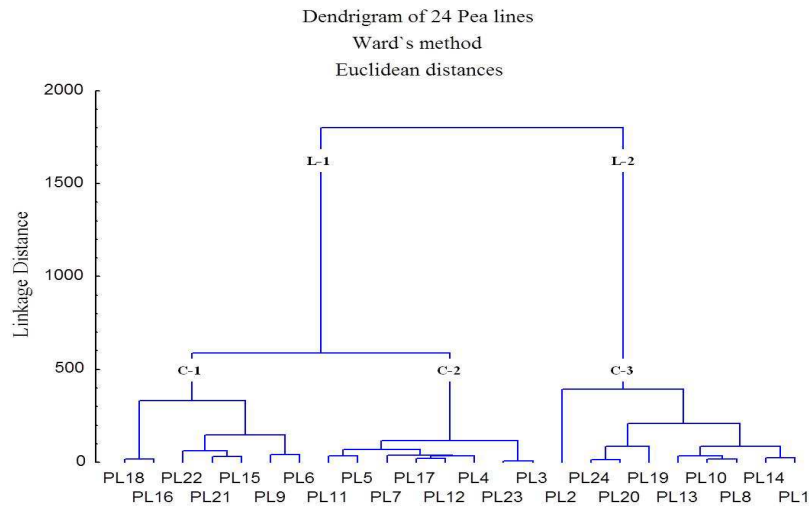


Figure 1: Indicating Dendrogram of 24 Genotypes of *Pisum Sativum* L. Based on Morphological Character

Table 1: Represented the Details of Morphological Traits

PL	SL	SM	RL	RM	RH
1	470	1.33	175	1.98	37
2	680	1.95	181	1.57	57
3	160	1.23	183	1.09	34
4	153	0.99	157	1.83	48
5	150	1.39	108	2.57	49
6	300	1	165	1.42	41
7	190	1.04	141	1.57	50
8	460	1.24	133	0.91	46
9	300	1.07	123	0.34	33
10	447	1.33	129	1.06	37
11	127	1.24	129	2.47	60
12	160	1.38	121	1.91	32
13	480	1.21	140	1.27	33
14	450	0.56	181	0.75	48
15	240	0.07	169	.68	52
16	300	1.17	312	0.91	60
17	170	1.03	125	0.95	41
18	310	1.21	303	1.23	47
19	400	1.01	110	1.66	32
20	370	1.36	166	1.61	38
21	220	.77	181	0.56	32
22	241	0.98	225	1.04	36
23	165	1.27	188	1.12	38
24	375	1.39	179	1.63	45

PL= Pea line SL= Stem length SW= Stem weight RL= Root length RW= Root weight RH= Root hair

Descriptive Statistics

Descriptive statistics of morphological traits was carried out, in order to find out the mean values and standard deviation of morphological traits of three clusters. Mean values and standard deviation are shown in table 2.

Cluster 1

Cluster- 1 consist of 8 genotypes, maximum root length and root hairs numbers were observed with mean valve of 200.875 with a standard deviation of 72.9862 and mean value of 45.125 with a standard deviation respectively as compared to other clusters. While stem mass and root mass was lower as compared to cluster 2 and 3. Stem length was intermediate between cluster 2 and 3 with a mean value of 254.75 and standard deviation of 62.2547.

Cluster 2

Cluster -2 consists of 7 genotypes, the root mass is greater than cluster 1 and 3 with mean values of 1.5771 and standard deviation of 0.57737. Other morphological characteristics like stem length, root length were lower as compared to other clusters. However, stem mass and root hairs number were greater than group 1 and less than group 3 with mean values of 1.1771 and standard deviation of 0.18936 and 41.71 and standard deviation of 7.40977 respectively.

Cluster -3

Cluster 3 consists of 9 genotypes, in this cluster highest value of stem length and stem mass was observed with mean values of 459.11 and standard deviation of 92.25 and 1.2644 and standard deviation of 0.36538. While the lowest value of root hairs numbers was observed with minimum mean value 41.44 and standard deviation of 0.86 as compared to other clusters. Other values like root length and root mass have intermediate values between cluster 1 and 2. The mean values for root length and root mass were 154.44 and 1.4933 and standard deviation of 26.889 and 0.3979 respectively.

Table 2: Mean and Standard Deviation of Three Clusters based on Morphological Traits

Cluster-1			Cluster-2			Cluster-3		
N	Mean	St. Dev.	N	Mean	St. Dev.	N	Mean	St. Dev.
8	254.75	62.2547	7	164	13.30413	9	459.1111	92.25433
8	1.0963	0.31391	7	1.1771	0.18936	9	1.2644	0.36538
8	200.875	72.9862	7	149	29.22898	9	154.4444	26.88918
8	1.0813	0.66318	7	1.5771	0.57737	9	1.4933	0.3979
8	45.125	11.4198	7	41.7143	7.40977	9	41.4444	8.14112

CONCLUSIONS

24 genotypes were grown in glass house of university of Malakand for determination of morphological traits analysis. Root mass and root hairs increase with interval of time, stem length and root length become slow. These Genotypes show the tallest, medium and dwarf range of there length. Data were collected in three step and were taken after every 15 Days.

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