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DIVERSITY ANALYSIS IN LINSEED (*LINUM USITATISSIMUM* L.) GERMPLASM FOR BUD FLY RESISTANCE USING MORPHOLOGICAL AND MOLECULAR MARKERS

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ABSTRACT

Fourty seven genotypes were evaluated for a genetic divergence to identify potential parents for the linseed breeding program aimed at yield improvement to identify the desirable and potential parents for hybridization. *Mahalanobis D² statistics for ten characters viz.* days to 50% flowering (on a plot basis), days to 80% maturity (on a plot basis), days to 100% maturity (on a plot basis), plant height (cm), number of branches plant^{-1}, sepal thickness (µm), total number of capsule plant^{-1}, % bud fly infestation, seed yield plant^{-1} (g), 1000 seed weight (g). Mahalanobis D² statistics was used in this study for computing genetic divergence for the characters studied. The analysis of dispersion for ten characters using Wilk's criterion revealed a highly significant difference between genotypes for all ten characters. The forty seven genotypes were grouped into eight clusters by Tocher's method. The intra cluster distance range from 0.00 to 11.68. Cluster III possessed highest intra cluster distance (D² = 11.68) followed by cluster II (D² = 10.53) and cluster I (D² = 10.11). The maximum inter-cluster distance was between cluster IV and VI (D² = 51.96), followed by cluster I and cluster VI (D² = 42.56) whereas the minimum inter-cluster distance was found between cluster I and cluster V (D² = 11.87). The canonical analysis indicated that days to 50% flowering, total number of capsules plant^{-1}, % bud fly infestation, number of branches plant^{-1}, contributed in vector I accounting for 77.11% of total variation. The canonical analysis and cluster mean studied together revealed the importance of 50% flowering, sepal thickness, total number of capsules plant^{-1}, % bud fly infestation, plant height and seed yield plant^{-1} as important contributors towards the total divergence. Hence, these traits form the criterion for the selection of parents for hybridization program. Germplasms IC633096, Neela, EC99001, IC0499165 were used as a varietal development and germplasms IC0498472, IC0498660, IC993391, Neelum identified as potential and diverse parents for their use in crossing program.

Keywords **:** Germplasm lines, Linseed, D^2, Clusters, Vector, Canonical analysis, Cluster mean, Divergence

Introduction

Linseed, or flax, is an annual, self-pollinating, autogamous diploid plant with a chromosomal number of 2n=2x=30. It belongs to the *Linaceae* family, encompassing 14 genera and over 200 species (Kumar *et al*., 2016). Linseed is a globally important oilseed crop and it is grown on 32.23 lakh hectares around the world, yielding 30.68 lakh tonnes with an average productivity of 952 kg ha^{-1} (FAOSTAT, 2019). In India, it grown on 234.47 thousand hectares with the production of 156 thousand tonnes and productivity of

667 kg ha^{-1} (Anonymous, 2023). In Maharashtra, it grown on 7.16 thousand hectares with the production of 3.40 thousand tonnes and productivity of 475 kg ha^{-1}. (Anonymous, 2024).

Linseed fibre, obtained from the stem of plant, is more tensile than cotton. Due to its strength, non-elasticity, repeatability and recyclable nature, it is very attractive to be used as rope and thread, which is the major interest for its cultivation (Jhala and Linda 2010). After oil extraction, the cake is used for cattle as a protein stock and fine manure (Sankari, 2000). Different names know it at different locations like Arasi, Alsi, Jawas, Tisi and Chana. Linseed oil makes several daily use products, such as paint, varnishes, water-resistant fabric and linoleum (Dash *et al*., 2017). Linseed is the best herbal source of PUFA- Poly unsaturated fatty acids such as linoleic and linolenic (ω-3) acid, which are essential for humans since they can't be synthesized in the body.

Linseed is an important oilseed crop which is the only species in *Linaceae* family with economic values (Tadesse *et al*., 2010). It has nutrients and pharmaceutical uses and also used in animal fat and poultry diets (Khan *et al*., 2013). Linseed contains oil 30-40%, carbohydrate 28%, protein 21%, water 7.4% and also different mineral 3.4% making it an important industrial crop. (Khan *et al*., 2010). In India, the cultivation of linseed is challenged by several diseases and insect pests, resulting in significant yield losses. Notably, bud fly (*Dasyneura lini*) infestations can cause losses ranging from 20% to as high as 97%. Control measures for bud fly infestations include application of systemic insecticides or cultural practices etc. which incurs extra cost to linseed growing farmers. (Malik *et al.*, 2008).

Control measures for bud fly infestation include application of systemic insecticides or cultural planting etc which incurs extra cost to the linseed growing farmers (Malik *et al.*, 2008). Hence, development of resistant varieties is thus the eco-friendliest and widely accepted approach to integrate this problem. Resistance to bud fly can be linked to certain varietal characters like early maturity & sepal thickness (Malik, 2020). Hence the present investigation to screen 47 germplasm, selected as a subset from the core germplasm developed for bud fly resistance. (Nair *et al*., 2024) and to study the association of characters associated with bud fly resistance both under natural & artificial conditions.

Materials and Methods

The present investigation was undertaken during *rabi* 2023 at All India Coordinated Research Project on Linseed and Mustard research farm, College of Agriculture, Nagpur under deliberate late sown conditions both under natural and artificial conditions. Artificial screening technique for screening for bud fly resistance was devised (Nair *et al.*, 2024) These 47 germplasms were grown in randomized block design in three replications. Two checks Neela (Resistant check) & Neelum (Susceptible Check) were sown after every 10/ 20 rows of test germplasm. All the recommended package of practices was undertaken to raise a good crop. Data was recorded on five competitive plants for ten characters i.e., days to 50% flowering (on a plot basis), days to 80% maturity (on a plot basis), days to 100% maturity (on a plot basis), plant height (cm), number of branches plant^{-1}, sepal thickness (µm), total number of capsule plant^{-1}, % bud fly infestation at dough stage, seed yield plant^{-1} (g).

Mahalanobis D² statistics was used in this study for computing genetic divergence for the characters studied. Grouping of germplasms into different clusters and canonical analysis were done by using Tocher's method. Selection of parents for hybridization from different clusters was done based on mean statistical distance.

Results and Discussion

The data was subjected to analysis of variance to study the genetic differences among 47 germplasms for yield and yield contributing traits. The results showed that the analysis of variance were highly significant for the characters studied the analysis of dispersion for the test of significance of difference in the mean values based on the Wilk's criterion revealed highly significant difference among genotypes for ten characters. (Table 2).

The grouping of 47 genotypes into different clusters was done by Tocher's method and presented in Table 4 and Fig. 1. The entire genotypes (47) were grouped based on D² statistics into eight clusters. Cluster I was the largest comprising 20 genotypes, followed by Cluster II comprising 9 genotypes, cluster III comprising 8 genotypes, and cluster IV comprised of 3 genotypes, Cluster V comprised 1 genotypes, cluster VI comprised of 3 genotype and cluster VII comprising of 2 genotypes and cluster VIII comprising of single genotype. The promising check Neela was grouped into cluster III and check Neelum was grouped into cluster VII respectively. There were many genotypes distributed in other cluster which were highly deviating from the promising check and hence offers good scope for improvement. From the data it can be seen that cluster I and cluster II had maximum number of genotypes. Those clusters that did not have

any of the check varieties were genetically diverse from the checks and hence there is scope for the selection of potential genotypes for genetic improvement of yield and yield contributing characters.

The contribution of each character towards genetic divergence is presented in Table 3. Contribution of 1000 seed weight (g) was maximum (68.36%) followed by % bud fly infestation (24.70%), days to 50% flowering (3.89%), total number of capsule plant^{-1} (1.30%), days to 100% maturity (0.37%), sepal thickness (0.37%), number of branches plant^{-1} (0.37%) were important traits contributing towards genetic divergence and this study could be used in selecting desired genotypes for further selection and choice of parent for hybridization and creation of more variability.

The values of the first three canonical vectors and canonical roots are presented in Table 5 and Table 6. The first three canonical roots accounted for 96.59 percent of the observed variability in the material studied (λ_1 =77.11%, λ_2=16.64%, λ_3 = 2.84%). The overall contribution of the three canonical roots to the total variability among 47 genotypes was 96.59 percent suggesting the major portion of differentiation in the first three phases. This indicates that differentiation for ten characters among 47 genotypes were completed in three phases.

The further coefficient in the first three canonical vectors shows that out of ten characters days to 50% flowering, total number of capsules plant^{-1}, % bud fly infestation, number of branches plant^{-1}, contributed in vector I accounting for 77.11% of total variation. Characters days to 50% flowering, sepal thickness, total number of capsules plant^{-1}, plant height, seed yield plant^{-1}, were important characters in vector II which accounted for 16.64% of the total variation. Days to 50% flowering, days to 80% maturity, days to 100% maturity, sepal thickness, total number of capsules plant^{-1}, % bud fly infestation, plant height, seed yield plant^{-1} were important characters in vector III which accounted for 2.84% of total variation. From the data, it can be observed that the parents selected on the basis of characters like days to 50% flowering, sepal thickness, total number of capsules plant^{-1}, % bud fly infestation, plant height and seed yield plant^{-1} is expected to be genetically diverse.

Average intra and inter cluster distance among ten characters were worked out by Tocher's method and are presented in Table 7. Data shows that inter-cluster distance in most of the cases was higher than the intra-cluster distance. The intra cluster distance range from 0.00 to 11.68. Cluster III possessed highest intra cluster distance (D^2 = 11.68) followed by cluster II (D^2 = 10.53) and cluster I (D^2 = 10.11). The average inter-cluster distance was maximum between cluster IV and VI (D^2 = 51.96), followed by cluster I and cluster VI (D^2 = 42.56), cluster V and cluster VI (D^2 = 40.41), cluster III and cluster IV (D^2 = 37.69), cluster VI and cluster VII (D^2 = 33.02) and cluster VI and cluster VIII (D^2 = 32.68) suggesting more variability in genetic makeup of genotypes included in these clusters. The inter-cluster distance was found minimum between cluster I and cluster V (D^2 = 11.87). From the data it can be observed that the average intra-cluster distance was maximum in cluster III, cluster II, and cluster I and the average inter-cluster distance was maximum between cluster IV and cluster VI and also in between cluster I and cluster VI. Widely diverged clusters remain distinct in different environments. Therefore, the genotypes belonging to the distant clusters may be used in hybridization programme for obtaining a wide spectrum of variation among the segregates.

The cluster means for all ten characters are presented in Table 8 and discussed below. The comparison of cluster means for ten characters' understudy marked considerable genetic differences between groups. The highest cluster mean for days to 50% flowering was recorded by cluster VIII (71.67) and cluster I (59.37) while cluster V (48.00) followed by cluster VII (55.50) represented the lowest mean for days to 50% flowering. Highest cluster means for days to 80% maturity was recorded by cluster VII (97.67) followed by cluster VI (96.44) while cluster VIII (84.00) followed cluster V (86.33) represented the lowest mean for days to 80% maturity. Highest cluster means for days to 100% maturity was recorded by cluster VIII (115.67) followed by cluster VI (111.33) while cluster V (97.67) followed cluster IV (105.89) represented the lowest mean for days to 100% maturity. Highest cluster means for sepal thickness was recorded by cluster VIII (2.85) followed by cluster V (2.44) while cluster VII (0.45) followed cluster IV (0.74) represented the lowest mean for sepal thickness. Highest cluster means for total number of capsules plant^{-1} were estimated by cluster VII (46.73) followed by cluster III (36.86) and minimum cluster mean were estimated by cluster V (26.33) followed by cluster VIII (29.67). Highest cluster means for % bud fly infestation were estimated by cluster VII (55.17) followed by cluster IV (36.28) and minimum cluster mean were estimated by cluster VIII (0.00) followed by cluster V (5.69). The highest cluster mean for plant height was recorded by cluster III (53.72) followed by cluster II (52.24) while cluster VIII (48.27) followed by cluster IV (49.13) represented the lowest mean for

plant height. For the number of branches plant^{-1} highest cluster means were estimated by cluster V (7.20) followed by cluster VIII (6.27) and minimum cluster mean were estimated by cluster VI (4.93) followed by cluster II (5.13). For seed yield plant^{-1} highest cluster mean was estimated by cluster VIII (2.39) followed by cluster V (2.11) and minimum cluster mean was estimated by cluster VII (1.52) followed by cluster II (1.58). For 1000 seed weight highest cluster mean was estimated by cluster VI (10.14) followed by cluster III (8.23) and the minimum cluster mean estimated by cluster IV (3.92) followed by cluster V (5.35). Over all study for cluster means considering all the characters indicated that cluster VIII possessed the highest cluster mean for days to 50% flowering, days to 100% maturity, sepal thickness, number of branches plant^{-1}, seed yield plant^{-1}.

In the present study all possible combinations beyond the mean statistical distance ($\overline{D} = 10.63$) formed from different clusters have been arranged in descending order of magnitude of genetic distance and promising ten cluster combinations have been presented in Table 9. Other practical consideration like the % bud fly infestation, seed yield plant^{-1}, number of capsules plant^{-1} etc. should be taken into account while choosing the genotypes as parents.

SSR marker for polymorphism in linseed

Molecular marker-based diversity analysis for identification of genetically diverse parents and using them in breeding programme could augment linseed improvement. There are only a few reports of identification and use of molecular markers in linseed breeding programs (Soto Cerda *et al*. 2011, Wu *et al*. 2017; Choudhary *et al*. 2017b). SSR markers have been widely used for genetic analysis because of their abundance, co-dominance inheritance, high polymorphism, reproducibility and ease of assay by PCR (Pali *et al*., 2015).

The present study related to SSR marker polymorphism was conducted at Nuclear Agricultural and Biotechnology Division at BARC, Mumbai. The details of material used and methods adopted during course of investigation were described as under. 47 germplasms were taken for further study which are representative samples for bud fly reaction which included 22 resistant (R), 22 moderately susceptible (MS) and 3 susceptible (S). Total genomic DNA was extracted from young seedlings using the method described by Dellaporta. The quality of DNA was checked by nanodrop spectrophotometer.

DNA was isolated from 47 germplasms. Concentration of DNA was estimated using DNA Nanodrop Technology. To check the purity, absorbance ratio (A_{260}/ A_{280}) was calculated. DNA concentration varied from 75.9 ng/µl to 682.7 ng/µl and DNA purity ranged from 1.90 to 2.63.

Polymorphic Information Content (PIC)

The polymorphic information content (PIC) value of sixteen SSR loci were calculated across 47 germplasms and are presented in Table 10. Fourteen markers showed polymorphism. The PIC values calculated for these fourteen polymorphic primers were in the range of 0.05 (Lu-2840) to 0.74 (Lu-2332). The highest PIC value was found in one primer Lu 2332 (0.74) followed by Lu 2633 (0.69). Similar work was also conducted by Fayyaz *et al*. (2014) where twelve SSR primer combinations generated a total of thirty three alleles, of that thirty two were polymorphic loci, whereas only one was monomorphic locus.

Assessment of genetic diversity on the basis of SSR markers

Distance-based cluster analysis was performed and dendrogram was constructed using DARwin software (Dissimilarity Analysis and representation for windows). Neighbour Joining Tree Analysis distributed 47 germplasms into 10 clades. (Fig. 2)

Results suggested that, there were 10 clades. First clade consisted of 7 germplasms *viz.,* IC0498538, IC0499071, IC0498892, EC0041755, IC296039, IC0356192, IC0526166 from which 4 germplasms were moderately susceptible and 3 germplasms were resistant. Second clade consisted of 4 germplasms *viz.,* IC0096678, Neelum, EC0011748, EC0000564 from which 1 germplasm was resistant, 1 germplasm was susceptible and 2 germplasms were moderately susceptible. Third clade consisted of 4 germplasms *viz.,* IC0356165, IC633096, IC96742, IC0498605 from which 3 germplasms were moderately susceptible and 1 germplasm was resistant. Fourth clade consisted of 1 germplasm IC0118861 which was moderately susceptible. Fifth clade consisted of 4 germplasms *viz.,* IC0342801, IC0498786, IC0498844, IC0499191 from which 2 germplasms were resistant, 1 germplasm was susceptible and 1 germplasm was moderately susceptible. Sixth clade consisted of 4 germplasms *viz.,* IC0385383, IC0498382, IC0525919, IC0499014 from which 2 germplasms were moderately susceptible and 2 germplasms were resistant. Seventh clade consisted of 12 germplasms *viz.,* IC0498660, IC0498517, IC0208456, IC0385380, IC0259404, IC0499183, IC0499156, Neela, IC0346107, IC0118891, IC0498427, IC0498992 from which 7 germplasms were moderately susceptible and 5 germplasms were resistant. Eighth clade consisted of 3 germplasms *viz.,*

IC0498570, EC99001, IC0499165 in which all 3 germplasms were resistant. Ninth clade consisted of 4 germplasms *viz.,* IC0498449, IC0510931, IC0498434, IC424872 from which 1 germplasm was resistant, 1 germplasm was susceptible and 2 germplasm were moderately susceptible and tenth clade consisted of 4 germplasms *viz.,* IC0342805, IC0498795, EC0001476, EC993391 from which 1 germplasm was moderately susceptible and 3 germplasms were resistant.

Thus, there was no clear-cut distribution between bud fly resistant and susceptible germplasms. Thus, the markers were not linked to the trait of interest. Since, no literature is available on marker in linseed on bud fly resistance and genome sequencing of linseed is not published. Hence, further studies need to be undertaken to identify markers linked to bud fly resistance.

Conclusion

Significant differences were observed for 47 genotypes. The characters like days to 50% flowering, sepal thickness, total number of capsules plant^{-1}, % bud fly infestation, plant height and seed yield plant^{-1} were identified to contribute maximum towards genetic divergence from canonical analysis studied, cluster means to estimate, and contribution of individual characters to divergence. Fourty seven genotypes were grouped into eight clusters. Ten inter-cluster combinations were identified for selecting promising diverse genotypes to be included in the crossing program to get potential transgrates. Four genotypes *viz*., IC633096, Neela, EC99001, IC0499165 were used as a varietal development and germplasms IC0498472, IC0498660, IC993391, Neelum identified as potential and diverse parents for their use in crossing program.

Table 1 : List of 47 germplasms

Sr. No.	Label No.	Germplasms	Bud fly reaction
1	1485	IC0510931	S
2	1337	IC0498427	MS
3	1303	IC0385380	MS
4	483	IC0498538	MS
5	1075	EC0001476	MS
6	2439	IC0498786	MS
7	1246	IC0499183	MS
8	515	IC0498449	MS
9	1657	EC0011748	MS
10	1224	IC0118861	MS
11	1561	IC0499156	MS
12	999	IC0346107	MS
13	1309	IC0208456	MS
14	1764	IC0096678	R
15	666	IC0118891	R
16	103	IC0525919	R
17	492	IC0342801	R
18	487	IC0498660	R
19	493	IC0342805	R
20	Neela	Neela	R
21	507	IC0498517	R
22	945	IC0498844	R
23	122	IC0498992	R
24	1060	IC0499191	S
25	Neelum	Neelum	S
26	1326	IC0499014	MS
27	659	IC0498434	MS
28	1563	EC0041755	MS
29	1304	IC0356192	MS
30	2159	EC0000564	MS
31	1707	IC0356165	MS
32	1772	IC96742	MS
33	1227	IC0259404	MS
34	1123	IC0498605	MS
35	1300	IC0385383	MS
36	2610	EC993391	R
37	2612	IC633096	R
38	2657	EC99001	R
39	1324	IC0498795	R
40	1070	IC0499071	R
41	71	IC0499165	R
42	605	IC424872	R
43	901	IC0526166	R
44	76	IC0498892	R
45	1335	IC0498382	R
46	637	IC0498570	R
47	1422	IC296039	R

S = susceptible, MS= moderately susceptible, R= resistant

Table 2: Analysis of dispersion

Source of variations	df	Sum of squares	Mean squares
Varieties	46	1.4531E14	3.1590E12
Error	91	4.2992E03	4.7244E01
Total	137	1.4531E14	1.0607E12

Table 3: Contribution of different characters towards divergence

Sr. No.	Characters	Time ranked 1st	Per cent Contribution
1.	Days to 50% flowering	42	3.89%
2.	Days to 80% maturity	3	0.28%
3.	Days to 100% maturity	4	0.37%
4.	Sepal thickness	4	0.37%
5.	Total number of capsule plant^{-1}	14	1.30%
6.	% Bud fly infestation	267	24.70%

7.	Plant height	3	0.28%
8.	No. of branches plant^{-1}	4	0.37%
9.	Seed yield plant^{-1}	1	0.09%
10.	1000 seed weight	739	68.36%
	Total	1081	
	Tochers cut-off value	127.89	

Table 4: Grouping of genotypes into different clusters

Cluster	Number of genotypes	Name of the genotypes
I	20	IC0385380, IC0498449, IC0118861, IC0356165, EC993391, IC0498786, IC0499156, IC96742, IC0498434, IC0499191, IC0118891, IC0498382, IC0342805, IC0498992, EC0041755, IC0498892, IC0498844, IC0526166, IC0498570, IC424872
II	9	IC0342801, IC296039, IC0499165, IC0499071, IC0499183, IC0498605, IC0208456, EC0000564, IC0346107
III	8	IC0096678, IC0498517, IC0525919, Neela, IC633096, IC0498538, EC0011748, IC0385383
IV	3	IC0498427, IC0356192, IC0510931
V	1	IC0498795
VI	3	EC0001476, IC0259404, IC0498660
VII	2	Neelum, IC0499014
VIII	1	EC99001

Table 5: Three canonical roots and their contribution expressed as per cent of the total variation

Root	Eigen value	Contribution in per cent
λ1	8801.75488	77.11
λ2	1899.60718	16.64
λ3	324.91251	2.84
Total	11026.2746	96.59
Sum of all canonical roots	100	
Residual	3.41	

Table 6: Values of first four vectors

	Characters	Vector I	Vector II	Vector III
1	Days to 50% flowering	0.03328	0.02135	0.93359
2	Days to 80% maturity	-0.02241	-0.02126	0.16728
3	Days to 100% maturity	-0.00846	-0.04007	0.20458
4	Sepal thickness	-0.02896	0.32396	0.16903
5	Number of capsules plant^{-1}	0.00115	0.00449	0.05884
6	% Bud fly infestation	0.06107	-0.94179	0.07024
7	Plant height (cm)	-0.01501	0.01632	0.05546
8	Number of branches plant^{-1}	0.02321	-0.01455	-0.00687
9	Seed yield plant^{-1} (g)	-0.00118	0.02638	0.13383
10	1000 seed weight (g)	-0.99649	-0.06621	0.02399

Table 7: Average intra and inter cluster distance D^2 values in linseed

Cluster	I	II	III	IV	V	VI	VII	VIII
I	**10.11**	16.42	27.86	15.49	11.87	42.56	23.01	19.20
II		**10.53**	16.71	25.23	15.54	29.97	17.93	15.24
III			**11.68**	37.69	25.37	18.78	23.87	19.13
IV				**10.01**	21.02	51.96	25.12	30.03
V					**0.00**	40.41	26.52	16.09
VI						**9.82**	33.02	32.68
VII							**6.64**	28.08
VIII								**0.00**

$\overline{D}$ **= 10.63**

Table 8: Cluster means for ten characters

Cluster	Days to 50% flowering	Days to 80% maturity	Days to 100% maturity	Sepal thickness	Total capsules plant^{-1}	Bud fly infestation%	Plant height (cm)	No. of Branches plant^{-1}	Seed yield plant^{-1} (g)	1000 seed weight (g)
1	59.37	90.57	106.52	1.17	34.74	17.57	51.11	6.14	1.70	5.10
2	57.44	93.48	108.52	1.34	32.92	20.32	52.24	5.13	1.58	6.66
3	56.96	90.92	107.71	1.46	36.86	15.16	53.72	5.43	2.09	8.23
4	58.67	89.33	105.89	0.74	36.09	36.28	49.13	5.49	1.64	3.92
5	48.00	86.33	97.67	2.44	26.33	5.69	51.87	7.20	2.11	5.35
6	56.22	96.44	111.33	1.05	30.94	21.35	50.73	4.93	1.70	10.14
7	55.50	97.67	111.00	0.45	46.73	55.17	51.73	5.43	1.52	6.68
8	71.67	84.00	115.67	2.85	29.67	0.00	48.27	6.27	2.39	6.69
SD	**8.49**	**19.56**	**18.53**	**1.09**	**33.02**	**9.27**	**17.13**	**4.19**	**2.26**	**0.52**
Variance	**72.08**	**382.59**	**358.34**	**1.18**	**1090.32**	**85.93**	**293.43**	**17.55**	**5.10**	**0.27**

Table 9 : Selection of genotypes based on inter cluster distances and cluster means

Clusters	Distance between clusters	Varietal development	Selection based on seed yield plant^{-1} and % bud fly infestation
IV & VI	51.96		IC0498472 × EC0001476 IC0498660 × IC0498427
I & VI	42.56		EC993391 × EC0001476 IC0118891 × EC0001476 IC0498892 × EC0001476 IC0498660 × EC993391
V & VI	40.41		IC0498795 × EC0001476
III & IV	37.69	IC633096, Neela	
VI & VII	33.02		IC0498660 × Neelum IC0498660 × IC0499014
VI & VIII	32.68		EC99001 × EC0001476 IC0498660 × EC99001
IV & VIII	30.03	EC99001	
II & VI	29.97	IC0499165	
VII & VIII	28.08		EC99001 × IC0499014
I & III	27.86		IC633096 × EC993391 IC0498892 × Neela

Table 10 : Details of Informative markers based on PIC

Sr. No.	Marker	No. of alleles amplified	PIC
1.	Lu-2840	2	0.05
2.	Lu-2332	6	0.74
3.	Lu-2235	2	0.49
4.	Lu-2850	4	0.16
5.	Lu-3280	3	0.29
6.	Lu-2725	4	0.51
7.	Lu-2149	3	0.34
8.	Lu-2992	3	0.55
9.	Lu-2509	4	0.47
10.	Lu-869	2	0.37
11.	Lu-2633	6	0.69
12.	Lu-2968	3	0.38
13.	Lu-3205	1	0.0
14.	Lu-2693	1	0.0
15.	Lu-2420	3	0.29
16.	Lu-3212	4	0.29

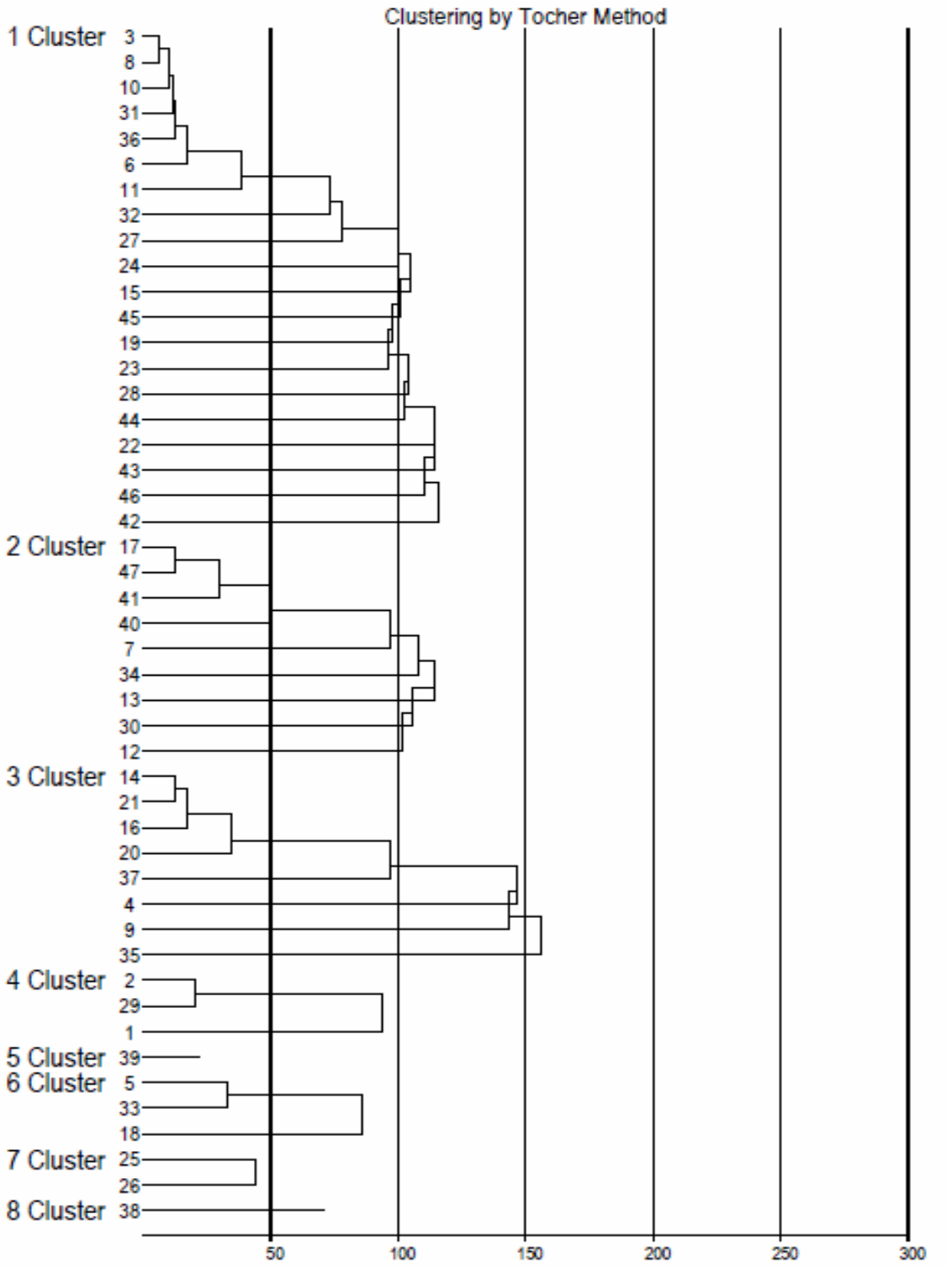

Fig. 1 : Dendrogram showing clustering of 198 germplasms by Tocher's method

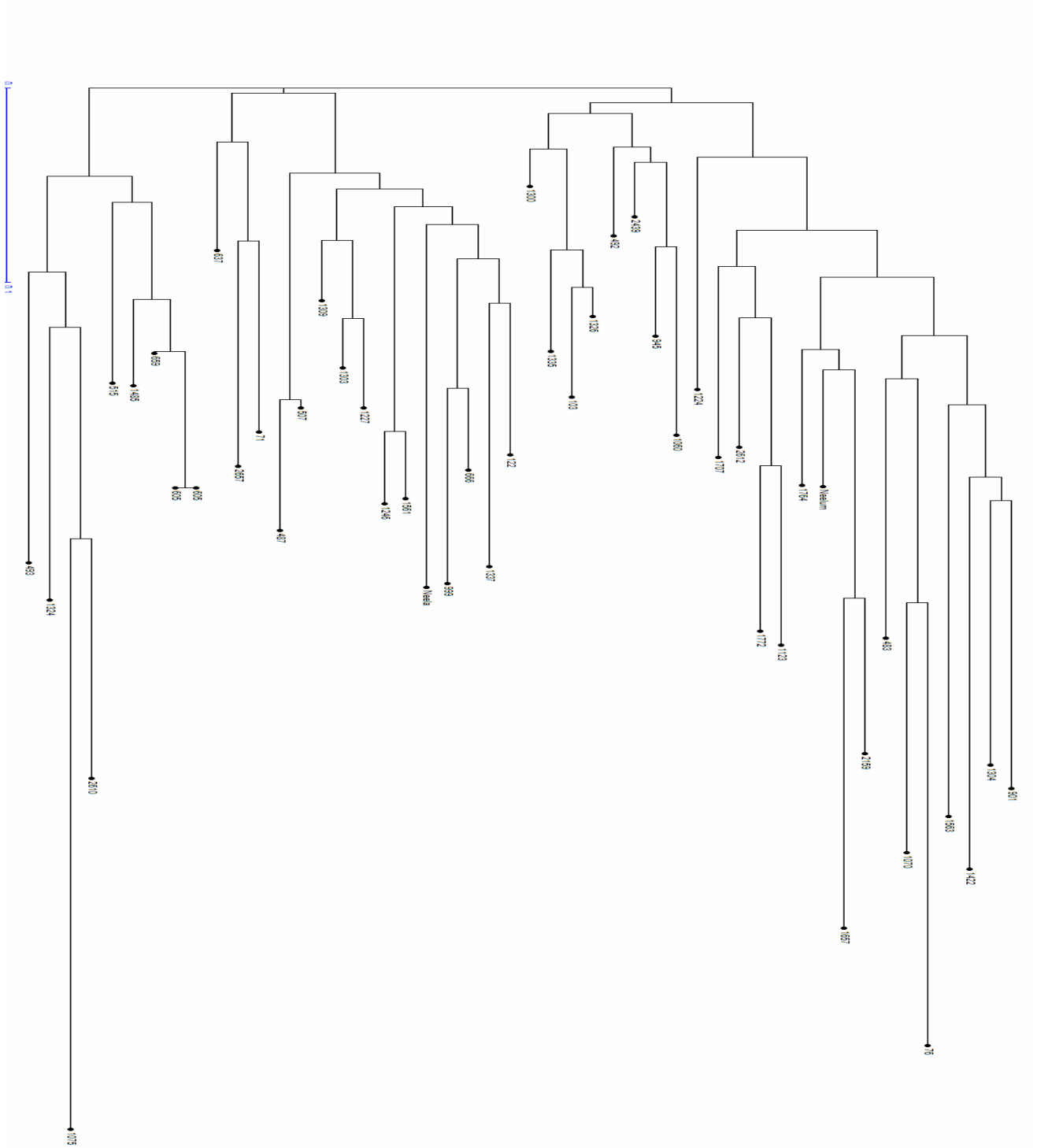

Fig. 2 : Linseed Neighbour Joining Tree of 47 germplasms

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