

ASSESSMENT OF GENETIC DIVERSITY AMONG OAT (*AVENA SATIVA* L.) GERMPLASM ACCESSIONS

RASHMI TOPPO¹, MAYURI SAHU^{2*}, ANJALI KAK³ AND NEHA BELSARIYA⁴

^{1,2&4}Department of Genetics and Plant Breeding, COA, IGKV, Raipur-492012 (Chhattisgarh) India

³Division of Germplasm Conservation, National Bureau of Plant Genetic Resources

*(e-mail : mayuri_pbg@rediffmail.com)

(Received : 19 May 2022; Accepted : 12 June 2022)

SUMMARY

Genetic divergence was studied for 130 Oat germplasm accession including 5 checks (JHO-851, RO-19, JHO-822, UPO-212, JO-1). Experiment was conducted in augmented design in Rabi 2019-20. All the 130 germplasm accessions were grouped into 12 clusters. Cluster I comprised by highest number of genotype followed by cluster III, cluster V, cluster X, and cluster VI. Seven cluster II, IV, VII, VIII, IX, XI, XII had lowest number of genotype. Wide range of intra cluster distance obtained. Highest intra cluster distance obtained by cluster VI represent the high genetic diversity among the genotypes. The highest inter cluster distance found between Cluster X and XI. Highest genetic divergence contributed by 1000 seed weight, green fodder yield and seed yield per plant.

Key words : Genetic divergence, intra cluster distance, inter cluster distance, genetic diversity

Oat (*Avena sativa* L.) is dual purpose crop usually grown as grain as well as forage purpose. Crop Oat is hexaploid having chromosome number ($2n = 42$) belongs to family Poaceae. As a best dualpurpose crop Oat gives good forage yield after first cutting and grain can be obtained by its subsequent growth period. Oats are recognized as the world's most significant cereal crop and are a major source of necessary nutrients for human consumption (Boczkowska and Tarczyk 2013). Oat consumption is frequently increased due to nutritional benefits such as antioxidants and high soluble fibre content. Oats contain antioxidants such as avenanthramides, alpha-tocopherol, and alpha-tocotrienol, as well as total dietary fibre and beta- glucan (Oliver *et al.*, 2010). The total area covered under oat cultivation in world is 27 mha and production is 40 mt (FAOSTAT2019). The total area covered under oat cultivation in the country is about 5,00,000 ha. (Anonymous 2012). Average yield varies from 45 to 55 tons of green fodder and 200-400 kg grain per hectare. Green fodder production is important for animals to provide balanced nutrition (Anonymous 2002; Phogat *et al.*, 2021). The purpose of this study was to analyse the genetic diversity of the Oat. This study's findings will aid in describing Oat germplasm, as well as the selection and use of varied genotypes to improve the variability and productivity of commercial oats for further crop improvement.

MATERIALS AND METHODS

Experiment was conducted in Rabi 2019-20 in Research Cum Farm Instructional, Department of Genetics and Plant Breeding, IGKV, Raipur (C.G.). Total 130 germplasm accessions including 5 checks (JHO-851, RO-19, JHO-822, UPO-212, JO-1) were evaluated in augmented design. The whole experimental field was divided into 5 blocks with 30 germplasm line in each block. Each check is replicated at every block and other 125 germplasm were grown in a single row. The study materials used are given in (Table 1). According to descriptor 'Indian grassland and Fodder Research Institute, Jhansi, India.' (Roy *et al.*, 2017) 19 quantitative traits were evaluated to assess genetic diversity.

RESULTS AND DISCUSSION

Genetic divergence can be described as the degree of differentiation between or within the species. Intra and inter specific differences are the base for any crop improvement programmes. Genetically divergent parents are important to get wide array of recombination for any hybridization programme. The knowledge of genetic diversity among the accession is necessary for crop improvement (Choudhary *et al.*, 2015).

Cluster analysis was conducted on the basis

of values of D^2 by using Tocher method. All the 130 germplasm accessions were grouped into 12 clusters (Table 2). Cluster I comprised by 66 genotypes followed by cluster III (33), cluster V (14), cluster X (9), and cluster VI (4). Seven cluster II, IV, VII, VIII, IX, XI, XII had 1 genotype indicating the high genetic divergence present between these clusters and this is by the impact of selection and isolation which prevent the gene flow and natural or human selection. Highest number of genotype in cluster I was also reported by (Yadav *et al.*, 2011; Krishna *et al.*, 2014; Jaipal and Shekhawat 2016). Clustering pattern of genotypes revealed that there is ample amount of genetic divergence present among themselves. Genotypes belongs to the same sources were clustered into different groups indicating changes in the different characters under selection. Genetic drift, selection pressure and environment could be the cause of this changes which leads to high genetic diversity instead of genetic distance (Marsan *et al.*, 1998; Senior *et al.*, 1998; Wende *et al.*, 2013).

Intra and inter cluster values were presented in (Table 3). Intra cluster distance ranges from 0 to 1506.42. This wide range of values indicates the ample of diversity present. Highest intra cluster distance obtained by cluster VI contains 4 genotypes represent the high genetic diversity among the genotypes. It is followed by cluster X having 9 genotypes, cluster III having 30 genotypes and cluster V having 14 genotypes. These clusters had high genetic divergence.

The inter cluster distance varied from 429.41 to 23009.13. The result of this analysis indicated the presence of commendable amount of genetic divergence in the study material. The highest inter cluster distance found between Cluster X and XI have relatively higher mean for the trait plant height, leaf width, number of nodes on the main culm, peduncle length, green fodder yield, dry matter yield, leaf dry weight per plant, stem dry weight per plant and days to maturity. So, selection can be done based on these characters. Genotypes which fell under cluster X and XI i.e. (GP-30, GP-17, GP-12, GP-21, EC/246146, JHO-851, IC/014555, EC/209215, EC/0107524 and EC/097519) will also show high genetic diversity. Lowest inter cluster distance was observed between cluster II and IX therefore genotypes (EC/097520, EC/097532) which belongs to these clusters were less diverse. From the study it was observed that values of inter cluster distance is higher than the intra cluster distance which indicates that high genetic divergence found between the genotypes.

Cluster means of different genotypes

represented the genetic difference between the clusters. Cluster means for different characters are given in (Table 4). Cluster VII had highest cluster mean for seed yield per plant and 1000 seed weight whereas culm diameter and days to maturity had lowest indicated genotypes with early maturity were high grain yielder. Similarly, cluster X had highest cluster mean for days to maturity and lowest cluster mean for green fodder yield, leaf dry weight per plant, seed yield per plant and 1000 seed weight indicating late maturity genotypes had decreased green fodder yield and seed yield. Highest cluster mean for plant height, flag leaf length, flag leaf width, number of nodes on the main culm, peduncle length and lowest cluster mean for days to 50% flowering were recorded in cluster VI. Highest cluster mean for plant height in cluster VI was also reported by (Yadav *et al.* 2011).

As peduncle length is associated with high seed yield it can be affected by days to 50% flowering. Cluster IX reported highest cluster for number of leaves per plant, number of tiller per plant and leaf: stem ratio whereas lowest for plant height, peduncle length, dry matter yield per plant and stem dry weight per plant indicated leaf: stem ratio will increase by decreasing the stem dry weight. It also represented that dry matter yield will decrease if stem dry weight will decrease which convey that the yield of both these traits were associated. Highest cluster mean for green fodder yield, dry matter yield per plant, leaf dry weight per plant and stem dry weight per plant were observed in cluster XI whereas this cluster observed lowest cluster mean for number of leaves per plant, number of nodes on the main culm and number of tiller per plant. Lowest cluster mean for flag leaf length was recorded in cluster XII whereas days to 50 % flowering and culm diameter had lowest.

Percent contribution by different traits toward divergence were the major deciding factor for selection of particular trait for use in hybridization programme. Different traits contributing towards divergence is given in (Table 5). Trait 1000 seed weight contributed largest (16.62%) towards genetic divergence followed by green fodder yield (14%) and seed yield (12%). Leaf dry weight per plant followed by days to maturity and flag leaf length. This is similar with the findings of (Kumarmall and Vishwakarma 2006; Ahemadet al. 2011; Singh and Singh 2011) who also reported highest contribution by trait green fodder yield and seed yield per plant.

Principal component analysis (PCA) demonstrated genetic distance and relatedness between the genotypes in population. Similarity between the variables can be identify by principal

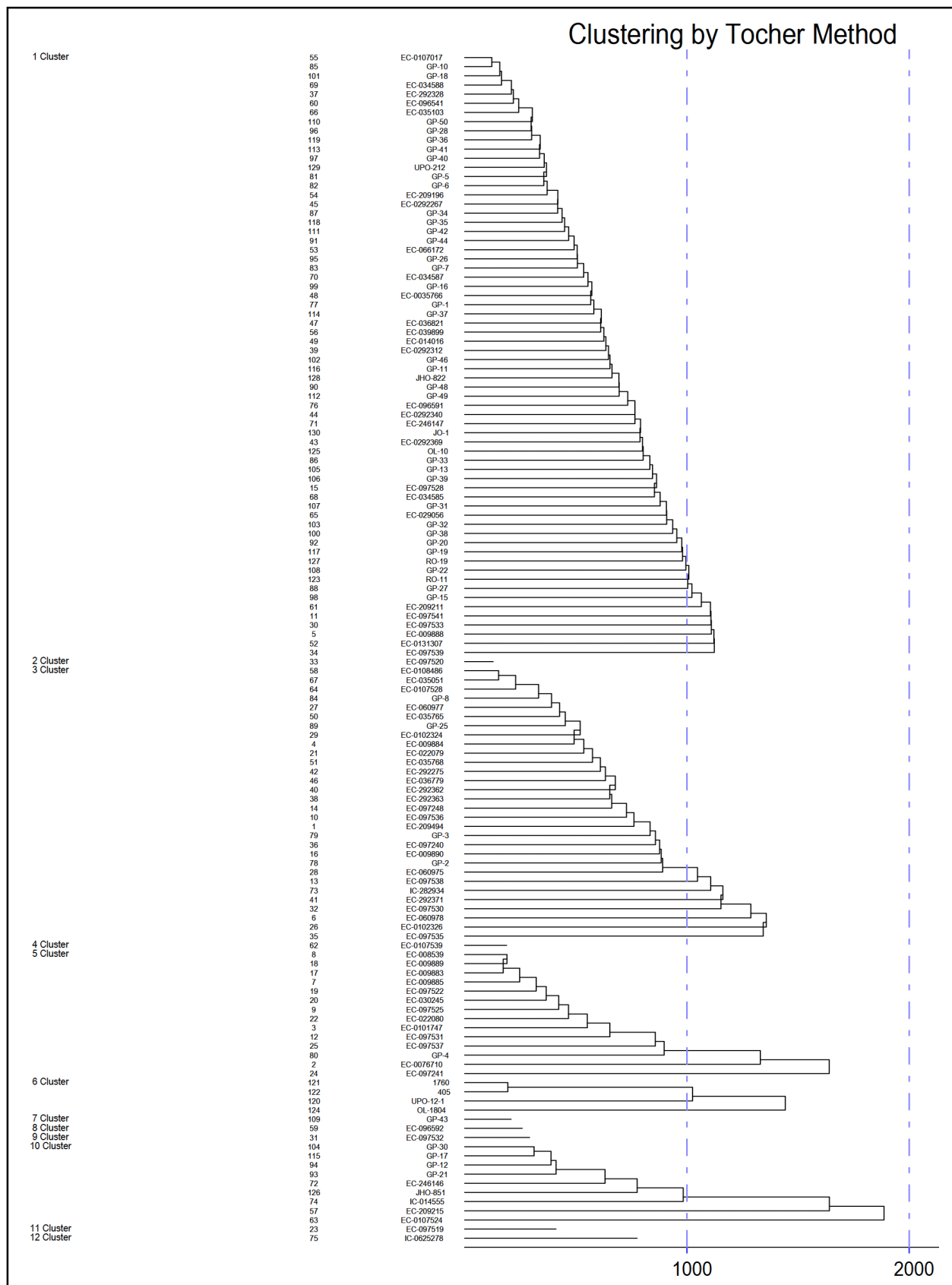


Fig. 1. Dendrogram showing genotypes falling under different clusters.

TABLE 1
Clustering pattern of different accessions of Oat (*Avena sativa* L.)

Cluster No.	No. of genotypes	% of total genotype	Name of genotype
I	66	50.77	EC/0107017, GP-10, GP-18, EC/034588, EC/292328, EC/096541, EC/035103, GP-50, GP-28, GP-36, GP-41, GP-40, UPO-212, GP-5, GP-6, EC/209196, EC/0292267, GP-34, GP-35, GP-42, GP-44, EC/066172, GP-26, GP-7, EC/034587, GP-16, EC/0035766, GP-1, GP-37, EC/036821, EC/039899, EC/014016, EC/0292312, GP-46, GP-11, JHO-822, GP-48, GP-49, EC/096591, EC/0292340, EC/246147, JO-1, EC/0292369, OL-10, GP-33, GP-13, GP-39, EC/097528, EC/034585, GP-31, EC/029056, GP-32, GP-38, GP-20, GP-19, RO-19, GP-22, RO-11, GP-27, GP-15, EC/209211, EC/097541, EC/097533, EC/009888, EC/0131307, EC/097539
II	1	0.77	EC/097520
III	30	23.08	EC/0108486, EC/035051, EC/0107528, GP-8, EC/06097, EC/035765, GP-25, EC/0102324, EC/009884, EC/022079, EC/035768, EC/292275, EC/036779, EC/292362, EC/292363, EC/097248, EC/097536, EC/209494, GP-3, EC/097240, EC/009890, GP-2, EC/060975, EC/097538, IC/282934, EC/292371, EC/097530, EC/060978, EC/0102326, EC/097535
IV	1	0.77	EC/0107539
V	14	10.77	EC/008539, EC/009889, EC/009883, EC/009885, EC/097522, EC/030245, EC/097525, EC/022080, EC/0101747, EC/097531, EC/097537, GP-4, EC/0076710, EC/097241
VI	4	3.08	1760, 405, UPO-12-1, OL-1804
VII	1	0.77	GP-43
VIII	1	0.77	EC/096592
IX	1	0.77	EC/097532
X	9	6.92	GP-30, GP-17, GP-12, GP-21, EC/246146, JHO-851, IC/014555, EC/209215, EC/0107524
XI	1	0.77	EC/097519
XII	1	0.77	IC/0625278

component analysis (Venujayakanth *et al.*, 2017). Principal component analysis divided total variability into 6 PCs presented in (Table 6). All the 6 PCs contributed 65.60 % of total variability present in germplasm accessions. First principal component (17.19%) contributed most towards total variability which is followed by subsequent principal components i.e. PC II (13.89%), PC III (12.39%), PC IV (8.68%), PC V (6.94%) and PC VI (6.51%). First 4 PCs contributed 52.16% of total variability. In PC I trait green fodder yield contributed most heavily towards negative loading (-0.43571), followed by leaf dry weight per plant (-0.42560) and dry matter yield (-0.37168) whereas number of tiller per plant (0.33005) and number of leaves per plant (0.27582) showed high contribution towards positive loading. The trait days to 50% flowering (-0.35897) contributed most towards negative loading in PC II followed by leaf: stem ratio (-0.30870), days to maturity (-0.25790) and leaf width (-0.23773) whereas stem dry weight per plant (0.44969) contributed heavily toward positive loading followed by dry matter yield (0.38182) and seed yield per plant (0.30526).

In PC III number of leaves per plant (-0.24262) contributed most heavily towards negative loading whereas leaf length (0.45111), plant height (0.39867), flag leaf length (0.39111) and culm diameter (0.35478) contributed towards positive loading. In PC IV high negative loading showed towards leaf: stem ratio (-0.27682) and number of nodes on the main culm (-0.25152) whereas number of leaves per plant (0.44398), number of tiller per plant (0.42070) and days to maturity (0.30450) contributed most towards positive loading. In PCA analysis days to 50% flowering, number of leaves per plant, flag leaf width, no. of tiller per plant, dry matter yield per plant, leaf dry weight per plant and leaf: stem ratio contributed most heavily towards total variability.

The 3-D biplot of PCA I score and PCA II score (Fig. 3) showed that the genotypes falling in the same cluster are closer to each other. The clusters only had single genotype showed distant between the genotypes present in these clusters and had a desirable mean value for traits i.e. GP-43 (high seed yield and low maturity duration), EC/097532 (low plant height and peduncle length), EC/097519 (high green fodder

TABLE 2
Distance between different centriole (intra and inter cluster distance) of different genotypes of Oats (*Avena sativa* L.)

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	834.01										
II	1177.38	0									
III	2355.20	1104.19	972.27								
IV	1332.28	725.57	1535.59	0							
V	7364.43	4942.37	2834.89	5596.67	925.05						
VI	1596.41	2660.01	3190.99	2421.89	7701.12	1506.42					
VII	1311.88	1907.41	4259.75	2136.30	11341.12	3033.02	0				
VIII	1251.84	1721.59	4155.23	1710.81	11285.17	2700.98	523.37	0			
IX	1196.91	429.41	2120.71	786.98	7196.66	2932.41	1372.74	802.77	0		
X	1764.03	2271.02	4707.68	2349.33	11871.73	3062.69	1024.76	743.29	1548.97	1331.27	
XI	16192.89	12878.85	8557.65	13265.84	2644.84	15852.71	22136.30	22382.06	16429.80	23009.13	0
XII	2504.86	1438.70	1566.96	957.30	4205.59	2799.35	4583.61	3611.58	1865.39	4060.47	10651.32

TABLE 3
Cluster means of different characters

	DT 50% F	PH	NOL	FLL	FLW	LL	LW	CD	NON	NOT	PL	GFY	DMY	LDW	SDW	L: S	DTM	SY	1000 SW
Cluster 1	72.26	112.24	28.68	30.67	1.92	46.89	1.78	6.14	4.89	6.20	33.76	78.66	25.11	7.47	17.71	0.43	108.23	20.94	39.14
Cluster 2	77.0	92.42	28.80	31.72	1.98	49.80	2.04	6.19	4.60	6.00	34.20	93.80	21.40	8.40	13.00	0.64	112.00	13.20	38.00
Cluster 3	74.03	101.05	26.24	30.28	1.98	47.16	1.83	6.17	4.81	5.55	33.69	114.74	27.27	8.61	18.53	0.47	109.13	17.09	35.20
Cluster 4	76.00	95.94	38.60	25.84	1.62	39.72	1.84	6.16	5.40	7.20	33.30	89.80	36.40	10.20	26.20	0.39	109.00	12.60	31.00
Cluster 5	73.93	104.00	23.07	29.39	2.03	48.72	1.92	6.22	4.89	4.93	31.41	158.10	31.27	9.96	21.01	0.50	111.00	16.64	34.93
Cluster 6	12.25	132.33	25.25	32.45	2.04	48.92	1.81	6.44	5.75	6.05	36.66	82.05	30.80	10.20	20.50	0.49	108.50	20.65	27.75
Cluster 7	70.00	98.24	24.20	28.30	1.92	41.36	1.84	5.70	5.40	5.60	35.44	56.00	25.00	8.80	14.35	0.61	105.00	23.40	49.00
Cluster 8	72.00	101.24	37.20	29.92	1.82	40.88	1.92	6.16	5.40	6.60	30.58	56.40	19.40	7.20	12.20	0.59	108.00	17.00	34.00
Cluster 9	81.00	92.16	39.40	28.62	1.86	42.84	1.80	5.83	5.60	10.20	29.90	81.00	17.80	7.00	10.80	0.64	109.00	16.20	36.00
Cluster 10	76.78	101.6	31.18	28.07	1.92	46.63	1.80	5.82	5.16	6.62	36.38	55.22	21.67	6.91	14.76	0.49	109.56	19.44	33.33
Cluster 11	70.00	108.54	17.40	28.66	1.96	40.96	2.02	6.45	4.40	3.80	33.48	201.60	41.80	14.20	28.60	0.49	111.00	18.00	35.00
Cluster 12	92.00	104.34	31.40	24.82	1.96	40.20	1.88	6.46	4.60	5.80	30.90	105.00	33.60	11.80	21.80	0.54	116.00	10.80	15.00

DT50%F = Days to 50% flowering
PH (cm) = Plant height
NOL = No. of leaves per plant
FLL (cm) = Flag leaf length
FLW (cm) = Flag leaf width
LL (cm) = Leaf length
LW (cm) = Leaf width
CD (cm) = Culm diameter
NON = No. of node on the main culm
NOT = No. of tiller per plant
PL (cm) = Peduncle length
GFY (g) = Green fodder yield per plant
DMY (g) = Dry matter yield per plant
LDW (g) = Leaf dry weight per plant
SDW (g) = Stem dry weight per plant
L:S = Leaf: stem ratio
DTM = Days to maturity
SY (g) = Seed yield per plant
1000 SW (g) = 1000 seed weight

TABLE 4
Relative contribution of individual traits to the genetic divergence

Source	Contribution (%)	Times ranked first	Cumulative frequency
Days to 50% flowering	0.84	70	0.84
Plant height	3.00	250	3.84
Number of leaves per plant	6.34	528	10.18
Flag leaf length	0.13	11	10.31
Flag leaf width	4.50	375	14.81
Leaf length	2.10	175	16.91
Leaf width	4.00	333	20.91
Culm diameter	6.00	500	26.91
Number of nodes on the main culm	8.00	667	34.91
Number of tiller per plant	5.00	417	39.91
Peduncle length	7.00	583	46.91
Green fodder yield	14.00	1167	60.91
Dry matter yield	2.15	179	63.06
Leaf dry weight per plant	0.01	1	63.07
Stem dry weight per plant	0.19	16	63.26
Leaf: stem ratio	8.00	667	71.26
Days to maturity	0.12	10	71.38
Seed yield	12.00	1000	83.38
1000 seed weight	16.62	1385	100

yield a most desirable character) and IC/0625278 (high days to 50% flowering).

CONCLUSION

Clustering of germplasm accession and estimation of principal component analysis revealed that there is sufficient amount of genetic divergence present among the germplasm accessions which is prerequisite for breeding programme of Oat. Crossing between diverse group leads to creation of genetic variability and exploitation of heterosis (Molin et al. 2013). Germplasm accession namely, GP-30, GP-17, GP-12, GP-21, EC/246146, JHO-851, IC/014555, EC/209215, EC/0107524 and EC/097519 had highest inter cluster distance and can be used in breeding programme. Trait 1000 seed weight, green fodder yield and seed yield per plant contributed highest towards genetic divergence. Germplasm accession GP-43 (high seed yield and low maturity duration), EC/097532 (low plant height and peduncle length), EC/097519 (high

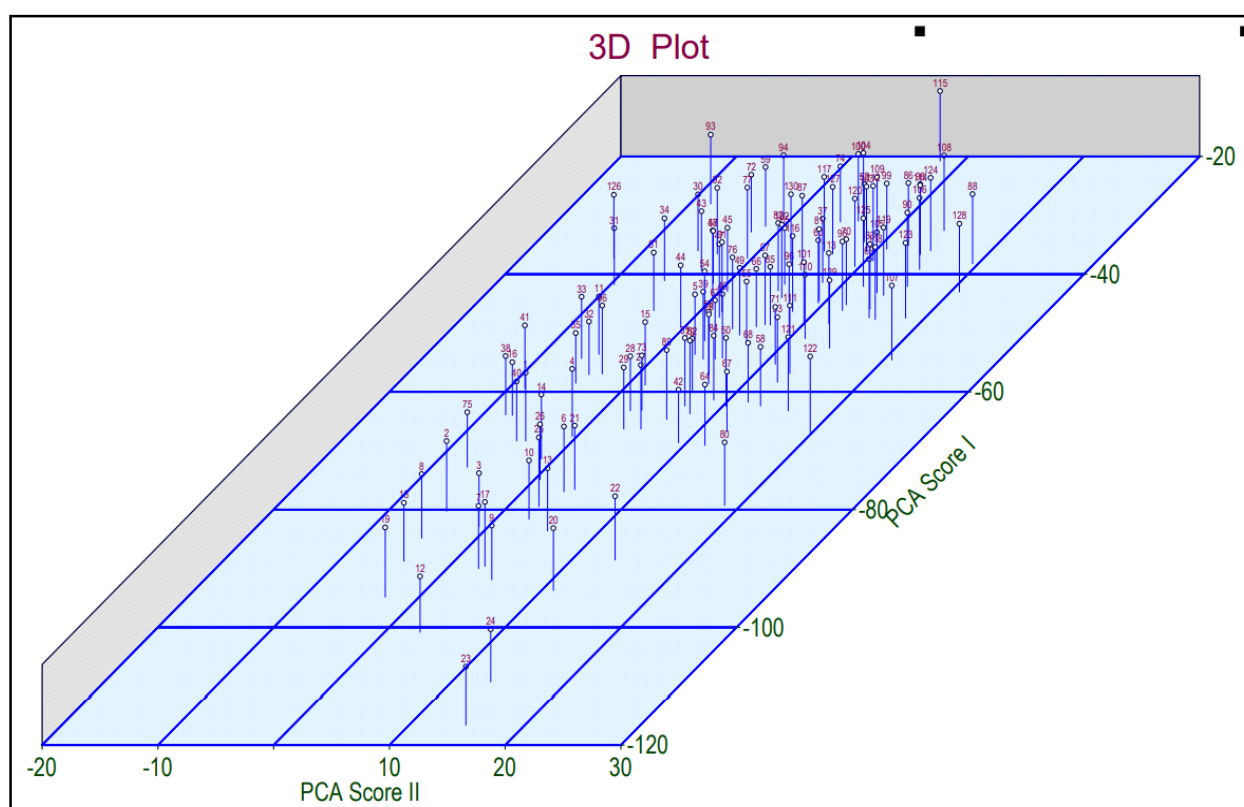


Fig. 2. 3D PCA plot.

TABLE 5
Principal component analysis in Oat (*Avena sativa* L.)

	PC I	PC II	PC III	PC IV	PC V	PC VI
Eigene value (Root)	3.26621	2.63987	2.35432	1.64967	1.31809	1.23655
% Var. Exp.	17.19057	13.89403	12.39117	8.68250	6.93733	6.50815
Cum. Var. Exp.	17.19057	31.08460	43.47577	52.15827	59.09560	65.60375
Days to 50% flowering	-0.09434	-0.35897	0.08422	0.01815	0.44146	-0.24354
Plant height	0.08188	0.24775	0.39867	0.00838	0.18269	0.09493
No. of leaves per plant	0.27582	-0.05646	-0.24262	0.44398	0.31798	0.07490
Flag leaf length	0.10030	0.06762	0.39111	0.19900	-0.03231	0.22161
Flag leaf width	-0.03457	-0.09915	0.31128	0.30700	-0.07636	0.07340
Leaf length	-0.05820	-0.07989	0.45111	-0.06169	0.06259	-0.16405
Leaf width	-0.14556	-0.23773	0.21144	0.27907	-0.10930	-0.03411
Culm diameter	-0.10472	-0.01543	0.35478	0.14824	0.07901	-0.03437
No. of nodes on the main culm	0.01345	0.14767	0.24918	-0.25152	0.42813	0.17600
No. of tiller per plant	0.33005	-0.03415	-0.15705	0.42070	0.25239	0.19896
Peduncle length	0.15715	0.20913	0.07939	-0.16805	0.25079	-0.30422
Green fodder yield	-0.43571	-0.02886	-0.03170	0.17190	-0.21224	-0.00537
Dry matter yield per plant	-0.37168	0.38182	-0.11156	0.15500	0.16867	0.02277
Leaf dry weight per plant	-0.42560	0.12880	-0.09603	-0.03641	0.24162	0.38440
Stem dry weight per plant	-0.28204	0.44969	-0.07390	0.24809	0.09248	-0.18284
Leaf: stem ratio	-0.13691	-0.30870	-0.03263	-0.27682	0.11794	0.60734
Days to maturity	-0.19508	-0.25790	-0.00114	0.30450	0.05439	0.03260
Seed yield per plant	0.24794	0.30526	-0.00885	0.02764	-0.02795	0.24542
1000 seed weight	0.14411	0.20470	0.16982	0.09959	-0.41675	0.25943

green fodder yield a most desirable character) and IC/0625278 (high days to 50% flowering) which belongs to solitary cluster could be used as parent in further hybridization programme of Oat.

ACKNOWLEDGEMENTS

The authors are thankful to Department of Genetics and Plant Breeding, Raipur (C.G.). We are grateful to the Dr. A. K. Sarawgi, Head of the Department of Genetics and Plant Breeding, for his immense support and valuable guidance.

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