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Estimation of Genetic Diversity among Genotypes of Fodder Oat based on Principal Component Analysis

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Abstract

The present investigation was planned to assess genetic diversity for fodder yield and yield contributing traits in fifty oat genotypes including two checks from different geographic regions and were evaluated in randomized block design with three replications at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture JNKVV Jabalpur during *rabi*, 2014. The traits were studied through principal component analysis (PCA). Out of eighteen, ten principal components (PC1 to PC10) exhibited more than 0.5 eigen values and showed about 89.52% total variability among the characters studied. PC1 accounts mostly for yield related traits like penultimate leaf area, panicle weight, axis branch number, spikelets panicle^{-1}, florets panicle^{-1} and grain yield. The combined variation among these traits was 23.342%. PC2 was contributed by both physiological and yield related traits which are days to 50% flowering, days to flower initiation, number of leaves plant^{-1} dry matter yield and grain fodder yield. PC3 include trait i.e. plant height. PC4 includes trait axis length. PC5 include by physiological trait i.e. days to maturity. PC6 include yield trait 1000 seed weight. On the basis of PC score germplasm like HFO-25**,** IC372418, IC372413 and JHO-11 can be used for development of new oat varieties. These information would be very useful to select potentially breeding lines for future oat improvement program.

Keywords: PCA, fodder, oat, dual purpose oat, green fodder yield, genetic diversity

1. Introduction

Oat (*Avena sativa* L.) is one of the most important cereal fodder crops of *rabi* season in North, Central and West Zone of the country. It is widely cultivated for use as food, feed and fodder. They are fast growing and produces significant amount of fresh fodder within short period (60–70 days) with adequate nutritional value (Bilal et al., 2017). In many parts of the world, oat is grown for grain as well as straw for bedding, hay, haylage, silage and chaff. Its grain makes a good feed particularly for horses, sheep and poultry. Oat is one of the most important cereal fodder crop having an excellent growth habit, quick cutting recovery, palatable, succulent and nutritious herbage. In recent years, with the advent of exaggerated dairy industry in our country, oat has fascinated the attention of breeders for its improvement due to its nutritious quality fodder for livestock and its grains as animal feed with high net energy gains (Ruwali et al., 2013). The nutritive value of oat forage is high and dry matter digestibility is in excess of 75% when fed to dairy cattle (Burgess et al., 1972). It provides soft and palatable fodder rich in crude protein (10–12%) and protein content of the hull-less oat kernel (groat) ranges from 12–24%, the highest among cereals (Lasztity, 1999). It also contains 20% dry matter, 10% crude protein, 91% organic matter (DM basis) (Gupta et al., 2004). The chemical composition of green fodder varies with the stage of harvest. Oat produces an abundance of excellent fodder at the time when other succulent better quality fodders are scarce and cannot be cut/grazed as a green feed, hay or silage crop. It forms an excellent combination when fed along with other cold season legumes, like berseem, Lucerne, senji, shaftal, pea and vetch. The total area covered under oat cultivation in the country is about 500 000 ha. The crop occupies a maximum area in Uttar Pradesh (34%), followed by Punjab (20%), Bihar (16%), Haryana (9%) and Madhya Pradesh (6%) (Panday et al., 2011).

2. Materials and Methods

In the present study, fifty germplasm (Table 1) were grown in randomized complete block design. The experiment was carried out at the Seed Breeding Farm, Department of Plant Breeding & Genetics, College of Agriculture JNKVV Jabalpur. The sowing of the experimental material was done on 23rd November 2014. Each plot was maintained of size 3×0.6 m² and having two rows for each treatment in each replication.

Table 1: List of rice genotypes selected for diversity analysis, with their place of origin.

Sl. No.	Germplasm	Source	Sl.No.	Germplasm	Source
1.	IC372442	IGFRI, Jhansi	26.	HFO-2	HAU- Hissar
2.	JHO-3	IGFRI, Jhansi	27.	HFO-3	HAU- Hissar
3.	IC372414	IGFRI, Jhansi	28.	HFO-4	HAU- Hissar
4.	IC372416	IGFRI, Jhansi	29.	HFO-5	HAU- Hissar
5.	IC372438	IGFRI, Jhansi	30.	PI486164	USA
6.	IC372443	IGFRI, Jhansi	31.	PI498912	USA
7.	IC372437	IGFRI, Jhansi	32.	PI486862	USA
8.	IC372452	IGFRI, Jhansi	33.	EC209638	USA
9.	JHO-10	IGFRI, Jhansi	34.	EC209568	USA
10.	JHO-11	IGFRI, Jhansi	35.	EC209341	USA
11.	IC372421	IGFRI, Jhansi	36.	CI9771	USA
12.	IC372445	IGFRI, Jhansi	37.	BGP-33	Brazil
13.	IC372461	IGFRI, Jhansi	38.	BGP-37	Brazil
14.	IC372415	IGFRI, Jhansi	39.	BGP-48	Brazil
15.	IC372425	IGFRI, Jhansi	40.	BGP-4	Brazil
16.	IC372423	IGFRI, Jhansi	41.	BGP13	Brazil
17.	JHO-18	IGFRI, Jhansi	42.	HFO-18	HAU- Hissar
18.	IC372432	IGFRI, Jhansi	43.	HFO-19	HAU- Hissar
19.	IC372422	IGFRI, Jhansi	44.	PA2672	GBPUAT-Pantnagar
20.	IC372413	IGFRI, Jhansi	45.	PA2857	GBPUAT-Pantnagar
21.	IC372418	IGFRI, Jhansi	46.	PA3562	GBPUAT-Pantnagar
22.	IC372428	IGFRI, Jhansi	47.	HFO-24	GBPUAT-Pantnagar
23.	IC372431	IGFRI, Jhansi	48.	HFO-25	GBPUAT-Pantnagar
24.	IC372419	IGFRI, Jhansi	49.	KENT	CHECK
25.	HFO-1	HAU- Hissar	50.	JO-1	CHECK

The row length was kept at 3 m, distance between rows was kept at 30 cm and plant to plant was 5 cm. Five competitive plants were randomly selected and tagged in each plot per replication for recording observation on eight fodder yielding characters, namely, plant height, number of leaves plant^{-1}, penultimate leaf area, tillers meter^{-1} row, internodal length, stem girth, dry matter yield and green fodder yield, and fifteen grain yield contributing characters, namely, days to 50% flowering, days to maturity, plant height, number of leaves plant^{-1}, penultimate leaf area, tillers meter^{-1} row, internodal length, panicle weight, axis length, spikelets panicle^{-1}, florets panicle^{-1}, dry matter yield, 1000 grain weight, green fodder yield and grain yield. However, days to 50% flowering were recorded on plot basis. Principal component analysis was also used to determine genetic variability for these traits. Genotypic means were used for the PCA with respect to each trait. The mean values of the observations were analysed using INDOSTAT software.

3. Results and Discussion

Principal component analysis, basically a well-known data reduction technique, initially floated by Pearson (1901) and later developed by Hotelling (1933), offers solution to this complex problem by transforming the original set of variables into smaller set of linear combinations that account for most of the variability of the original data set. The objective of principal component analysis is to identify the minimum number of components, which can explain maximum variability out of the total variability (Anderson, 1972 and Morrison, 1982) and also to rank germplasms on the basis of PC scores.

The first principal component i.e. PC1 accounted for maximum proportion of total variability in the set of all variables and remaining components accounted for progressively lesser and lesser amount of variation. The first principal component accounted for maximum variability i.e., 23.342% which

reduced gradually to 2.831% in ten principal components. The first ten principal components having eigen values greater than 0.5 altogether explained 89.52% (Table 2) of the total variation.Screen plot (Figure 1) explained the percentage of variance associated with each principal component obtained by drawing a graph between eigen values and principal component numbers. PC1 showed 23.342% variability with eigen value 4.201 which then declined gradually. Semi curve line is obtained after ten PC tended to become straight with little variance observed in each PC. The maximum variation was observed in PC1 in comparison to other nine PCs. So, selection of lines from this PC is useful.

Table 2: Eigen values, % variance and cumulative eigen values of oat germplasm

Character	PC	Eigen value	% variability	Cumulative %
DFF	PC1	4.201	23.342	23.342
DM	PC2	3.104	17.247	40.588
DFI	PC3	1.830	10.167	50.756
PH	PC4	1.698	9.434	60.189
NLPP	PC5	1.340	7.446	67.635
PLA	PC6	1.121	6.228	73.864
TPMR	PC7	0.928	5.156	79.020
IL	PC8	0.807	4.482	83.502
PL	PC9	0.575	3.194	86.696
PW	PC10	0.510	2.831	89.527
AL	PC11	0.471	2.617	92.143
ABN	PC12	0.397	2.204	94.347
SPP	PC13	0.335	1.862	96.209
FPP	PC14	0.236	1.309	97.518
DMY	PC15	0.213	1.181	98.699
1000SW	PC16	0.108	0.598	99.297
GY	PC17	0.084	0.468	99.765
GFY	PC18	0.042	0.235	100.000

DFF: Days to 50% flowering; DM: Dry matter; DFI: Days to flower initiation; PH: Plant height; NLPP: Number of Leaves plant^{-1}; PLA: Penultimate leaf area; DTM: Days to maturity, TPMR: Tillers per meter row; IL: Internodal length; PL: Peduncle length; PW: Panicle weight; AL: Axis length; ABN: Axis branch number; SPP: Spikelet panicle^{-1}; FPP: Florets panicle^{-1}; DMY: Dry matter yield; 1000SW: 1000 seed weight; GFY: Green fodder yield; SY: Grain yield

Rotated component matrix depicted in Table 3 revealed that the PC1 which accounted for the highest variability 23.342%. PC1 accounts mostly for yield related traitslike penultimate leaf area, panicle weight, axis branch number, spikeles panicle^{-1}, florets panicle^{-1} and grain yield. PC2 was

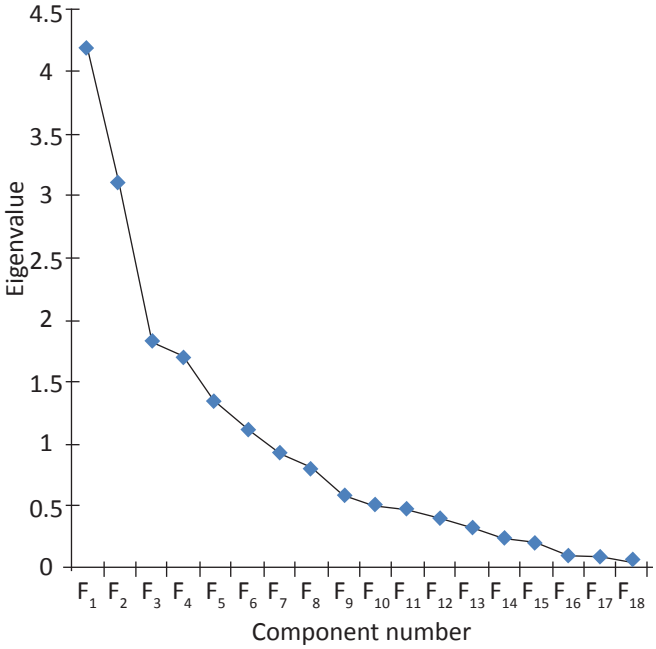

Figure 1: screen plot

Table 3: Rotated component matrix* for 18 variables of oat germplasm

TRAITS	PC1	PC2	PC3	PC4	PC5	PC6
DFF	-0.209	0.681	0.094	-0.284	0.102	0.205
DM	0.019	0.050	0.243	-0.038	0.841	-0.262
DFI	-0.262	0.568	0.194	0.068	-0.166	0.403
PH	0.362	0.221	0.671	-0.351	-0.028	0.101
NLPP	0.280	0.699	-0.017	-0.218	-0.317	-0.202
PLA	0.624	0.369	0.400	0.139	-0.051	0.017
TPM	0.387	0.329	-0.555	-0.198	-0.308	0.057
IL	0.246	0.279	0.461	0.451	-0.270	-0.405
PL	-0.105	-0.106	-0.041	-0.623	-0.333	-0.447
PW	0.829	-0.128	-0.147	-0.080	0.117	0.090
AL	0.239	0.238	0.165	0.696	-0.152	-0.033
ABN	0.633	0.050	0.189	-0.218	0.129	-0.282
SPP	0.701	-0.176	-0.247	0.217	-0.012	0.075
FPP	0.807	-0.261	-0.261	0.222	-0.001	0.144
DMY	-0.100	0.807	-0.410	0.111	0.197	-0.112
1000SW	0.484	0.147	0.190	-0.304	0.125	0.513
GY	0.850	0.031	-0.182	-0.186	0.122	-0.160
GFY	-0.115	0.772	-0.376	0.131	0.300	-0.117

Rotation Method: Varimax with Kaiser Normalization; *Rotation converged in 14 iterations; Maximum value in each PC has been highlighted

contributed by both physiological and yield related traits which are days to 50% flowering, days to flower initiation,

number of leaves plant^{-1}, dry matter yield and grain fodder yield. PC3 include trait i.e. plant height. PC4 includes trait axis length. PC5 include by physiological trait i.e. days to maturity. PC6 include yield trait 1000 seed weight. These results were in close correspondence with Tanoli et al. (2016) who revealed that plant height, leaf length, leaf width, number of tillers plant^{-1}, number of leaves tiller^{-1}, days to maturity, spike length, number of grains spikelet^{-1}, number of spikelets spike^{-1} and seed yield plant^{-1} are important principal component.

4. Conclusion

PC1 and PC6 were mostly related to yield traits. PC2, PC3, PC4 and PC5 were mostly related to physiological traits. As PC1 was constituted by most of the yield attributing traits, an intensive selection procedure can be designed to bring out rapid improvement of dependent traits i.e., yield by selecting the lines from PC1. Maximum positive value was recorded in HFO-25 (2.822), IC372418 (2.736), IC372413 (2.241) and JHO-11(1.957) HFO-25 (2.822) and was found to be common in PC1, PC 2 and PC5, IC372418 (2.736) found to be common in PC1, PC2 and PC4, IC372413 (2.241) found to be common in PC1, PC2 and PC6, while JHO-11 (1.957) presenting their contribution in PC1, PC3 and PC5. On the basis of PC score which is present in different germplasm like HFO-25**,** IC372418, IC372413 and JHO-11 can be used for development of new varieties in breeding programmes.

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