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Genetic diversity of genus *Avena* in north western-Himalayas assessed by morphological traits

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Introduction

Oat (*Avena sativa* L.) is a cool season, annual crop grown mainly in moist areas of temperate climates of the world serving as a food for mankind and forage for cattle. Oat is an important *rabi* fodder crop in India.In India, oat is also cultivated in Himalayan states like Kashmir, Himachal Pradesh and Uttarakhand. Oat in these regions have a wider adaptability, because of its excellent growing habitat, quick re-growth and better nutritional value (Misri, 2004). Oat breeding programme in Indian regions has not achieved much impetus due to a narrow genetic base of cultivated gene pool within the regionally adapted germplasm. The competition for utilization of land for food grains and fodder necessitates intensified efforts towards more efficient forage research and production, for which it is imperative to characterize and evaluate *Avena* species in order to identify donors for different traits and diversify primary oat gene pool. Historically, morphological traits have been important in the diversity analysis of crop species. The characterization of germplasm using morphological traits help the plant breeders to select the accessions to be utilized in hybridization programme.

Considering the potential forage value of oats and limited genetic information available at morphological level, present study was aimed to assess the genetic diversity of genus *Avena* using morphological characterization. The information generated from this study will be helpful in characterizing the genus *Avena* germplasm and in the selection and utilization of diverse genotypes to enhance variability and productivity of commercial oat for future crop improvement endeavors in the Indian North-Western Himalayan region.

Materials and Methods

The plant material used was a collection of 25 oat genotypes belonging to 16 *Avena* species out of which *A. sativa* (HJ-6, PLP-1, HFO-114, OS-6 and Kent) is the only cultivated one while the rest *i.e*. *A. sterilis* (HFO 872, EC 131639, HFO-878, PI 292561, CI 8077, PI 295932), *A. insularis* (EC 425098), *A. vaviloviana* (EC 415201), *A. maroccana (*IG 03-482), *A. fatua* (EC 131307), *A. brevis* (IG 03-470), *A. nuda* (EC 108467), *A. barbata* (HFO 58), *A. pratensis* (HFO 502), *A. abyssinica* (IG 03-456), *A. strigosa* (EC 4620), *A. murphyi* (EC 7120), *A. byzantina* (EC 9889), *A. orientalis* (HFO 103) and *A. longiglumis* (EC 108457) are the wild one. The data were recorded on 15 (13 morphological and 2 quality) quantitatively measured traits for 2 years (2011-12 and 2012–2013) namely days to 50 % flowering (DF), plant height (PH), leaves per plant (LP), tillers/plant (TP), green forage yield/plant (GFP), leaf stem ratio (LSR), fresh fodder yield/plant (FY), dry matter (DM), dry matter yield/plant(DMY), crude protein content (CP), crude protein yield/plant (CPY), days to 75% maturity (DSF), biological yield/plant (BY), seed yield/plant (SY), harvest index (HI) and 100-seed weight (HW).Traits were measured as per standard procedure on 5 randomly selected plants from each genotype and the mean from each genotype was used for analysis. The analysis of morphological data and to draw conclusions, mean values of 2-year observations were taken. The data were analyzed for Principle Component Analysis (PCA) and cluster analysis. The statistical analysis was carried out using SAS statistical software (SAS institute, 2012).

Results and Discussion

The objective of the present study was to assess the genetic diversity of genus *Avena* (diploid, tetraploid and hexaploid species) for 15 (13 morphological and 2 quality) quantitatively measured traits. ANOVA, Principal Component Analysis (PCA) and cluster analysis (wards method) was used to visualize the association among different traits. In the present study, high levels of variability among 25 *Avena* genotypes were observed as results of the analysis of variance were found significant for all the traits studied. These findings infer a greater scope for possible exploitation and selection to improve these traits in commercial genotypes. The variation ranges of some of the traits were in accordance with

previously reported results (Kumar *et al*., 2006). The dendrogram constructed using agro-morphological traits resulted in the establishment of eight distinct clusters (Fig.1). The average genetic similarity coefficient between genotypes was found to be 0.70. The commercial cultivars *viz*., HJ-6,0S-6, Kent and HFO-14 were grouped in two clusters with average similarity ranged from 0.50-0.75.

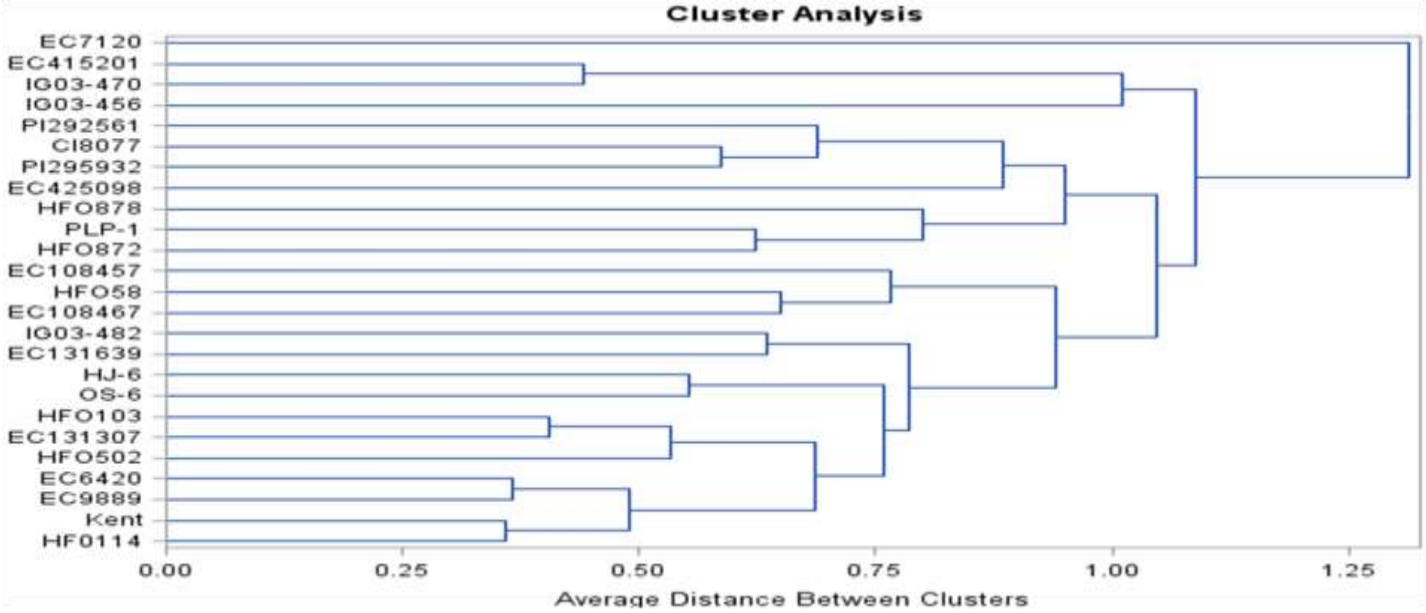

Fig.1 Dendogram of 25 oat genotypes revealed by wards method

However, in the dendrogram, distinctness of commercial oat cultivar PLP-1 was observed, as it out clustered into separate group from rest of other commercial cultivars, and grouped with all of the *A. sterilis* genotypes *viz*., HFO872, HFO878, PI295932, CI8077 and PI292561. The formation of eight distinct clusters in this study suggests the existence of variation among the genotypes for all the traits studied.

The PCA was performed to know the interrelationships among different parameters and to acquire knowledge about the diversity of different *Avena* species. The first two PCA components provided a reasonable summary of the data and explained 47.2 % of the total variation (Fig.2, Left side), while subsequent components contributed each 7.1 % or less. The first principal component (PC1) was the most important and explained 28.6 % of the total variance. PC1 was attributed to FY, HI, SY, BY, DMY, CPY, CP, TP, PH and DM traits. Of the variation among accessions, 18.6 % was attributed to the second principal component. PC2 was attributed to LSR, HW, LP, DSF and DF. PCA grouping were almost similar to the distribution of cultivars based on dendogram analysis. Three main groups were formed in PCA, in which one group had all commercial cultivars (OS-6, Kent, HJ-6 and HFO-114) with most of non-cultivated hexaploid species like *A. sterilis* (EC131639) and *A. byzantina* (EC 9889). Second group includes the commercial cultivar PLP-1, with all the hexploid species of *A. sterilis* viz., HFO 872, HFO 878, PI 292561, PI 295932), and almost similar grouping of PLP-1 was observed in dendogram analysis, depicting the similarity between PLP-1 and *A.sterilis* species. Third group contains 4 tetraploid species viz., *A. insularis* (EC425098), *A. vaviloviana* (EC415201), *A. abyssinica* (IG 03-456) and *A. insularis* (EC425098) and two diploid species *A. murphyi* (EC 7120) and *A. brevis* (IG 03-470). Again grouping pattern was similar to dendogram analysis, further supporting the evidence of similarity between these species.

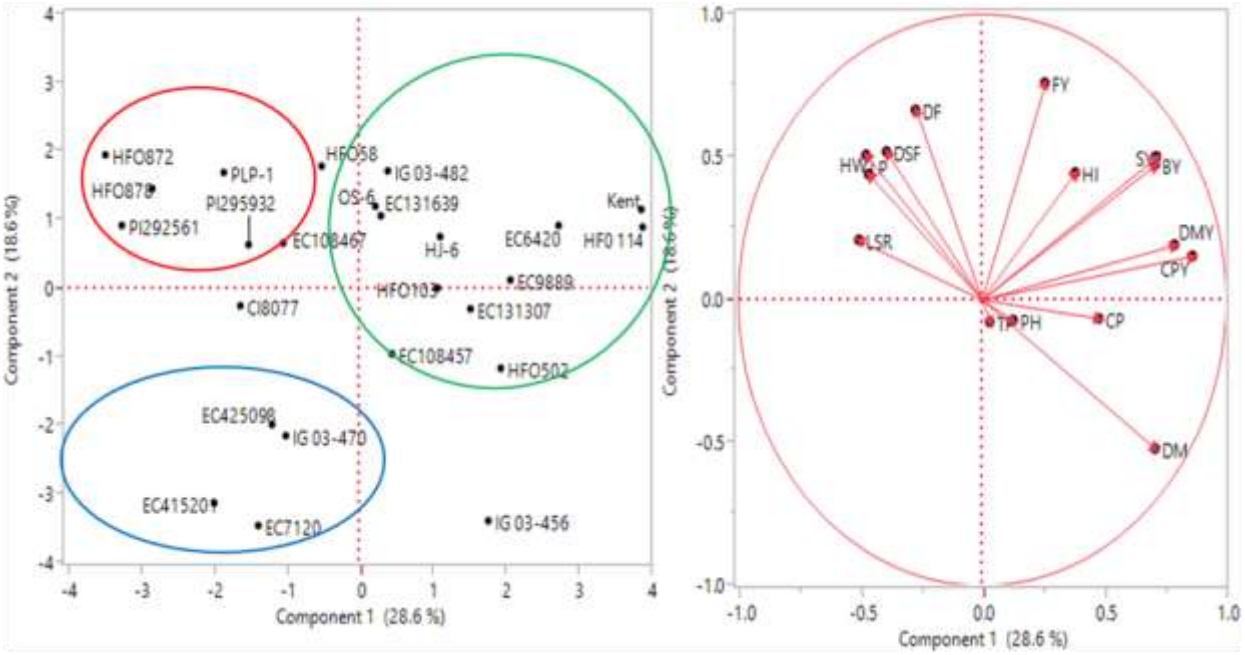

Fig.2 Scatter plot of principle coordinates 1 and 2 of 25 *Avena* genotypes, based on dissimilarity matrix.

Nevertheless, the inclusion of commercial cultivars in same group may be the fact that these are closely related to each other, depicting narrow genetic base between these commercial cultivars. Commercial cultivars grouped together with a few wild relatives like *A. strigosa*, *A. sterilis*, indicate the involvement of the nearest genetically similar wild relatives in their genealogy. These findings are supported by Choubey *et al*. (1985), which showed that *A. strigosa*, *A. sterilis*, and *A. fatua* were widely used for breeding oat cultivars in India.

The low genetic diversity among commercial oat cultivars may have consequences both for the vulnerability of crops to new diseases and for their ability to respond to changes in climate and agricultural practices.It is thus imperative and urgent to exploit the genetic diversity present in wild relatives or land races for breeding new cultivars and broadening the genetic variation in commercial oat cultivars. Furthermore, diversity analysis revealed that distinct species like A. *sterilis* (CI 8077), *A. byzantina* (EC9889), *A. sterilis* (PI 292561) and *A. strigosa* (HFO 505) can be used in wide hybridization programme for the introgression of desirable traits, to develop novel cultivars with improved traits. Potentiality of *A. byzantina*, *A. sterilis*, *A.insularis* and *A. strigosa* towards improvement of cultivable oat species in terms of various agro-morphological traits, quality parameters, biotic and abiotic stresses have been reported by Loskutov (2009).

Conclusion

The classification of 25 genotypes which include both commercial cultivars and wild relatives may be of wider application as it will avoid repetition of genetically similar genotypes in hybridization programme.

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