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Evaluation of Diversity and the Relationship of *Avena* Species Based on Agronomic Characters

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Abstract

Phenotypic diversity based on morphological traits was estimated in 114 accessions from 25 *Avena* species. Analyses showed that there was abundant genetic diversity in all species. In the quantitative characters, shattering habit had the highest phenotypic coefficient of variation (140.42%), and wheel layers had the lowest one (17.31%). In qualitative characters, color of glumelle had the highest genetic diversity index (H=1.3), while grain color had the lowest one (H=0.41). Correlation analysis of quantitative characters showed that the plant height (PH) and grain number per panicle (GNP) were the main factors which can increase yield. Principal component analysis (PCA) showed that 89.3% of the total variation of quantitative characters could be explained by the first five components. Comprehensive evaluation of agronomic characters revealed that several accessions, including accessions CN 25766 and CN 25787 (*A. hispanica*), PI 545459 (*A. fatua*), CN 21703 (*A. hirtula*), Ciav 8330 (*A. maroccana*), PI 636073 and CN 64226 (*A. sativa*) were to be promising parents in high grain yield and lodging resistance breeding. Based on agronomic characters, diploid species *A. lustanica* and *A. wiestii* were different from other diploid As genome species. *A. Murphyi* was closest to hexaploids in the three AACC tetraploid.

Abbreviations: AAFC, Agriculture and Agri-Food Canada; AFLP, amplified fragment length polymorphism; ARS, Agricultural Research Service; CV (%), coefficient of variation; EL(cm), ear length; ETP, effective tiller number per plant; GNP, grain number per panicle; GYP (g), grain yield per plant; H′, genetic diversity index; ITS, internal transcribed spacer; LR, lodging resistance; PCA, principal component analysis; PH (cm), plant height; RAPD, random amplified polymorphic DNA; SH, shattering habit; USDA, United States Department of Agriculture; WL, wheel layers

Keywords: Correlation analysis; Principal component analysis; Clustering analysis; Agricultural characters; *Avena*

Introduction

Oat (*Avena sativa* L.) is a small coarse cereal used all over the world for food and feed. Despite an important cereal, the area under cultivation of oat has been continuously decreasing during the past few decades (Buerstmayr *et al.*, 2007). However, recent demands for human consumption in oat have been gradually increased, particularly owing to its nutritional benefits. Oat has been shown to be a nutritious source of protein, carbohydrate, fibre, vitamins and mineral as well as of some compounds (polymers of fructose and antioxidant molecules, etc.) with beneficial effects on health (Peterson *et al.*, 2005; Islamovic *et al.*, 2012). Moreover, oat has also been shown to better tolerate various abiotic stresses such as cool-wet climates and dry soils with low fertility (Hoffmann, 1995).

The yield improvement was related to the better agronomic practices and application of specific breeding programs. However, yield improvement through principles of plant breeding has been suggested as cheapest strategy under range of environments (Redaelli *et al.*, 2008). Further improvement in the yield through breeding and selection depends on the novel genetic variability in the elite breeding material. Germplasm collections have been important source of novel genetic variability and could be utilized in the crop improvement programs. However, it is also important to evaluate and characterize the germplasm to determine magnitude of genetic variability within agronomical important plant traits and also to estimate genetic diversity within germplasm. High genetic diversity within parental cultivar could result in higher degree of heterosis, trangressive segregants and act as buffer against yield reduction due to biotic and abiotic stresses (Buerstmayr *et al.*, 2007).

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Traditionally oat has been evaluated for the effective tiller number, spikelets per spike, shattering habit, grain yield per plant and heading time. Selection has been shown to be based on multiple breeding characters, and it was concluded that parents must have at least one outstanding trait (Yan and Frégeau-Reid, 2008). Previous evaluation of oat germplasm showed that elite germplasm showed low genetic variability for agronomic important plant traits, while wild species were rich source of resistance to biotic and abiotic stresses (Christoffers *et al.*, 2002; Peng *et al.*, 2011). However, introgression between different plant species was difficult due to genome differentiation discovered through cytological (Ladizinsky, 1973; Rajhathy and Thomas, 1974), morphological (Baum, 1977), molecular approaches and C-banding technique (Alicchio *et al.*, 1995). Major genomic divergence were found between the A and C genomes in *Avena* (Rajhathy and Thomas, 1974; Drossou *et al.*, 2004). In this study, we evaluated agronomic characters and analyzed the relationship of 114 accessions of 25 *Avena* L. species originating from different growing regions, based on correlation, principal component and cluster analyses. The purpose of this study was: (1) to identify some outstanding accessions on the basis of agronomic traits; (2) determining correlations among the quantitative traits; (3) phenotypic diversity within germplasm and quantitative traits.

Materials and Methods

Plant Material and Field Trails

Experiments were carried out during 2010-2012 cropping seasons for two years at the experimental plots of Sichuan Agricultural University in Wenjiang (Chengdu) (30°41′N, 103°49′E). Seeds of the 114 oat accessions were obtained from Agriculture and Agri-Food Canada, United States Department of Agriculture, Agricultural Research Service, National Small Grain Research Facility, and National Small Grains Collection (Table 1). The 114 oat accessions were sown at the end of October and harvested in early June. The plot size was 3 m^2, with 5 rows that were 2 m long and 0.3 m apart. All 114 cultivars were primarily germinated in petri dishes, and then transplanted them to the field plots. Crop management was done for oat production according to local practice.

Characters Investigation

Ten representative plants were chosen to evaluate each character of all materials. Eighteen agronomic characters were investigated for all accessions, including awn, awn shape, awn color, color of glumelle, color of lemma, grain shape, grain color, grain pubescence, grain plumpness, ear shape, PH, ear length (EL), wheel layers (WL), effective tiller number per plant (ETP), GNP, shattering habit (SH, proportion of shattered seeds to all seeds of a plant). Lodging resistance was evaluated and plants were characterized as (LR, lodging: the inclination was more than 45°; moderate resistance: the inclination was between 15-45°; lodging-resistant: the inclination was under 15°), and grain yield per plant (GYP).

Statistical Analysis

Mean value and their standard deviation, coefficient of variation (PCV, %), frequency distribution, genetic diversity index and ranges were estimated for all traits. Genetic diversity index (H′) was calculated by Shannon-wiener index: $H'=-\sum Pi \ln Pi$, and $Pi=Ni/N$, N was the number of the same sample (Qi *et al.*, 2008). Correlation coefficients among the quantitative characters were also computed using statistical software. Principle component analysis (PCA) was used to determine the importance of different characters in the explanation of polymorphism in materials. Cluster analysis was adopted to measure the hierarchical similarity among materials (Iannucci *et al.*, 2011). SPSS 18.0 and NTSYSpc 2.1 were used to analyze the data.

Results

Variation of Quantitative Characters in *Avena* Species

Evaluation of germplasm depicted significant variation within the tested quantitative characters (Table 2). PH range was 67.6 to 214 cm, there were 82 accessions having PH higher than 120 cm. The EL has a minimum 16 cm and maximum 58 cm. Species shorter than 100cm of PH and 20 cm of EL were PI 367381 (*A.eriantha*, C_pC_p),CN 21405 (*A.ventricosa*, C_vC_v), INS-4(*A. insularis*, AACC), all with C genome. WL has the minimum PCV of 17.31% (phenotypic). The accessions having more than 9 WL were all diploids with A_sA_s genome, while accessions, which have WL less than 5.5 generally belong to C genome, including *A. eriantha, A. cluda, A. ventricosa and A. insularis.* Prominent differences were found of ETP, accession CN 23036 (*A. occidentalis*) has the maximum ETP, while all accessions of *A. sativa* had less than 10 ETP. The range of GNP was 10 to 253, species *A. sativa* had more than 150 GNP, and C genome species had the least GNP. It was interesting to find that *A. sativa* accessions PI 636073, CN 2811, CN 21957 had high GYP (30 g), while some accessions less than1g of GYP. Half of the accessions were lodging-resistant, and most of the lodged accessions belong to *A. sativa*. Wild species were susceptible to the shattering at maturity, while cultivated belong to A_sA_s, AABB and AACCDD genome species were shattering resistant.

Variation of Qualitative Characters in *Avena* Species

Data transformation was carried out in qualitative traits for quantification and statistical analysis (Table 3).

Table 1: 114 accessions of 25 *Avena* L. species used in this study

Species	Haplome	No	Accession No.	Origin or source
A. abyssinica	AB	1	PI 411163	Seraye, Eritrea
		2	PI 411173	Tigre, Ethiopia
		3	PI 411359	Eritrea
A. agadiriana	AB	4	CN 25837	Africa: Morocco
		5	CN 25854	Africa: Morocco
		6	CN 25856	Africa: Morocco
		7	CN 25863	Africa: Morocco
		8	CN 25869	Africa: Morocco
A. atlantica	A_s	9	CN 25849	Africa: Morocco
		10	CN 25859	Africa: Morocco
		11	CN 25864	Africa: Morocco
		12	CN 25887	Africa: Morocco
		13	CN 25897	Africa: Morocco
A. barbata	AB	14	PI 296229	Northern, Israel
		15	PI 337802	Izmir, Turkey
		16	PI 337826	Central Greece, Greece
		17	PI 282723	Northern, Israel
		18	PI 337731	Macedonia, Greece
		19	PI 367322	Beja, Portugal
A. brevis	A_s	20	Ciav 1783	Lower Saxony, Germany
		21	Ciav 9113	Europe
		22	PI 258545	Portugal
A. canariensis	A_c	23	CN 23017	Canary Islands, Spain
		24	CN 23029	Canary Islands, Spain
		25	CN 25442	Canary Islands, Spain
		26	CN 26172	Canary Islands, Spain
		27	CN 26195	Canary Islands, Spain
A. clauda	C_p	28	CN 19205	Iran
		29	CN 19242	Turkey
		30	CN 21378	Greece
		31	CN 21388	Algeria
		32	CN 24695	Turkey
A. damascena	A_d	33	CN 19457	Syria
		34	CN 19458	Syria
A. eriantha	C_p	36	Ciav 9050	England, United Kingdom.
		37	PI 367381	Madrid, Spain.
A. fatua	ACD	38	PI 447299	Gansu, China.
		39	PI 544659	South Dakota, United States.
		40	PI 545459	Mexico, Mexico.
		41	PI 560776	Van, Turkey.
A. hirtula	A_s	43	CN 19739	Algeria.
		44	CN 21674	Corsica, France.
		45	CN 21703	Morocco.
		46	CN 22633	Tunisia.
A. hispanica	A_s	47	CN 25676	Portugal.
		48	CN 25727	Portugal.
		49	CN 25766	Portugal.
		50	CN 25778	Portugal.
		51	CN 25787	Portugal.
A. insularis	AC	123	sn	Sicily, Mt. Bubonia, Italy
		124	6-B-22	Sicily, Gela, Italy
		125	INS-4	Sicily, Gela (reselection),Italy
A.*longiglumis*	A_l	52	Ciav 9087	Oran, Algeria.
		53	Ciav 9089	Libya.
		54	PI 367389	Setubal, Portugal.
A. lusitanica	A_s	55	CN 25414	Spain.
		56	CN 25885	Morocco.
		57	CN 25899	Morocco.
		59	CN 26441	Spain.
A. maroccana	AC	61	Ciav 8330	Morocco.
		62	Ciav 8331	Khemisset, Morocco.

Table 1: Continued

Table 1: Continued

A. murphyi	AC	63	CN 21989	Spain.
		64	CN 25974	Morocco.
A. sativa ssp.nuda	ACD	65	Ciav 9009	Ontario, Canada
		66	PI 401795	Netherlands.
		67	PI 401812	Germany.
A. occidentalis	ACD	68	CN 4547	Canary Islands, Spain
		69	CN 23036	Canary Islands, Spain.
		70	CN 25942	Morocco.
		71	CN 25956	Morocco.
		72	CN 26226	Canary Islands, Spain.
A. sativa	ACD	73	PI 40650	Gansu, China.
		75	Ciav 1946	Xizang, China.
		76	PI 93751	Colonia, Uruguay
		77	PI 103669	New South Wales, Australia.
		78	PI 103670	New South Wales, Australia.
		79	PI 175021	Uttar Pradesh, India.
		80	PI 194896	Gonder, Ethiopia.
		81	PI 258641	Georgia.
		82	PI 258644	China.
		83	PI 258649	Chernivtsi, Ukraine.
		84	PI 258655	Irkutsk, Russian Federation.
		85	PI 258656	Dzavhan, Mongolia.
		86	PI 258657	Georgia.
		87	PI 258658	Poland
		89	PI 258663	Krym, Ukraine
		90	PI 258665	Kabardino-Balkaria,Russian,Federation
		91	PI 258666	Armenia.
		92	PI 258677	Ankara, Turkey.
		93	PI 258685	China.
		94	PI 258724	Kirov, Russian Federation
		95	PI 258726	Sakhalin, Russian Federation
		96	PI 258734	Kirov, Russian Federation.
		97	PI 411426	Nevsehir, Turkey.
		99	PI636013	Heves, Hungary.
		100	PI 636073	South Australia, Australia
		101	CN 2811	New South Wales,Australia,(Sunrise)
		102	CN 21957	Ethiopia.
		103	CN 24942	Iran.
		104	CN53095	Malmohus, Sweden (GoldenRain)
		105	CN 64226	Rio Grande do Sul, Brazil(BAGE)
		107	CN82122	Xinjiang, China(XINYUAN)
A. sterilis	ACD	109	PI 411503	Alger, Algeria.
		110	PI 411656	Tigre, Ethiopia.
A. strigosa	A_s	111	PI 83722	New South Wales, Australia.
		112	PI 158246	Lugo, Spain.
		113	Ciav 9066	Ontario, Canada
		114	PI 436082	Los Lagos, Chile.
A. vaviloviana	AB	115	PI 412761	Eritrea.
		116	PI 412766	Shewa, Ethiopia.
A. ventricosa	C_v	117	CN 21405	Algeria.
A. wiestii	A_s	120	PI 53626	Giza, Egypt.
		121	Ciav 9053	Ontario, Canada
		122	PI 299112	Chile.

Glume colour had the highest H' (1.3). Evaluation of the germplasm showed that 44% accessions had yellow lemma. Lemma color (yellow and white) was equally distributed within germplasm (Table 3). Germplasm was also characterized for presence of awn, within germplasm 5 accessions were awnless,68 percent of the accessions had dense awn, while remaining had low density of awn. Grain shapes were characterized into three types. 89% of the accessions had spindle shape or long barrel grain shape. Yellow colored grains were most predominant in germplasm, about 86% of the accessions were with yellow grain color and 71 black grain color. The variation among the fuzzes of seeds was obvious. Less fuzzes, medium and dense fuzz possessed 34%, 34% and 32%, respectively. In the present study, only nine accessions had shrunken seeds, while others were medium or plumb. In order to maximize their exposure to the sunshine, most species had spikelets scattering all around the spike-stalk.

Correlation Analysis of Quantitative Characters

Correlation analysis was estimated to identify the key traits

Table 2: Estimates of variability among quantitative characters

Characters	Mean	Min	Max	Std. Deviation	Range	Variation coefficient (%)
PH	138.66	67.60	214.00	29.96	146.40	21.61
EL	32.19	15.40	57.60	10.24	42.20	31.82
WL	7.66	4.20	11.40	1.33	7.20	17.31
ETP	24.69	2.00	81.40	14.73	79.40	59.66
GNP	84.85	10.00	253.20	49.18	243.20	57.95
LR	2.18	1.00	3.00	0.90	2.00	41.59
SH	0.16	0.00	0.80	0.22	0.80	140.42
GYP	10.20	0.17	29.97	7.92	29.80	77.66

Note: PH, plant height(cm); EL, ear length(cm); WL, wheel layers; ETP, effective tiller number per plant; GNP, grain number per panicle; LR, lodging resistance: 1) lodging 2)moderate resistance 3) lodging-resistant; SH, shattering habit(%); GYP, grain yield per plant(g)

Table 3: Phenotypic diversity among qualitative characters

Characters	Frequency distribution					Genetic diversity index
	0	1	2	3	4	
Awn	0.04	0.31	0.65	—	—	0.78
Awn shape	0.04	0.11	0.85	—	—	0.51
Awn color	0.04	0.08	0.88	—	—	0.45
Color of glumelle	—	0.44	0.20	0.18	0.18	1.30
Color of lemma	—	0.50	0.50	—	—	0.69
Grain shape	—	0.46	0.43	0.11	—	0.96
Grain color	—	0.86	0.14	—	—	0.41
Grain fuzz	—	0.34	0.34	0.32	—	1.10
Grain plumpness	—	0.08	0.46	0.46	—	0.91
Ear shape	—	0.87	0.11	0.02	—	0.44

Notes: Awn: 0. awnless, 1. week, 2. strong; Awn shape: 0. awnless, 1. straight awn, 2. curving awn; Awn color: 0. awnless, 1. yellow, 2. black; Color of glumelle: 1. yellow, 2. brown, 3. black, 4. white; Color of lemma: 1. yellow, 2.white;Grain shape: 1.spindle shape, 2. long barrel shape, 3.ellipse; Grain color: 1.yellow, 2.black; Grain fuzz: 1.less, 2.medium, 3. dense; Grain plumpness: 1.shrunken, 2. medium, 3. plump; Ear shape: 1. spread all around, 2. spread side, 3.sidely compact

Table 4: Correlation coefficient based on mean values of quantitative characters

Characters	EL	WL	ETP	GNP	LR	SH	GYP
PH	0.752**	0.554**	-0.324**	0.626**	-0.149	-0.006	0.077
EL		0.456**	-0.433**	0.611**	0.004	-0.036	-0.119
WL			-0.035	0.676**	0.009	-0.126	0.109
ETP				-0.264**	0.132	0.229*	-0.041
GNP					-0.141	-0.181	0.133
LR						0.121	-0.369**
SH							-0.074

*, ** mean significant at the 0.05 and 0.01 level, respectively. Note: PH, plant height(cm); EL, ear length(cm); WL, wheel layers; ETP, effective tiller number per plant; GNP, grain number per panicle; LR, lodging resistance: 1) lodging2)moderate resistance 3) lodging-resistant; SH, shattering habit(%); GYP, grain yield per plant(g)

associated with high yield. PH was highly significant correlated with EL, WL and GNP (Table 4). There was a negatively significant correlation between PH and ETP. No significant ($P \geq 0.05$) relations were found between PH with GYP, while LR and SH were negatively related to PH but insignificant. Significant ($P \leq 0.05$) correlations were found among EL with WL and GNP. Negative significant ($P \leq 0.05$) correlation was found between EL and ETP. The correlation among EL with GYP and SH was negative and insignificant. Correlation between WL and GNP was significant. ETP had significantly negative correlation with both of GNP and GYP. There was negative highly significant correlation between LR and GYP. SH and GYP had negative correlation.

Principal Component Analysis (PCA) of Quantitative Characters

In order to determine relationships between characters, we estimated relationship among eight quantitative characters in *Avena* species (Table 5). There were only three principal components, with the PC1 contained 38.015% of the total variation estimated, and PC2 17.972%, PC3 13.835%. The factor loading was used to determine the characteristics of each principal component. Relative higher factor loading of PC1 was PH, EL and GNP, and was named as plant height component; PC2 had a higher factor loading of LR and SH, and named as lodging resistance component. However GYP had a negative effect of lodging and shattering. The highest factor loading of PC3 was ETP, and was named as effective tiller number component. On the basis of these results, accessions with high PC1, PC3 and low PC2 may be selected from germplasm.

Cluster Analysis

All accessions were classified into three groups at a Euclidian distance of 15% (Fig. 1). Group I to III contained

Table 5: Analysis of principal component of eight quantitative characters i.e. pH, plant height (cm); EL, ear length (cm); WL, wheel layers; ETP, effective tiller number per plant; GNP, grain number per panicle; LR, lodging resistance: 1) lodging 2) moderate resistance 3) lodging-resistant; SH, shattering habit(%); GYP, grain yield per plant (g)

Components	Total Variance Explained			Principal component Matrix			
	Initial Eigenvalues			Characters	Component		
	Total	% of Variance	Cumulative %		1	2	3
1	3.041	38.015	38.015	PH	0.865	0.096	0.103
2	1.438	17.972	55.987	EL	0.836	0.290	-0.140
3	1.107	13.835	69.822	WL	0.733	0.102	0.394
4	0.942	11.771	81.592	ETP	-0.476	0.142	0.702
5	0.619	7.743	89.336	GNP	0.859	-0.018	0.152
6	0.373	4.666	94.001	LR	-0.184	0.769	-0.046
7	0.287	3.582	97.583	SH	-0.207	0.368	0.531
8	0.193	2.417	100	GYP	0.129	-0.766	0.348

Table 6: Mean values of each cluster based on the dendrogram

Group	PH	EL	WL	ETP	GNP	LR	SH	GYP
I	146.67	33.61	7.84	22.20	101.05	1.00	0.11	15.01
II	136.89	33.20	7.86	25.43	81.10	3.00	0.17	7.43
III	130.80	27.57	6.89	26.70	69.35	2.00	0.15	9.60

Note: PH, plant height(cm); EL, ear length(cm); WL, wheel layers; ETP,effective tiller number per plant; GNP, grain number per panicle; LR, lodging resistance: 1) lodging2)moderate resistance 3) lodging-resistant; SH, shattering habit(%); GYP, grain yield per plant(g)

35, 56 and 23 accessions, respectively. Accessions came from the same species had the tendency to cluster together. However, *A. sativa* accessions belonging to 20 countries and different regions were scattered in different cluster. Each group showed the performance for specific agronomic characters (Table 6). All plant material of group I displayed lodging, showed the highest PH, GNP and GYP together with the least ETP from diploid species *A. hispanica*(As), *A. strigosa* (As), *A. damascene*(Ad), tetroploid AABB genome species *A. vaviloviana*, *A. abyssinica*, hexaploid *A. sativa*, *A. sterilis* and *A. occidentalis*. All lodging-resistant accessions (contained diploids (As, Al, Cp), tetroploieds (AC, AB) and hexaploids) were grouped in II cluster, while other traits were of medium level. Accessions in the third group were medium lodging, had the shortest PH, EL and least GNP and high shattering rate. There were two subgroups in group III. The first subgroup contained diploid *A. ventricosa* (Cv) and *A. canariensis* (Ac), tetroploid *A. insularis*(AACC). The second subgroup including two As diploid *A. lusitanica*, *A. wiestii*, and hexaploid *A. sativa*.

Cluster analysis of *Avena* species with diploid A haplomes performed independently (Fig. 2). Several species were scattered among the two groups, which may related with geographical distributing. Five species with the AsAs genome together with the AlAl genome species were clustered in group I. Group II contained other two species with the AsAs genome *A. lustanica*, *A. wiestii*, and *A. canariensis* (AcAc), *A. damascene* (AdAd).

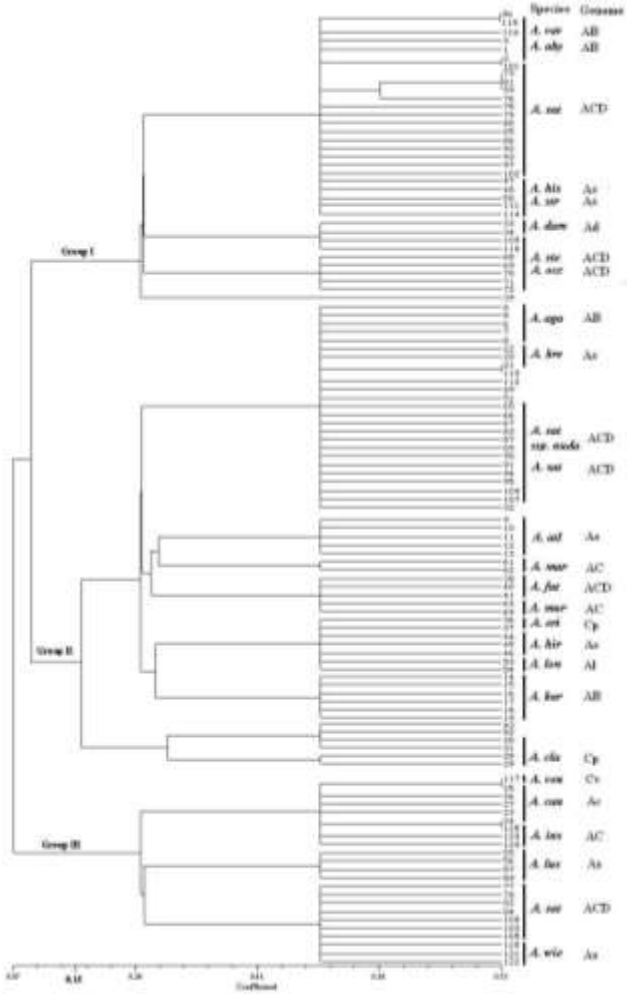

Fig. 1: Dendrogram for 114 accessions of *Avena* based on quantitative traits

Discussion

Increasing yield potential of field crop is the ultimate objective of plant breeding and to reduce gap between the demand and supply of the grains. Hence, to improve yield and quality of oat, presence of sufficient genetic diversity in the germplasm is an important prerequisite (Qi *et al.*, 2008).

Present studies showed high genetic diversity within and among worldwide collections of different *Avena* species.

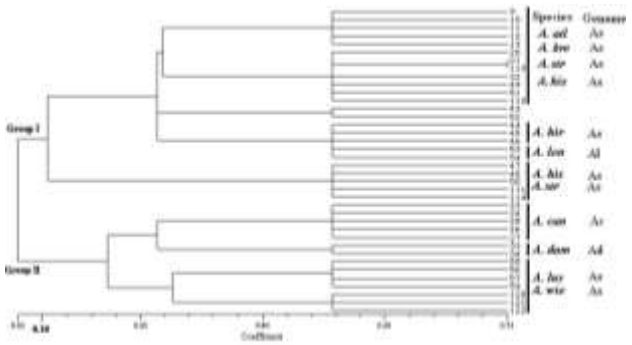

Fig. 2: Dendrogram for 10 diploid A genome species of *Avena* based on quantitative traits

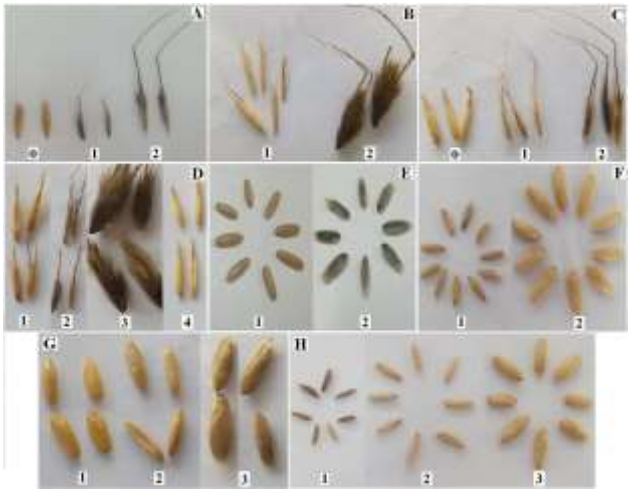

Fig. 3: (A) Awn: 0. Awnless 1. Week 2.Strong; (B) Awn shape: 1.Straight awn 2. Curving awn; (C) Awn color: 0. Awnless 1. Yellow 2. Black; (D) Color of glumelle: 1. Yellow 2. Brown 3. Black 4. White (E) Grain color: 1. Yellow 2. Black (F) Grain yield per plant: 1. GYP=0.17 g 2. GYP =29.97 g: (G) Grain pubescence: 1. Less 2. Medium 3.Much (H) Grain plumpness: 1. shrunken 2. medium 3. plump

As regards genetic diversity of agronomic traits, studies have shown the configuration of panicle and spikelet had differential contribution to the yield and quality (Griffiths *et al.*, 2012). Our studies indicated that low yielding species had the few WL and GNP with the scrubby plant type and lodging susceptible. Johnston *et al.* (1981) also indicated that lodging may result in substantial oat yield and kernel quality losses. Shattering habit was an important selection criterion as well. Some species had the tendency to shatter before maturity. Therefore, seeds had to be harvested before it mature. Substantial variation also existed for qualitative traits. Awn movement was related to the water absorption and seeds germination (Raju and Ramaswamy, 1983), dense awn accessions germinated quickly.

Our results showed positive relationship of PH with GYP which was in contrast to the previous reports showing negative relationship among two traits (De Vita *et al.*, 2007). Oat germplasm also showed negative relationship between the GYP and ETP, which was in contrast to the previous finding of Peltonen-Sainio and Järvinen (1995). It was noteworthy that negative correlation was found between PH with LR and SH, this was not consistent with result of Buerstmayr *et al.* (2007) which showed that PH and LR were positively correlated. Study showed that all dwarf genotypes were lodging resistant whereas tall genotypes were susceptible to the lodging. However, our studies showed that tall accessions (≥163 cm) were lodging-resistant, whereas some accessions (≤90 cm) were susceptible to the lodging. This may be due to variation in stem diameter, tissue strength. GNP had positive correlation with GYP, this was in good agreement with the results of Buerstmayr *et al.* (2007), while not in line with Dumlupinar *et al.* (2011) who showed negative correlation between GNP and GWP. In our study, the PH and GNP were the main factors affecting seed yield, while ETP, LR and SH factor would reduce yield. Variation in correlations between economical traits with respect to the previous finding was due to utilization of germplasm having different genetic back ground.

Multivariate analysis was used to quantify diversity and assess relative contributions of plant traits to the total variability in germplasm collections (Rezai and Frey, 1990). According to PCA, high yield accessions should have high PC1, PC3 and low PC2. However, none of trait was able to explain full variation. Similar conclusion was also made by Iannucci *et al.* (2011) in evaluation of Turkish oat germplasm.

Comprehensive evaluation of germplasm revealed few lodging resistance accessions with high GYP (20 g). These accessions may be utilized as parents to produce trangressive segregants. Distant hybridization between cultivated oats, species *A. wiestii* (Peng *et al.*, 2010a), *A. strigosa* (Chen and Armstrong, 1994; Nikoloudakis *et al.*, 2008), *A. maroccana* and *A. murphyi* (Peng *et al.*, 2008; Peng *et al.*, 2010b) may be attempted due to their cytological and chromosomal similarities. Moreover, gene cloning could also attempted to transfer the lodging-resistant gene to cultivated oats.

Analysis for *Avena* species with diploid A haplome showed the species with AsAs genome were scattered among the species with AcAc, AdAd and AlAl genomes (Fig. 2), indicating that *Avena* species with the AsAs genome were more divergent than the other diploid A genome species. This was in agreement with the molecular studies carried out with ccSSR markers (Li *et al.*, 2009). ITS sequences research indicated that *A. wiestii* was different from other A genome species (Peng *et al.*, 2010b) while AFLP study based on 25 *Avena* speices showed that species *A. lusitanica* was more related to *A. damascena* (Fu and Williams, 2008); Ac-genome species *A. canariensis* had close relationship with *Avena wiestii* (AsAs) (Li *et al.*, 2000),

which were in agreement with our result that *A. canariensis* (AcAc) and *A. damascene*(AdAd) stayed with the other two AsAs genome species *A. lustanica* and *A. wiesti* in group II (Fig. 2). The two Cp genome species *A. eriantha* and *A. clauda* were both clustered into group II (Fig. 1), indicating their close relationship to each other than to *A. ventricosa* (Cv genome), this was supported by RAPD and AFLP molecular markers analyses (Drossou *et al.*, 2004). Species with A and C genomes scattered among group I to III and not clearly divided into two groups (Fig. 1), this was not in line with results of RFLP and RAPD marker analyses that major genomic divergence existed between the A and C genomes (Drossou *et al*., 2004).

Although three AABB tetraploids *A. abyssinica*, *A. vaviloviana* and *A. barbata* were interfertile, *A. abyssinica* was more closely related to *A. vaviloviana* than to *A. barbata* (Drossou *et al.*, 2004), ITS sequence results of Nikoloudakis *et al.* (2008) indicated the AABB species *A. agadiriana* is different from the other three. These conclusions were supported by our result that AABB genome species *A. vaviloviana*, *A. abyssinica* clustered into group I, while *A. barbata* and *A. agadiriana* clustered into different subgroups of group II (Fig. 1). Meiotic chromosome pairing of hybrids between AsAs autotetraploids and AABB tetraploids revealed that B genome chromosomes had high homology with the As genome (Sadasivaiah and Rajhathy, 1968). The C-banding patterns (Fominaya *et al.*, 1988) and genomic in situ hybridization experiments (Katsiotis *et al.*, 1997) revealed close relationship of the A and B genomes. Our results also suggest that diploids *A. hispanica* (As), *A. strigosa* (As), *A. damascen e* (Ad) grouped together with two AABB genome species *A. vaviloviana* and *A. abyssinica* (Fig. 1).

Tetroploid AACC species *A. murphyi* and hexaploid *A. fatua* were in the same subgroup, tetroploid *A. maroccana* in another subgroup, both in group II, while *A. insularis* was in group III, indicating that *A. murphyi* was closest to hexaploids in the three AACC tetraploid. Our results supports Ladizinsky and Zohary (1971), who showed that tetraploid species *A. murphyi* was donor of the AC-genomes of the hexaploid species. However, our result contradict with the finding that *A. insularis* (AC) was the tetraploid ancestor of hexaploids (Ladizinsky, 1998). Previous research also suggested that species *A. strigosa* (Chen and Armstrong, 1994; Jellen *et al.*, 1994), or *A. weistii* (Li *et al.*, 2000; Fu and Williams, 2008) were the donor of A genome within the polyploid oats, which was in agreement of our results that *A. strigosa* and *A. weistii*, clustered with the different accessions of *A. sativa*, respectively (Fig. 1).

In conclusion, we found several outstanding accessions CN 25766 and CN 25787 (*A. hispanica*), PI 545459(*A. fatua*), CN 21703 (*A. hirtula*), Ciav 8330(*A. maroccana*), PI 636073 and CN 64226(*A. sativa*) could be exploited as donor of high yield and lodging resistance. These useful traits may introgressed through distant hybridization. This study also extends the knowledge of the relationships among *Avena* species. Results showed that diploid species *A. lustanica* and *A. wiestii* were different from other diploid As genome species, and had close relationship between *A. canariensis* and *A. damascene*. Furthermore, our study showed *A. murphyi* was closest to hexaploids in the three AACC tetraploid. Further research in oat with more population materials based on morphological, cytological and molecular evidence would help to determine more information regarding *Avena* L.

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