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# PHENETIC STUDIES IN *AVENA* SPECIES AND POPULATIONS OF IRAN

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## Abstract

A multivariate statistical analysis was performed on morphological characters of sixty-one populations of *Avena eriantha* Dur. *A. clauda* Dur., *A. barbata* Pott ex Link., *A. wiestii* Steud., *A. fatua* L., *A. sterilis* ssp. *ludoviciana* L. and *A. sativa* L. Factor analysis revealed that intraspecific morphological variations are due to quantitative characters. Interspecific as well as intersectional relationships were investigated using cluster, discriminant analysis and ordination method based on principal components supporting the Baum's classification.

**Keywords:** *Avena*; Gramineae; Cluster analysis; Principal components; Ordination; Discriminant analysis

## Introduction

The genus *Avena* L. of tribe Aveneae comprises about 27 species throughout the world [2] and mainly grow in the regions with Mediterranean climate. The number of *Avena* species reported from Iran varies from 7 to 10 [2,3,7]. Although these species grow wildly through Iran, they mainly occur in west and northwest regions (Fig. 1). *Avena* species are predominantly inbreeders and annuals with the exception of *A. macrostachya* Bal. ex Cosson & Dur. Which is a perennial outbreeding species from north Africa [8].

Although the available literature dealing with classification, morphology and cytogenetics of *Avena* [1,2] indicates the importance of these taxa, no report is available on biosystematics of *Avena* from Iran. This study considers the phenetic analysis of morphological characters in some *Avena* species/populations in Iran with the objective to investigate intra-specific variation and the species inter-relationships. It is also attempted to define qualitative and quantitative characters discriminating the species studied.

Baum [2], based on morphological characters such as the glumes relative length i.e. equal or unequal, presence/absence of scar in the florets, number of rows of cilia along edges of keels and genomic constitution, placed *Avena* species into 7 sections, which is followed here too.

## Materials and Methods

### *Plant Material*

Sixty one populations of 7 *Avena*, *A. eriantha* Dur., *A. clauda* Dur., *A. barbata* Pott ex Link., *A. wiestii* Steud., *A. fatua* L., *A. sterilis* ssp. *ludoviciana* L. and *A.*

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**Table 1.** The *Avena* species code, their localities and voucher number

| Species | Sp. Code | Locality | Voucher | Collector |
|---|---|---|---|---|
| *A. barbata* Pott ex Link | b1 | Fars, Hosseinabad | 19491 | Iranshahr & Mossavi |
| | b2 | Kerman, Jebalbarez montain | 19533 | Reshinger & Allen |
| | b3 | Fars,Kazeron,Rahdar | 5028 | Forooghi |
| | b4 | Tehran,road to Ghom | 18249 | Amin & Bazargan |
| | b5 | Khozestan Behbahan-Aghajari road | 38746 | Assadi & Aboohamzeh |
| | b6 | Fars,Firoozabad-Shiraz road | 41381 | Assadi & Sardabi |
| | b7 | Bakhtaran,Rijah | 19492 | Iranshahr & Dezfoolian |
| | b8 | Fars,Shiraz | 99146 | Koobaz & Heidari |
| | b9 | Fars,Shiraz,Eram garden | 99145 | Koobaz & Heidari |
| | b10 | Kohkiloyeh-Boyerahmad | 16627 | |
| *A. clauda* | c1 | Golestan,Gonbadkavoos, Malek-Ali hill | 19497 | Sharif |
| | c2 | Golestan,Gonbadkavoos, Agribodagh | 19495 | Mirzaiyan |
| | c3 | Ardebil,Moghan, Parsabad | 19529 | Manoochehri |
| | c4 | Golestan, Gonbadkavoos, Agribodagh | 19493 | Sharif |
| | c5 | Khozestan, Masjedsoleyman | 70199 | Mozafarian |
| | c6 | Kohkiloyeh-Boyerahmad, Dogonbadan-Noorabad road | 38530 | Assadi & Abohamzeh |
| | c7 | Golestan, Gonbadkavoos, Agribodagh | 23870 | Assadi |
| | c8 | Gilan, Roodbar,Darestan | 99142 | Koobaz & Darestani |
| *A. eirantha* Dur | e1 | Ardebil, Moghan,Aslandooz | 122 | Olfat |
| | e2 | Ardebil, Mogan,Parsabad | 27460 | Pabo |
| | e3 | Golestan, Gonbadkavoos, Maravehtapeh | 55481 | Assadi & Massoomi |
| | e4 | Golestan, Gonbadkavoos | 27458 | Pabo |
| | e5 | Golestan, Gonbadkavoos, Dasht1 | 98412 | Zehzad & Sonboli |
| | e6 | Golestan, Gonbadkavoos, Dasht2 | 98411 | Zehzad & Sonboli |
| | e7 | Golestan, Gonbadkavoos, Dasht3 | 99143 | Koobaz & Heidari |
| | e8 | Gilan, Roodbar, Darestan | 99144 | Koobaz & Darestani |
| *A. fatua* L. | f1 | Sistan-Baloochestan, Kakoli mountion | 52948 | Mozafarian |
| | f2 | Sistan-Baloochestan,Zabol | 63431 | Mozafarian |
| | f3 | Sistan-Baloochestan,kharestan | 53030 | Mozafarian |
| | f4 | Mazandaran,Polesefid | 73390 | Assadi |
| | f5 | Tehran,Varamin | 19528 | Manoochehri |
| | f6 | Markazi,Mahalat | 98413 | Heidari |
| | f7 | Tehran,Bagherabad | 98401 | Koobaz&heidari |
| | F8 | Esfahan,Nazvan Park | 98403 | Azarani |
| | F9 | Markazi,Arak | 98402 | Heidari |
| | F10 | Khorasan,25km to Ghochan | 623 | |

**Table 1.** Continued

| Species | Sp. Code | Locality | Voucher | Collector |
|---|---|---|---|---|
| *A.sativa* L. | s1 | Tehran, Karadj | 19536 | |
| | s2 | Golestan,Gonbadkavoos | 2/2/27/3 | Soodmand |
| | s3 | Lorestan | 26326 | Ronehmark |
| | | 50km to south-west Aligodarz | | |
| | s4 | West Azarbayjan, | | |
| | | Makoo-Kooy road | 41092 | |
| | s5 | Golestan, Gonbadkavoos | 27/2 | |
| *A. sterilis* | | | | |
| ssp. *ludoviciana* L. | | | | |
| | l1 | Ghazvin, Koohin | A-66 | Zehzad |
| | l2 | Fars, Shiraz, near Marvdasht | 98414 | Pakravan |
| | l3 | Golestan, Gonbadkavoos, Dasht | 98404 | Zehzad & Sonboli |
| | l4 | Tehran,Varamin, Bagherabad | 98407 | Heidari & Koobaz |
| | l5 | Golestan, Gonbadkavoos, | | |
| | | Tangehrah1 | 98405 | Zehzad & Sonboli |
| | l6 | Tehran, Darake | 99151 | Koobaz |
| | l7 | Golestan, Gonbadkavoos | | |
| | | Tangehrah2 | 98406 | Zehzad & Sonboli |
| | l8 | Markazi, Arak | 98410 | Heidari |
| | l9 | Tehran, Elahieh | 98408 | Azarani |
| | l10 | Markazi, Mahalat | 98409 | Heidari |
| *A. wiestii* | | | | |
| Steud | w1 | Golestan, Gonbadkavoos | 99147 | Heidari & Koobaz |
| | w2 | Tehran, Tochal | 99149 | Heidari & Koobaz |
| | w3 | Tehran, Darband | 99150 | Heidari & Koobaz |
| | w4 | Golestan,Gonbadkavoos, | | |
| | | Malek-Ali tapeh | 19530 | |
| | w5 | Esfahan,Kashan | 19531 | Iranshahr |
| | w6 | Kerman, Jebalbarez | 19532 | Reshinger & Allen |
| | w7 | Khozestan, Behbahan | 164 | Roohipoor |
| | w8 | Fars, Noorabad-Dogonbadan | | |
| | | road | 38462 | Assadi & Abohamzeh |
| | w9 | Bakhtaran, Halate Mehran | 19535 | Behbodi |
| | w10 | Golestan, Gonbadkavoos | 99148 | Heidari & Koobaz |

*sativa* L. were studied morphologically. Details of the localities and the voucher numbers are presented in Table 1. For morphometric analyses, minimum 10 and maximum 50 plants were studied from each population (in those cases which voucher specimens were studied less than 10 plants were studied). Voucher specimens are deposited in TARI, IRAN and Herbarium of Shahid Beheshti University (HSBU).

### *Morphometry*

In total 45 quantitative and qualitative morphological characters were studied (Table 2). Characters were selected based on those reported by Baum [1,2] and our own field studies (Table 2). For phenetic analyses the mean of quantitative characters were used while qualitative characters were coded as binary/multistate characters [9]. Variables were standardized (mean=0, variance=1) for multivariate statistical analyses [4,11].

In order to group the species having morphological similarities, cluster analysis using single linkage (nearest neighbor), UPGMA (unweighted paired group mean average) and WARD (minimum variance spherical clusters) [5] as well as ordination based on principal component analysis (PCA) were performed [6,10]. The Euclidean distance/squared Euclidean

distance was used as dissimilarity coefficient in cluster analysis of morphological data.

In order to determine the most variable morphological characters among the species/ populations, factor analysis based on principal components analysis (PCA) was performed. Invariable characters were omitted before factor analysis.

**Table 2.** Morphological characters and their coding range

| |
|---|
| 1- Ligule shape at anthesis or younger, 0-1 |
| 2- Ligule length, mm |
| 3- Shape of panicle, 0-1 |
| 4- Length of spikelet without awn, mm |
| 5- No. of florets, 0-5 |
| 6- Glumes relative length, 0-1 |
| 7- Mode of disarticulation (dispersal unit), 0-1 |
| 8- Mode of disarticulation in florets, 0-2 |
| 9- Scar, 0-1 |
| 10- Shape of scar in the first floret, 0-5 |
| 11- Place of awn insertion, 0-5 |
| 12- Shape of tip in lemma, 0-8 |
| 13- Vestiture bellow awn insertion, 0-1 |
| 14- Rows along cilia along edges of keels, 0-2 |
| 15- Type of lodicule, 0-1 |
| 16- Rachila length, mm |
| 17- pedicel length, mm |
| 18- Prickles, 0-2 |
| 19- Anther length, mm |
| 20- Leaf diameter, mm |
| 21- Knee of awn, 0-3 |
| 22- Vestiture back, 0-3 |
| 23- Awn length in the first floret, mm |
| 24- Awn length in the second floret, mm |
| 25- Upper glume length, mm |
| 26- Lower glume length, mm |
| 27- No. of nerves in the upper glume, n |
| 28- No. of nerves in the lower glume, n |
| 29- Lemma length in the first floret |
| 30- Lemma length in the second floret |
| 31- Palea length in the first floret |
| 32- Palea length in the second floret |
| 33- Glume diameter in the upper glume, mm |
| 34- Glume diameter in the lower glume, mm |
| 35- Teeth of lemma ending, mm |
| 36- Stem node indumentum, 0-2 |
| 37- Panicle length, cm |
| 38- Seed length in the first floret, mm |
| 39- Seed length in the second floret, mm |
| 40- Seed diameter in the first floret, mm |
| 41- Seed diameter in the second floret, mm |
| 42- Leaf indumentum, 0-1 |
| 43- Rachis length, cm |
| 44- Callus length, mm |
| 45- Periphery ring, 0-1 |

Canonical discriminant analysis (DA) was performed to check the grouping of the sections against the proposed classification of Baum [2]. For each section, predicted group membership was estimated from canonical discriminant scores using Bayes' rule [7] and checked against actual group membership, followed by grouping of the species based on the first two discriminant factors. Multivariate statistical analyses used STATISTICA version 5 (1995) and SPSS version 9 (1998) softwares.

## Results and Discussion

### *Interpopulation (Intraspecific) Variations*

Cluster analysis and ordination of *A. barbata* populations produced similar results (Fig. 2). Two main clusters/groups are formed in both analyses. The

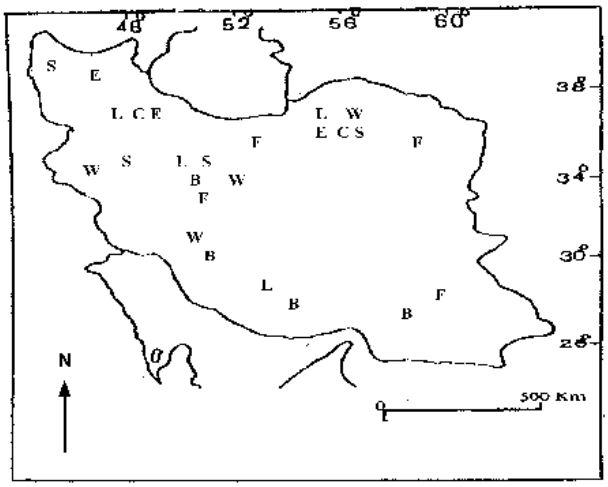



**Figure 1.** Distribution map of the *Avena* species. Abbreviations: B = *A. barbata*, C = *A. clauda*, E = *A. eriantha*, F = *A. fatua*, L = *A. ludaviciana*, S = *A. sativa*, W = *A. weistii*.

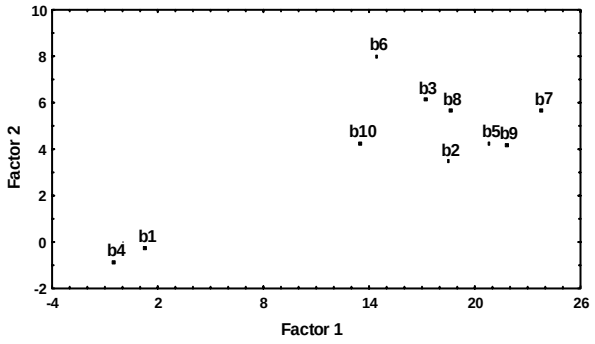



**Figure 2.** Ordination of *A.* barbata populations on the first two PCA axis. Species/populations code as in Table 1.

**Table 3.** Factor loading (showing high correlation) of morphological characters in *A. barbata* populations. Characters as in Table 2

| Character | Factor 1 | Factor 2 | Factor 3 | Factor 4 | Factor 5 |
|---|---|---|---|---|---|
| 2 | -.10824 | .72975 | .55721 | -.14356 | .15653 |
| 4 | .90870 | .13528 | -.18976 | -.00711 | -.26402 |
| 17 | .91069 | .08432 | .17018 | .01841 | .08518 |
| 19 | -.27245 | -.38778 | .11461 | .76234 | .22676 |
| 20 | -.03892 | .83197 | .14827 | .32772 | -.33314 |
| 22 | -.22023 | -.01107 | .11153 | .75636 | -.16414 |
| 23 | .84718 | -.04491 | -.31072 | -.08408 | .29923 |
| 24 | .91610 | .01631 | -.00490 | -.35876 | .14915 |
| 25 | .95158 | .16458 | .04867 | -.07840 | -.07111 |
| 26 | .96740 | .18634 | -.05634 | -.07676 | -.09501 |
| 28 | .51608 | .74591 | -.09887 | .20396 | .20135 |
| 29 | .88284 | .02095 | -.15421 | -.16457 | -.15370 |
| 30 | .96790 | .01223 | -.17644 | -.14978 | .01514 |
| 31 | .98873 | -.00685 | -.02880 | .08256 | .03226 |
| 32 | .92615 | .30642 | .11994 | .09781 | .06884 |
| 34 | .77350 | .22866 | .49318 | -.18350 | .14389 |
| 37 | -.35828 | .79131 | -.12868 | -.17599 | .20053 |
| 38 | .82427 | -.27072 | -.37790 | .04344 | -.14218 |
| 39 | .72689 | -.39077 | -.21061 | .15337 | -.14222 |
| 41 | .40827 | -.78651 | .23684 | -.20795 | .01522 |
| 42 | .52215 | .01096 | .70048 | .39735 | -.12681 |
| 43 | -.19313 | .77008 | .13624 | -.43193 | .01229 |

populations of Ghom and Hoseinabad (b1 & b4) show more similarity in morphological characters and form the first group, while other 8 populations form the second group.

Factor analysis revealed that the first 4 factors comprise about 79% of total variation (Table 3). In the first factor which comprises about 39 % of total variance, characters like the length of palea in the first and second florets, length of the lower glume, pedicel, rachis, seed and size of spikelet possessed the highest correlation (>0.70). This factor separates Ghom and Hoseinabad populations from the others (Fig. 2). The length of rachis, ligule, size of the anther and leaf indumentum showed the highest correlation with the factors 2-4. Therefore these are the most variable morphological characters among *A. barbata* populations. Variation in these quantitative characters may be due to effect of environment in which the plants grow.

Cluster analysis and ordination based on PCA factors of *A. clauda* populations produced similar results (Fig. 3). These Populations due to morphological differences are placed in separate distant clusters/ groups. Such a difference is even present in plants collected from close by localities as observed in Gonbadekavoos populations. Two of these populations are placed close to each other (c1 & c7 in Fig. 3) while the other two are separated from the others (c2 & c4).

Factor analysis of morphological characters revealed that the first 3 factors comprise about 70% of total variance, in which the length and diameter of seed in the first and second florets, length of rachila and the lower glume as well as diameter of upper glume possessed the highest correlation (>0.70). Therefore these are the most variable morphological characters among *A. clauda* populations.

Cluster analysis and ordination based on PCA analysis among *A. eriantha* populations produced similar results (Fig. 4). Three main clusters/groups are formed; populations of Ardebil, Pabo & Dasht1 (e1, e4 & e5 in Fig. 4) form the first group; populations of Maravejtapeh, Dasht 2 & 3 (e3, e6 & e7) form the second group while Parsabad and Darestan (e2 & e8) form the third one.

Factor analysis revealed that the first 3 factors comprise about 71% of total variance. Characters like seed length and diameter in the first and second florets, length and diameter of lower and upper glumes, length of lemma and awn, number of florets, length of callus and anther possessed the highest correlation (>0.70). Therefore these are the most variable morphological

characters among *A. eriantha* populations.

Cluster analysis and ordination based on PCA analysis of *A. fatua* populations produced similar results (Figs. 5 and 6) producing two main clusters/groups. Populations of Kakoli mountain, Zabol, Kharestan, Polesefid and Bagherabad (f1-f4 & f7 in Fig. 5) form the first main cluster/group, while the other populations form the second main cluster. In this cluster, populations of Mahalat, Esfahan and Ghoochan (f6, f8 & f10) show more similarity in morphological characters and form the first sub-cluster, while populations of Varamin and Arak (f5 & f9) form the second sub-cluster.

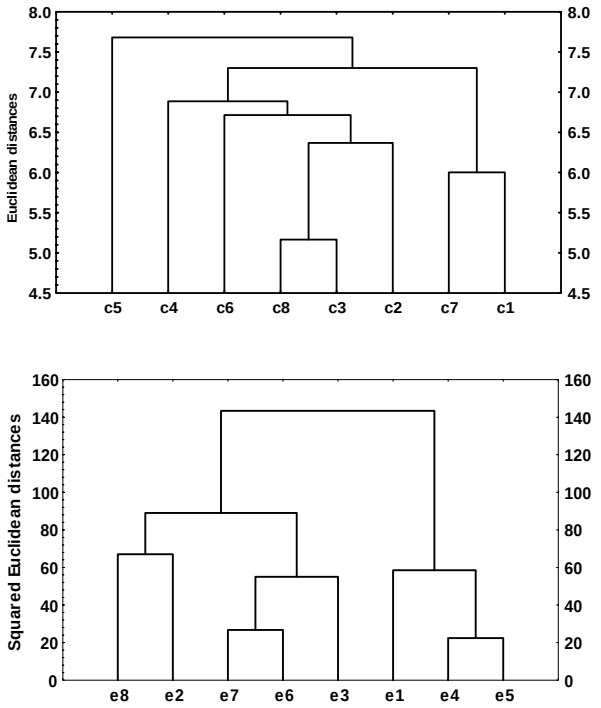
Factor analysis of morphological characters revealed that the first 3 factors comprise about 69% of total variance. In the first factor (which comprises about 44% of total variance), characters like the length of awn in the first and second florets, length of lemma and glume, size of spikelet and anther, possessed the highest correlation (>0.70). This factor separates members of the main clusters of Fig. 5 from each other. In factor 2 (which comprises about 14% of total variance), characters like presence/absence of scar and lodicule spines possessed the highest correlation (>0.70). This factor separates the two sub-clusters of the second main cluster in Figure 5. (i.e. f6, f8 & f10 from f5 & f9).

Cluster analysis and ordination of populations of *A. sativa* produced 2 main clusters/groups (Fig. 7). Two populations of Gonbadekavoos (s2 & s5) showed morphological similarity and form the first cluster, while 3 populations of Karaj, Lorestan and Azarbayejan form the second cluster.

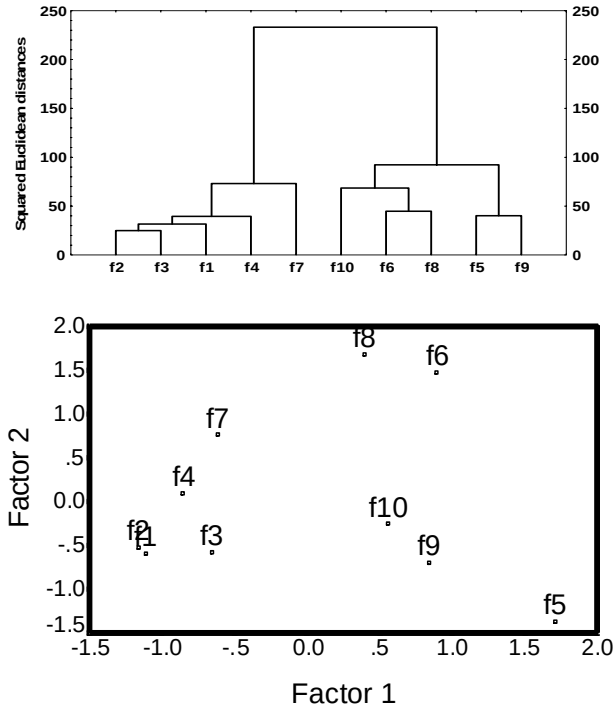
Factor analysis revealed that the first 2 factors comprise about 81% of total variance. In the first factor (which comprises about 64% of total variance), characters like the size and diameter of seed in the first and second florets, length of glume, palea, lemma, awn and spikelet, possessed the highest correlation (>0.70). This factor separates the main two clusters/groups from each other.

Cluster analysis and ordination based on the first two PCA factors of *A. wiestii* populations produced similar results (Figs. 8 & 9). Kerman and Fars populations (w6 & w8 in Fig. 8) form the first cluster and due to morphological difference stand in a separate cluster far from the others. Eight other populations form the second cluster in which Bakhtaran and Khoozestan populations (w9 & w7) are joined to the others with some distance (Fig. 8).

Factor analysis revealed that the first 3 factors comprise about 72% of total variance. In the first factor (which comprises about 46% of total variance), characters like the length and diameter of seed in the




**Figures 3 & 4.** Cluster analysis (single linkage & WARD) of *A. clauda* and *A. eriantha* populations.
Species/populations code as in Table 1.




**Figures 5 & 6.** Cluster analysis (WARD) and ordination of *A. fatua* populations.
Species/populations code as in Table 1.

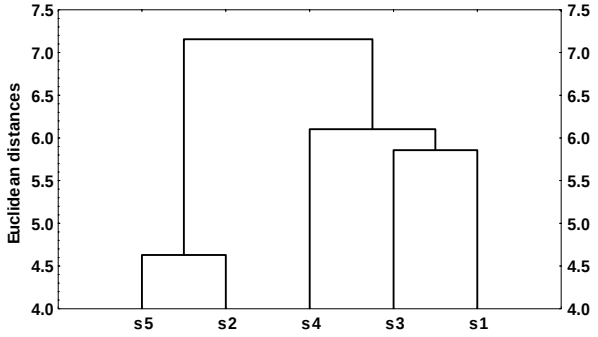
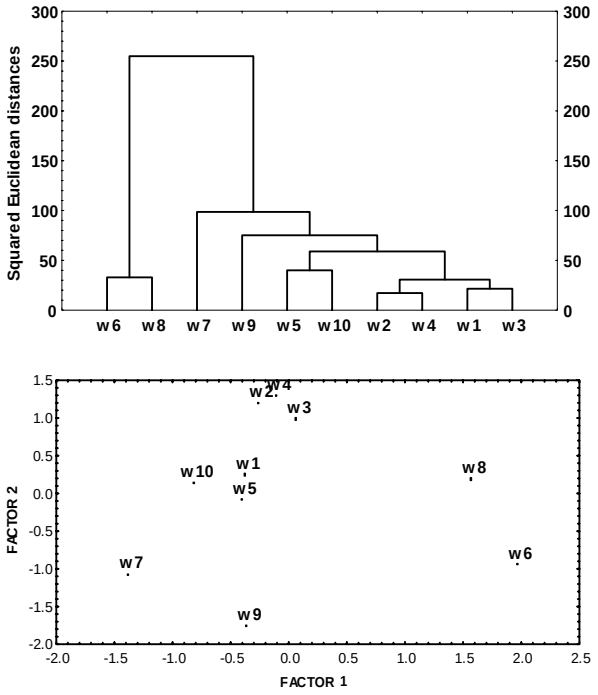



**Figure 7.** Cluster analysis (single linkage) in *A. sativa* populations. Species/populations code as in Table 1.




**Figures 8 & 9.** Cluster analysis (WARD) and ordination of *A. wiestii* populations. Species/populations code as in Table 1.

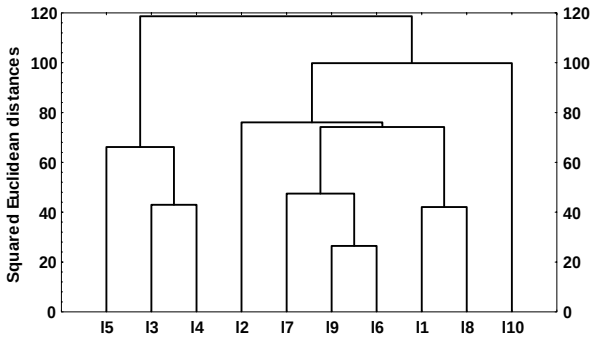



**Figure 10.** Cluster analysis (WARD) of *A. sterilis* ssp. *ludoviciana*. Species/populations code as in Table 1.

first and second florets, length of palea, lemma and glume possessed the highest correlation (> 0.70). This factor separates Kerman and Fars populations from the others (Fig. 9). In the second factor (which comprises about 14% of total variance), length of rachis and spike possessed the highest correlation. This factor separates Bakhtaran and Khoozestan populations from the members of second cluster in Figure 8.

Cluster analysis of *A. sterilis* ssp. *ludoviciana* populations produced two main clusters (Fig. 10), in which two different populations of Golestan along with Tehran population (l3-l5 in Fig. 10) form the first cluster, while the other 7 populations form the second main cluster. Ordination of these populations supported the clustering result.

Factor analysis of morphological characters revealed that the first 4 factors comprise about 70% of total variance. The characters of awn length, glume, spike and rachis, size of spikelet, ligule and anther possessed the highest correlation (> 0.70) in the first factor, while diameter of glume possessed the highest correlation in the second factor.

In general, factor analysis of morphological characters revealed that inter-population variation observed in *Avena* species studied is mainly due to differences in their quantitative characters. Due to lack of difference in qualitative morphological characters as well as chromosome number (unpublished data) among the populations studied, no attempt is made to create a taxonomic group below the species rank.

### *Interspecific Relations*

The species studied here belong to 3 different sections: 1- *A. clauda* and *A. eriantha* belong to the section *Ventricosa* Baum that includes diploid species possessing C genome. 2- *A. wiestii* and *A. barbata* belong to the section *Tenuicarpa* Baum which includes diploid and tetraploid species with AA and AABB genomes. 3- the species of *A. sativa*, *A. sterilis* ssp. *ludoviciana* and *A. fatua* belong to the section *Avena* Baum that includes hexaploid species possessing AACCDD genomes.

The phenogram obtained from cluster analysis and ordination plot based on PCA analysis of 61 populations studied are presented in Figures 11 and 12. Two main clusters are formed separating diploid and tetraploid species from hexaploids. The species of *A. barbata* and *A. wiestii* (tetraploid) are placed close to each other forming the first sub-cluster, while species of *A. clauda* and *A. eriantha* (diploid) form the second sub-cluster.

The major hexaploid species cluster has two sub-clusters. *A. fatua* and *A. sterilis* ssp. *ludoviciana* show

more similarity and form the first sub-cluster, while *A. sativa* stands apart from the other hexaploid species forming the second sub-cluster. Separation of diploid, tetraploid and hexaploid species in different groups supports Baum's classification [2]. However separation of *A. sativa* from the other hexaploid species is complex. The species of *A. clauda* and *A. eriantha*, *A. barbata* and *A. wiestii* as well as *A. sterilis* ssp. *ludoviciana* and *A. fatua* occupy similar geographical areas (Fig. 1) and are placed very close in the cluster analysis and ordination plot. The description of these species share several common features, therefore a comparison of data matrix among the species for quailtative characters and a t-test analysis was performed for quantitative characters between pairs of species.

### *A. clauda and A. eriantha*

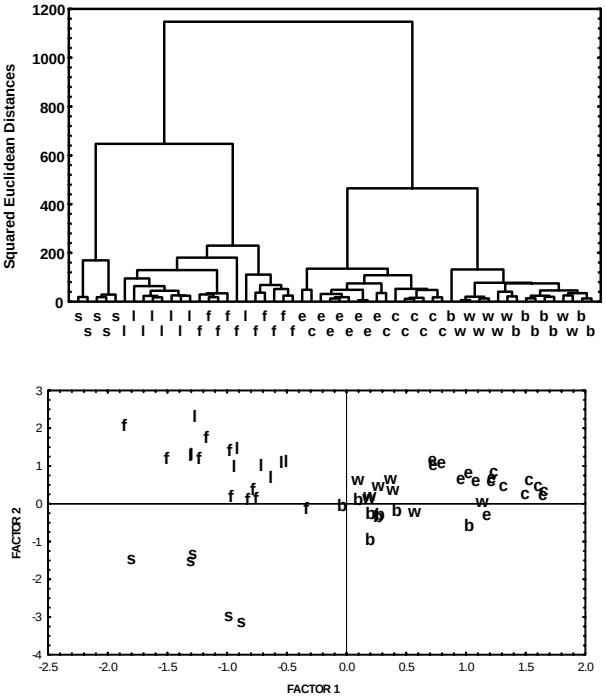
The qualitative characters separating *A. clauda* and *A. eriantha* were as following: Scar was present in all the florets of adult plant in *A. clauda* while it was only present in the last floret of *A. eriantha*. Lodicule spine and leaf indumentum were present in *A. clauda* while absent in *A. eriantha*. The quantitative characteristics of awn, glume and seed showed a significant difference between these two species (Table 4).

### *A. barbata and A. wiestii*

Important qualitative characters separating these two species were as following: place of awn insertion was at 1/3 to 1/4 of lemma in *A. barbata* compared to 1/4 and lower in *A. wiestii*. Lemma of *A. barbata* was biaristulate, while it was biaristulate or bisetulate-biaristulate in *A. wiestii*. Lodicule in *A. barbata* was *A. sativa* type while it was *A. fatua* in *A. wiestii*. The quantitative characteristics of spikelet, awn, lemma and seed showed a significant difference between these two species (Table 5).

### *A. sterilis ssp. ludoviciana and A. fatua*

These two hexaploid species differ mainly in qualitative characters were as following: scar was present in *A. ludoviciana* while absent in *A. fatua*. Place of awn insertion was from 1/3 of lemma in *A. sterilis* ssp**.** *ludoviciana* while it was from 1/3 to 1/4 in *A. fatua*. The length of lemma in the second floret was the only quantitative character showing a significant difference between *A. sterilis* ssp. *ludoviciana* and *A. fatua* (mean value was 10.89 mm in *A. sterilis* ssp. *ludoviciana* and 12.31 mm in *A. fatua*).




**Figures 11 & 12.** Cluster analysis (WARD) and ordination of *Avena* species. Species code as in Table 1.

### *A. sativa and A. sterilis ssp. ludoviciana + A. fatua*

Qualitative characters separating *A. sativa* from *A. ludoviciana* and *A. fatua* were as following: 1-glume was non-disarticulating in *A. sativa* but disarticulating in both *A. sterilis* ssp. *ludoviciana* and *A. fatua*. 2-scar was absent in *A. sativa* while present in both *A. sterilis* ssp. *ludoviciana* and *A. fatua*, 3-the relative length of glumes were equal in *A. sativa* while unequal in both *A. sterilis* ssp. *ludoviciana* and *A. fatua*, 4-A surrounding ring was present in *A. sterilis* ssp. *ludoviciana* and *A. fatua* while absent in *A. sativa* and 5- the lodicules was of *A. sativa* type in *A. sativa* while was of *A. fatua* type in *A. sterilis* ssp. *ludoviciana* and *A. fatua*. *A. sativa* differ significantly from *A. sterilis* ssp. *ludoviciana* in several quantitative morphological characters such as length of lemma and palea as well as diameter of glume.

Baum [2] states that although most *Avena* species are very similar to each other in their general habit and gross morphology, using the micromorphologic criteria appear to be the most definitive and immediate methods for recognizing the specific taxa of *Avena*. He used Stabrool's method of character analysis and considered morphological characters such as type of lodicule, type and size of epiblast, mode of disarticulation, relative length of glumes, shape of scars, configuration of

lemma tip, vestiture of back of palea and some few more characters important for the formulation of the *Avena* species.

Difference in qualitative morphological characters among *A. sativa* and two other hexaploid species of *A. sterilis* ssp. *ludoviciana* and *A. fatua* as well as their separation in cluster analysis/ordination plot may suggest inclusion of *A. sativa* in a separate sub-section from *A. sterilis* ssp. *ludoviciana* and *A. fatua*.

In order to determine the most variable morphological characters among *Avena* species studied here, factor analysis based on PCA was performed after varimax rotation. Analysis revealed that the first 4 factors comprise about 61% of total variance in which characters like relative length of glumes, scar, lemma tip, vestiture bellow awn insertion, type of lodicule, leaf indumentum and periphery ring showed the highest correlation (Table 6). Quantitative features of spikelet, pedicel, awn, glumes and seed also showed high correlation with these factors. Therefore these morphological characters show variation among the species studied and are in agreement with those reported by Baum and adding a few more quantitative characters.

### *Inter-Sectional Relationships*

An attempt was made to investigate the inter-sectional relationships as revealed by multivariate statistical analysis using the present data and those reported by Baum [2]. For this purpose a pooled data matrix of 17 characters X 35 OTUs was formed which was used in a canonical discriminant analysis (DA). The groupings obtained (Fig. 13) supports that of Baum [2], separating almost the 7 different *Avena* sections into different groups. However a better separation of sections *Avenotrichon*, *Ventricosa* and *Agraria* (sections 1-3 in Fig. 13) is observed. Some members of sections *Tenuicarpa*, *Ethiopica*, *Pachycarpa* and *Avena* (sections 4-7 in Fig. 14) show mixed distribution.

The actual membership of the OTUs versus their predicted group membership (sections) produced 100% correct classification for all the sections except sections 4 and 7 (*Tenuicarpa* & *Avena*) with about 91% correct classification. It is interesting to see that *A. sativa* specimens included in the analysis (from present study and that of Baum) are separated from the other members (numbers 34 and 35 in Fig. 14) of section *Avena* and may support inclusion of *A. sativa* in a new sub-section as suggested earlier.

According to Baum [1], characters which on intuitive grounds or after character analysis exercise are thought to be most important for discrimination between OTUs, are not necessarily most important for discrimination between grouping of the OTUs. In the *Avena* data, the "good" characters by which the species can be keyed out, do not possess at all the same discriminatory capacity for the sections [1].

In short, the main findings of the present study may be summarized as: 1- intraspecific morphological variations observed in *Avena* species are due to quantitative characters. 2 - phenetic analyses of morphological characters grouped diploid, tetraploid and hexaploid species in distinct clusters/groups supporting Baums' classification. 3 - morphological characters for distinguishing studied *Avena* species are presented.

**Table 4.** Quantitative characters showing significant difference between *A. clauda* and *A. eriantha*

| Character | Mean value | |
|---|---|---|
| | *A. clauda* | *A. eriantha* |
| Length of rachila | 1.08 ± 0.20 | 2.20 ± 0.10 |
| Length of awn in The first floret | 35.31 ± 0.21 | 40.76 ± 0.18 |
| Length of awn in The second floret | 31.46 ± 0.23 | 35.95 ± 0.20 |
| Number of lines on the lower glume | 3.00 ± 0.17 | 3.75 ± 0.21 |
| Diameter of upper Glume | 4.61± 0.20 | 5.50 ± 0.14 |
| Diameter of lower Glume | 2.43 ± 0.19 | 3.14 ± 0.20 |
| Diameter of seed in the first floret | 0.98 ± 0.09 | 1.36 ± 0.10 |
| Diameter of seed in the second floret | 0.80 ± 0.08 | 1.07 ± 0.09 |
| Callus length | 1.45 ± 0.20 | 2.28 ± 0.17 |

**Table 5.** Quantitative characters showing significant difference between *A. barbata* and *A. wiestii*

| Character | Mean value | |
|---|---|---|
| | *A. barbata* | *A. wiestii* |
| Length of spikelet | 18.25-23.20 | 19.80-23.00 |
| Length of pedicel | 1.52 ± 0.18 | 1.56 ± 0.10 |
| Length of awn in The first floret | 32.33 ± 0.34 | 35.77 ± 0.27 |
| Length of lemma in The second floret | 13.57 ± 0.19 | 14.94 ± 0.10 |
| Diameter of seed in the first floret | 1.27 ± 0.07 | 1.04 ± 0.08 |

**Table 6.** Factor loading (showing high correlation) of morphological characters in *Avena* species. Characters as in Table 2

| Character | Factor 1 | Factor 2 | Factor 3 | Factor 4 |
|---|---|---|---|---|
| 4 | .82557 | .26259 | -.10541 | -.16876 |
| 6 | -.62053 | .43639 | -.49663 | -.32780 |
| 7 | -.17122 | .80165 | .53255 | .04980 |
| 8 | -.13097 | -.01370 | .68623 | -.25362 |
| 9 | -.04498 | .61477 | -.02589 | .14786 |
| 10 | -.17122 | .80165 | .53255 | .04980 |
| 12 | .00525 | -.02202 | -.10895 | .63595 |
| 13 | .47709 | .06233 | .77286 | .33393 |
| 15 | .05455 | .76405 | -.24624 | .21212 |
| 17 | .72590 | .05455 | -.20141 | .10064 |
| 23 | .44509 | .71167 | .07099 | -.13015 |
| 24 | .13831 | .87072 | .30674 | -.07848 |
| 25 | .79699 | .24302 | -.15184 | -.20263 |
| 26 | .90963 | -.13372 | .27846 | .14290 |
| 27 | .66213 | -.34291 | .14778 | .39486 |
| 28 | .75293 | -.38544 | .30925 | .35420 |
| 30 | .34652 | .65759 | .04342 | -.43503 |
| 31 | .89212 | -.03292 | .06661 | -.00061 |
| 32 | .84892 | .30046 | .06566 | .11978 |
| 33 | .70517 | -.19315 | -.41505 | .24154 |
| 34 | .80326 | -.39348 | .08923 | .28709 |
| 35 | -.50028 | .44172 | .03292 | -.61335 |
| 37 | .73955 | -.09796 | -.12060 | -.04231 |
| 38 | .65688 | .10537 | -.09131 | .45164 |
| 39 | .80318 | -.03948 | .18126 | .25268 |
| 40 | .65073 | -.06782 | -.18081 | .50552 |
| 41 | .67364 | .00946 | -.02912 | .46487 |
| 42 | -.01345 | .12267 | .71479 | -.14545 |
| 43 | .72230 | -.01708 | -.01160 | -.09723 |
| 45 | -.17122 | .80165 | .53255 | .04980 |

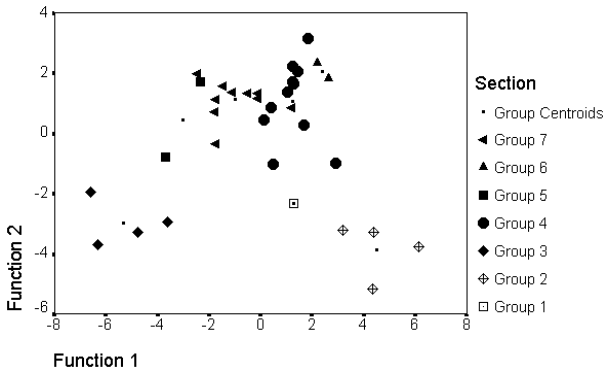



**Figure 13.** Grouping of the *Avena* sections based on DA. Sections: 1- *Aventrichon* (Holub) Baum, 2- V*entricosa* Baum, 3- *Agraria* Baum, 4-Tenuicarpa Baum, 5- *Ethiopica* Baum, 6- *Pachycarpa* Baum and 7- *Avena* Baum.

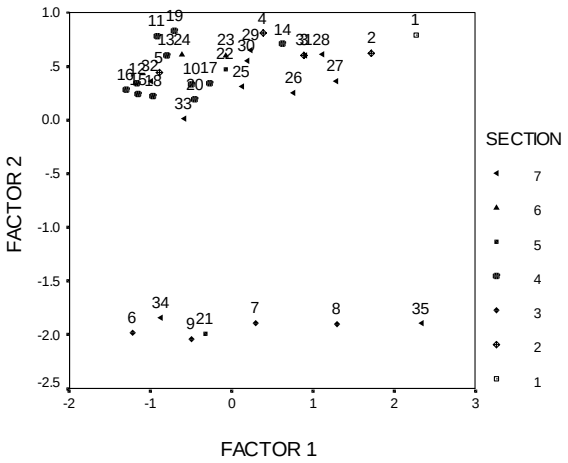



**Figure 14.** Ordination of the *Avena* species/populations based on factor analysis.

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