

Study of Morphological Traits of Secondary *Tritipyrum* genotypes

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Abstract: Soil salinity is an increasing threat for agriculture and is a major factor in reducing plant productivity; therefore, it is necessary to obtain salinity-tolerant varieties. Intergeneric hybridization is one way to transferring desirable genes into field crops. *Tritipyrum* is a new salt tolerant that produced from crossing between wheat cultivars and *Thinopyrum bessarabicum*. *Tritipyrum* genotypes have undesirable traits. In order to improve primary *Tritipyrum* lines by D genome, 21 crosses between 6x bread wheat cultivars (2n=6x=42, AABBDD) and primary *Tritipyrum* lines (2n=6x=42, AABB^bE^b) was carried out and 49 F₁ seeds was produced. F₁ seeds were sown and following were measured some morphological traits. Cluster analysis by Ward method established three groups. Factor analysis showed three factors defined 68.61 percent data variation, as a whole. Share of each factor from first to third is 36.14, 20.53 and 11.94 percent, respectively.

Key words: Tritipyrum • Factor analysis • Cluster.

INTRODUCTION

Agricultural productivity is severely affected by soil salinity because salt levels that are harmful to plant growth affect large terrestrial areas of the world [1]. *Thinopyrum bessarabicum* is an osmo conformer, being able to with stand up to 350 mol/m³ of NaCl and have the potential to play a major role in the production of salt tolerant wheat, through gene introgression and the production of a new salt-tolerant cereal, *Tritipyrum* [2]. A new cereal, *Tritipyrum*, is a amphiploid between *Triticum spp.* and *Thinopyrum spp* [3]. Although *Tritipyrum* has brittle rachis and meiotic instability but it is an important crop for breeding because of its desirable traits such as salt tolerant and multiple pistil seed character [3]. These problems might to overcome through substitution of E^b genome chromosomes by D genome chromosomes, particularly the substitution of 5E^b chromosome with 5D chromosome in wheat, which carrying a dominant gene/s for salt tolerant [3].

Various algorithms have been used in studying of genetic diversity in cluster analysis of which, UPGMA and Ward's methods are the most popular approaches. Of the algorithms, UPGMA, Ward's, SLINK and CLINK, applied for cluster analysis and exploring genetic diversity and grouping of plant materials in the past,, the UPGMA

is the most valid method in accordance with the relationship of family based on their genetic material [1]. Estimation of genetic distance is one of appropriate tools for parental selection in wheat hybridization programs. Some appropriate methods, cluster analysis, PCA and factor analysis, for genetic diversity identification, parental selection, tracing the pathway to evolution of crops, centre of origin and diversity and study interaction between the environment are currently available [1,4]

Factor analysis is used to reduce number of variables into some hidden factors, as well as to identify principal components of the yield, to classify traits on the basis of intra-relations between them and to research genetic diversit [5] so Factor analysis can be complementary of stage regression analysis and path coefficient analysis and presents additional information [1].

The present study was performed to determine most effective traits to improve *Tritipyrum* genotypes yield.

MATERIALS AND METHODS

Materials: Iranian 6x bread wheat cultivars (male: Omid, Navid, Roshan, Alvand, Catlicum, Double haploid, Kavir, Nichnejad, Chamran, Morvarid, Sefidkhosheh, Okta, Bahareh Baft, Falat, Kerifla)

Primary 6x Tritipyrum cultivars [female: (Ka/b)(Cr/b), (Ka/b)(Cr/b)[F₂] (Ka/b)(Cr/b)[F₃] Ka/b, St/b, Cs/b, Ne/b, Ma/b, Az/b, Cr/b, La/b, La(4B/4D)/b, (Ma/b)(Cr/b),(St/b)(Cr/b)]

The crossing program with 14 primary 6x *Tritipyrum* lines (female) and 15 hexaploid wheat cultivars (male) was carried out in south east of Iran, SBUK university (Table 1). Female parents were sown at December 2007 and their spikes were emasculated, then pollinated by fresh pollen from male wheat cultivars about 1 to 3 days after emasculation. F₁ seeds were sown at 2008 and following traits were measured No. of tillers, plant height, stem length, No. of leafs, No. of nods, inter nod length, flag leaf length, flag leaf width, No. of spikes, No. of spikelets/spike, awn length, spike diameter and leaf (before flag leaf) length. Cluster analysis based on Wards method and factor analysis were performed using the statistical software SAS program.

RESULTS AND DISCUSSION

From 21 crosses between primary 6x *Tritipyrum* and 6x Iranian bread wheat cultivars (Table 1), 49 F₁ seeds were obtained, particularly from 6x bread wheat (cv; Omid) with all primary 6x *Tritipyrum* lines which showed the relatively adequate cross ability between parents and also indicates that producing NPSSTIG genotypes is feasible. The data matrix of average values for 26 samples (cultivars and harvests) for all 13 variables was analyzed by the cluster analysis (Fig.1). Results of Cluster analysis by Ward method established three groups. The first group contain 7 genotypes:omid×St/b, Navid×La/b, Navid×(Ka/b)(Cr/b), Navid×(St/b)(Cr/b), Navid×Az/b and Navid × (Ma/b)(Cr/b). genotypes of first group have higher mean in number of tillers, number of spike and

leaf(befor flag leaf) length traits. The second group contain 12 genotypes: Omid×Cr/b, Omid×St/b, Omid×La/b, Omid×Az/b, Omid× (St/b)(Cr/b), Roshan× (Ka/b)(Cr/b), Bahareh Baft× (St/b)(Cr/b).genotypes of second group have higher mean in plant height, number of leaves, number of nodes, number of spikelets/spike and awn length traits. third group contain 7 genotypes: Omid×Az/b, Alvand×Ma/b, Okta×St/b, Roshan×Ne/b, Roshan× (Ka/b)(Cr/b), Chamran×Cr/b and Kerifla×La/b. genotypes of this group have higher mean in number of tillers, plant height, stem length, number of leaves, number of nodes, inter node length, flag leaf length, flag leaf width, number of spikes, number of spikelets/spike, awn length, spike diameter traits.

Factor analysis was used to evaluate and comprehend complex relations of traits, as well as to identify hidden factors. Factor analysis complemented on the basis of special values which are larger than one and was done by considering three factors. These three factors justified 68.61 percent data variation, as a whole. Share of each factor from first to third is 36.14, 20.53 and 11.94 percent, respectively. Factor analysis results show that first factor has positive factorial coefficients for plant height, stem length, number of leaves, inter node length, flag leaf length, number of spikletes/spike and awn length. The second factor has positive coefficients for number of tillers, flag leaf width, number of spikes and leaf (before flag leaf) length. The third factor has positive factorial coefficients for stem length, flag leaf width and spike diameter.

Walton [10] used factor analysis to identify growth and morphological traits relevant to yield in spring wheat and they introduced four factors which include yield components, morphological traits, spike.

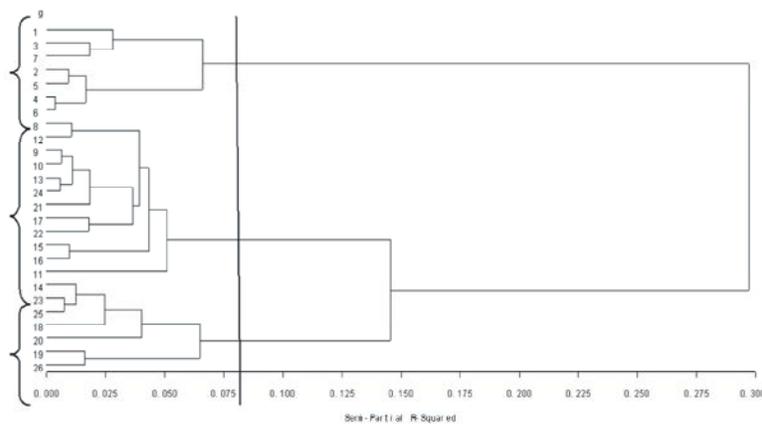


Fig.1: The diagram of 26 genotypes for 13 studied variable using cluster analyzing (Ward method).

Table 1: F₁ seeds derived from crossess between 6x bread wheat with 1 primary 6x Tritipyrum lines.

Crosses	F ₁	Crosses	F ₁	Crosses	F ₁
Omid× (St/b)(Cr/b)	3	Omid×(Ka/b)(Cr/b)[F5]	1	Caticum×St/b	1
Omid×Ne/b	2	Omid×Cr/b	2	Caticum× La(4B/4D)/b	1
Omid×Ka/b	2	Omid×La(4B/4D)/b	2	Navid×(Ka/b)(Cr/b)	5
Omid×St/b	2	Alvand×(Ma/b)(Cr/b)	1	Navid×Ka/b	4
Omid× (Ma/b)(Cr/b)	2	Alvand×Ka/b	4	Roshan×(Ka/b)(Cr/b)	3
Omid×(Ka/b)(Cr/b)	2	Alvand× La(4B/4D)/b	2	Roshan×Ne/b	1
Omid×Az/b	7	Caticum×La/b	1	Roshan×Cr/b	1
Total	20			13	16

Table 2: The results of Factor analysis

Traits	Factor 1	Factor 2	Factor 3
No. of tillers	-0.31	0.77	0.23
Plant height	0.79	0.22	0.36
Stem length	0.66	0.14	0.50
No. of leaves	0.67	-0.40	0.27
No. of nodes	0.53	-0.23	0.43
Inter nod length	0.63	0.45	-0.15
Flag leaf length	0.62	0.47	-0.26
Flag leaf width	0.56	0.51	-0.50
No. of spikes	-0.27	0.80	0.32
No. of spikelets/spike	0.77	0.13	0.05
Awn length	0.86	-0.20	-0.40
Spike diameter	0.27	0.13	-0.50
Leaf(befor flag leaf) length	-0.41	0.59	0.18
Eigen value	4.69	2.66	1.55
Proportional Variance	36.14	20.53	11.94
Cumulative Proportional Variance	36.14	56.07	68.61

REFERENCES

- Mollasadeghi, V., R. Shahryari, A.A. Imani and M. Khayatnezhad, 2011. Factor Analysis of Wheat Quantitative Traits on Yield under Terminal Drought. *American-Eurasian J. Agric. and Environ. Sci.*, 10(2): 157-159.
- King, I.P., C.N. Law and K.A. Cant, 1997. *Tritipyrum*, a potential new salt-tolerant cereal. *Plant Breeding.*, 116: 127-132.
- Hassani, H.S., P.D. Caligair and T. Miller, 2003. The chromosomal assessment of salt tolerant substituted *Tritipyrum* using genomic fluorescent in situ hybridization. *Iranian J. Biotechnol.*, 1(3): 169-178.
- Eivazi, A.R., M.R. Naghavi, M. Hajheidari, S.M. Pirseyedi, M.R. Ghaffari, S.A. Mohammadi, I. Majidi, G. H.Salekdeh and M. Mardi, 2007. Assessing wheat (*Triticum aestivum* L.) genetic diversity using quality traits, amplified fragment length polymorphisms simple sequence repeats and proteome analysis. *Ann. Appl. Biol.*, 152: 81-91.
- Azizi, F., A.M. Rezaie and A.M. Mir Mohammadi Meibodi, 2001. Evaluation genetic and phenotypic variation and factor analysis on morphological traits in bean genotypes, *J. Science and Technology of Agriculture and natural Resources*, 5: 127-140.