

IDENTIFICATION OF SUPERIOR WHEAT GENOTYPES USING MULTIPLE-TRAIT SELECTION METHODS BASED ON AGRONOMIC CHARACTERS AND GRAIN PROTEIN CONTENT UNDER RAIN-FED CONDITIONS

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Several plant breeding methods have been successfully used to improve genetic resources in many crops such as wheat. However, selection of genotypes based on multiple traits is a complex task for the breeders. The selected genotypes should display high performance in a series of desired traits. The GT-biplot and the multiple selection index have been proposed to identify a superior genotype based on various desired traits. In the present study, thirty wheat genotypes were assessed using randomized complete block design with three replications under rain-fed conditions to evaluate the genotypes by using two different multiple-trait selection methods (i.e. the GT-biplot and the multiple selection index) for agronomic traits and grain protein content. Results indicated that almost the same genotypes (G7, G9 and G16) were selected as superior entries by the both methodologies. Among the superior selected genotypes, the entries G9 (394.6 gr/m²) and G16 (388.9 gr/m²) showed higher grain yield. Furthermore, the entry G7 had the highest level of grain protein (15.91%) in the flour and the entry G18 (40.9%) revealed highest harvest index. In addition, the both methods were appropriate to identify superior wheat genotypes based on the multiple traits but the multiple selection index could be simpler and fast, if proper weights would be selected.

Key words: Genotypes x traits, GT-biplot, Multiple selection index, Selection indices, Superior wheat genotype

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the major staple food and the most nutritious cereal among others for billions of people in the world (FAO, 2013; NAWAZ *et al.*, 2020; POSPISIL *et al.*, 2020). The grains contain 60–75% starch and 10–18% protein (ŠRAMKOVÁ *et al.*, 2009). The

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gluten proteins in the seed endosperm impart to wheat dough stickiness and unique bread-baking qualities (ŠRAMKOVÁ *et al.*, 2009). The human population is growing very fast. The estimation showed that with current projections will be more than nine billion by 2050 (GERLAND *et al.*, 2014). During the last century, a lot of precious research projects were done in the domain of wheat breeding through genetic manipulations. However, increasing world population and changing the community needs will cause the breeders to speed up their efforts to develop food products. One of the main challenges of the coming decades will be imperative to ensure food security. While production should to be increase, also the quality must be maintained (BATTENFIELD *et al.*, 2016). Maintaining these two together is a major challenge for the breeders. In most plant breeding programs grain yield is used as the only selection index and other quantitative or qualitative features are less considered, simultaneously. An “ideal” genotype must show superior levels for a number of target traits (YAN and FREGEAU-REID, 2018). Two basic approaches for selecting the ideal genotype are presented, (i) independent culling which is discard a genotypes with the below minimum value requirement for a trait, no matter, how the genotype is good for the other traits. (ii) Index selection which is ranking the genotypes based on an index that is a linear combination of the desired traits (YAN and FREGEAU-REID, 2018; XU *et al.*, 2017; YAN *et al.*, 2008). The use of a selection index was originally proposed by SMITH (1936). He argued that since genotypic worth could not be directly evaluated, it might be best estimated by a linear function of observable phenotypic values. BAKER (1986) declared that the maximum response to index selection will be achieved if the correlation between genetic worth and the index is maximized. Instead of using direct selection of different traits in different plants, plant breeders have had more success using the index selection to gain expected responses (GRAVOIS and MCNEW, 1993; JANNINK *et al.*, 2000). The weights and culling points can vary in different studies based on researcher’s views. Obviously, giving different weights to the desired traits can lead to different results. The genotype \times trait (GT) biplot analysis is a different method were used by YAN and RAJCAN (2002) as a graphical tool for analysis of multi-trait dataset. The GT biplot could be used by three major goals: first, evaluation of genotypes on the basis of multiple traits; second, visualization of the genotype by trait relationships; and third, illustration of genetic correlation among traits (YAN and FRÉGEAU-REID, 2008). Selection technique has been applied to evaluate the genotypes on the basis of multiple traits in wheat (SABAGHNIA and JANMOHAMMADI, 2014), durum wheat (MOHAMMADI and AMRI, 2011), rice (SABOURI *et al.*, 2008; SAMONTE *et al.*, 2013), canola (DEGHANI *et al.*, 2008), maize (HEINZ *et al.*, 2012; SAFARI DOLATABAD *et al.*, 2010), oat (YAN and FRÉGEAU-REID, 2008), sugar beet (OBER *et al.*, 2005), and papaya (VIVAS *et al.*, 2012). The objectives of this study were (i) assessment of the relationships among important agronomic traits by GT biplot, and (ii) to select superior genotype based on multiple traits by two different methods i.e. the multiple selection index and the GT-biplot (iii) comparing two methodologies and determining the advantages of one over the other.

MATERIALS AND METHODS

Plant Materials and Experimental field

The rain-fed experiment was carried out at research farm of Razi University, Kermanshah, located in west of Iran (47° 20' N latitude, 34° 20' E longitude and 1351.6 m altitude) in 2010-2011. Climate in the region is classified as semi-arid with mean annual rainfall

of 478 mm. Minimum and maximum temperature at the farm were -27 and 44°C, respectively. Each genotype planted in 3×1.25 m plot with 25 cm inter-row distances. The soil texture of the research farm was sandy-loam. Thirty wheat genotypes (Table 1) were planted in randomized complete block design (RCBD) with three replications. Seeds were pretreated with the commercial fungicides to minimize the probability of seed- and soil-borne diseases. The seeds planted in early October 2010 and harvested in late July 2011. The grain yield and yield components measured from two meters of two middle rows of each plot at harvest time. Phenotypic data were collected for grain yield per square meter (GYld), 1000-grain weight (TGW), number of spikes per square meter (NSPM), number of seeds per spike (NSPS) and biomass per square meter for calculating harvest index (HI). The harvest index was derived from the percentage of division of grain yield on biomass. Total nitrogen in the grain flour was determined calorimetrically after Kjeldahl digestion with peroxymonosulfuric acid (HACH *et al.* 1985). Briefly, the grain flour was weighed in an analytical balance with a sensitivity of 0.001 g, and placed in a digestion flask. 4 ml concentrated H₂SO₄ were added to each flask. Digestion was carried out at 430°C until the solution was completely clear. In the early stages of digestion, 8 ml of hydrogen peroxide was added to the flask in several parts. The digestion was complete after 8- 10 minutes. The volume was brought to 100 ml with distilled water after the digestion flask reached room temperature. A 0.5 ml aliquot of the digest was withdrawn and mixed with 24.5 ml of a 0.1 g⁻¹ polyvinil alcohol solution and 1.00 ml of Nessler's reagent. The absorbance of samples recorded at 450 nm. The absorbance was converted into concentration by means of a linear calibration curve. The grain protein content (GPC) or crude protein (CPr) was calculated as $N \times 5.7$.

Table 1. Thirty bread wheat genotypes used for rain-fed environment.

Code	Pedigree	Code	Pedigree
G1	F103-L-1-12//PONY/OPATA	G16	Pishtase
G2	OR F1.158/FDL//BLO/3/SH14414/CROW/4/C ICWH99381-0AP-0AP-OMAR-6MAR	G17	KAR-1//RMNF12-71/JUP'S'
G3	PYN/BAU//VORONA/HD2402	G18	QAFZAH-25
G4	KATILA-13	G19	Marvdasht
G5	Pishgam (Bkt/Zhong)	G20	Chamran
G6	Zarin	G21	M-81-13
G7	CA8055//KS82W409/STEPHENS	G22	TEVEE'S//CROW/VEE'S'
G8	Bolani	G23	M-83-17
G9	Shahriar	G24	M-83-6
G10	WS-82-9	G25	M-82-6
G11	SABALAN/4/VRZ/3/OR F1.148/TDL//BLO	G26	Jcam/Emu"s"//dove"S"/3/Alvd/4/MV17/Attila
G12	KARIM	G27	Shiraz
G13	Atila2/PBW65	G28	STAR/SHUHA-4
G14	KAUZ'S/MACHETE	G29	KATILA-1
G15	M-79-7	G30	Pishgam (Bkt/Zhong)

Statistical analysis

Analysis of variance (ANOVA) was performed using SAS software (SAS INSTITUTE, 2003) and the differences between means were compared using least significant difference (LSD) test at the 0.05 and 0.01 probability level. In this study, data presented as mean values for each trait. The grain yield (Gyld), 1000-grain weight (TGW), number of spikes per square meter

(NSPM), number of seeds per spike (NSPS), harvest index (HI) and grain protein content (GPC or CPr) ranked according to their trait values. To evaluate the genotypes, multiple selection index (MSI) were calculated based on standard data according to below formula:

$$MSI_i = \frac{(w_1 p_{i1}) + (w_2 p_{i2}) + \dots + (w_j p_{ij})}{w_1 + w_2 + \dots + w_j} = \sum w_j p_{ij} / \sum w_j$$

Where w_i is weight factor for each trait, p_{ij} is standardized phenotypic value of each trait for each genotype and MSI_i is the multiple selection index value for each genotype (SMITH, 1936). Given that the phenotypic values (p_{ij}) should be unitless, standardization was done using the following formula:

$$p_{ij} = \frac{x_{ij} - x_{min}}{x_{max} - x_{min}}$$

where x_{ij} is the mean value of genotype i and trait j , x_{min} and x_{max} are the minimum and maximum values for the same trait, respectively. Due to the main target which was to enhance the grain yield and the sub-targets that were to improve the yield components and the protein content of flour, the relative weight for each trait (w_i) is the coefficient of multiple determination (R^2) of these traits which was computed by regressing of each of the traits with other traits (RENCHER, 2002). The multiple selection index computed by the excel software. The GT biplot method proposed by YAN and RAJCAN (2002) was used to investigate genotype and trait interactions. The used statistical model is based on the following formula:

$$\frac{T_{ij} - \bar{T}_j}{S_j} = \sum_{n=1}^2 \lambda_n \xi_{in} \tau_{jn} + \varepsilon_{ij}$$

where T_{ij} is the mean value of genotype i for trait j , \bar{T}_j is the mean value of all genotypes in trait j , S_j is the standard deviation of trait j between the genotype means, λ_n is the singular value for principal component n , ξ_{in} and τ_{jn} are scores for genotype i and trait j on principal component n , respectively, and ε_{ij} is the residual associated with genotype i in trait j . A GT-biplot is constructed by plotting the first principal component (PC1) scores of the genotypes and the traits against their corresponding scores for the second principal component (PC2) resulting from singular-value decomposition (SVD) of trait-standardized data. In the "Relationship between testers" view of the GT-biplot, the correlation coefficient between any two traits is approximated by the cosine of the angle between their vectors. Due to the different units of different traits, the standardization is necessary to remove the units. The GenStat 12th edition software was used for GGE biplot analysis.

RESULTS AND DISCUSSIONS

Analysis of variance (Table 2) indicated that the wheat genotypes differed significantly for grain yield (Gyld), harvest index (HI), number of seeds per spike (NSPS), number of spikes per square meter (NSPM) and 1000-grain weight (TGW). Grain protein content (GPC) was not statistically significant among the genotypes but used in further analysis. The predicted relative

weight values for the multiple selection index of SMITH (1936) show the impact of each trait on the final genotype selection (Table 3).

Table 2. Analysis of variance (ANOVA) for 30 wheat cultivars under rain-fed condition.

SV	df	GYld	HI	NSPM	NSPS	TGW	GPC
Block	2	12239	9.85	3224	133.3*	6.66	30.6**
Genotype	29	8109*	61.10*	13547*	117.8**	39.37**	1.91
Error	58	4454	32.63	7154	31.48	7.25	1.2
CV%		22.27	18.52	16.86	14.12	11.51	7.57

GYld: grain yield; HI: harvest index; NSPM: number of spikes per square meter; TGW: 1000-grain weight; NSPS: number of seeds per spike; GPC: Grain protein content; * significant at the 5%; ** significant at 1% probability levels; ns: non-significant.

The highest relative weight values were assigned to the grain yield (0.93) and the 1000-grain weight (0.91). So, the grain yield and the 1000-grain weight were the most important factors affecting the selection of genotypes based on multiple traits. On the other hand, grain protein content and harvest index with the lowest relative weight values (0.28 and 0.47, respectively), which make them smallest influencing factor on selection of superior genotypes (Table 3). YAN *et al.* (2018) states that the 1000-grain weight and the number of seeds per spike is highly correlated with grain yield in the semi-arid region and can be used as selection indicators for wheat breeding in these regions. However, one of the important goals of wheat breeding for rain-fed production, in addition to developing high yielding genotypes, is good flour quality due to increased protein content in grains (TADESSE *et al.*, 2017). Also they stated that harvest index could be an important trait when all available water is exhausted in the final growth season. Among 30 studied wheat genotypes, the entries G7, G9, G16 and G18 occupied highest performance in all traits based on computed multiple selection index (Table 3 and Figure 1).

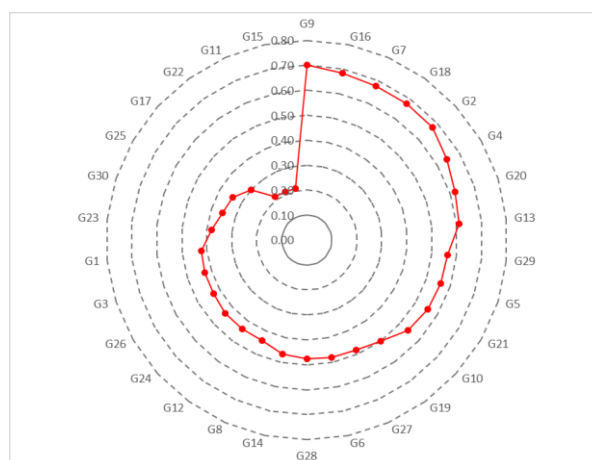


Figure 1. Multiple selection index of 30 wheat genotypes for six desired traits

Table 3. Means, relative weight and the multiple selection index (MSI) computed according to SMITH (1936) and ranked based on MSI of the 30 wheat genotypes

Traits name:	GYld	HI	NSPM	NSPS	TGW	GPC		
Relative weight:	0.93	0.47	0.87	0.90	0.91	0.28		
Gen ID	GYld (gr/m ²)	HI (%)	NSPM	NSPS	TGW (gr)	GPC (%)	MSI	Ranked
G1	279.59	28.92	548	40.84	18.63	14.11	0.42	23
G2	376.52	31.39	580	35.64	28.15	14.31	0.67	5
G3	273.54	29.03	493	39.46	21.4	15.71	0.43	22
G4	336.16	35.45	564	27.54	32.53	14.51	0.64	6
G5	331.00	36.80	401	45.72	25.83	15.05	0.56	10
G6	308.12	29.06	392	53.29	22.17	14.75	0.48	15
G7	377.19	31.30	539	43.2	24.28	15.91	0.68	3
G8	274.57	30.27	525	36.09	23	14.62	0.44	18
G9	394.60	33.00	509	45.83	25.45	15.17	0.70	1
G10	325.63	34.48	371	46.53	28.07	14.44	0.54	12
G11	204.75	26.13	412	40.29	18.87	14.54	0.21	29
G12	290.24	27.98	596	32.42	22.3	13.16	0.44	19
G13	349.44	33.91	532	35.92	27.78	13.97	0.61	8
G14	293.55	33.33	591	36.18	20.8	12.52	0.47	17
G15	210.12	26.91	437	39.35	19.08	13.02	0.21	30
G16	388.89	32.01	531	42.9	25.65	14.92	0.68	2
G17	242.05	22.42	529	31.81	21.77	13.81	0.30	27
G18	360.53	40.90	563	36.45	26.77	13.96	0.67	4
G19	294.71	27.43	534	49.54	19.5	14.21	0.50	13
G20	326.28	38.95	481	35.83	29.42	15.77	0.62	7
G21	312.66	32.65	502	46.41	22.2	15.14	0.56	11
G22	208.31	23.90	419	39.25	19.1	15.18	0.21	28
G23	265.63	30.29	387	49.81	20.55	14.65	0.38	24
G24	286.51	29.10	457	41.65	22.78	15.16	0.44	20
G25	248.95	30.02	435	44.18	19.42	14.64	0.34	26
G26	269.63	36.16	529	31.88	24.08	13.36	0.43	21
G27	292.45	32.51	526	39.32	21.68	14.75	0.48	14
G28	277.69	29.62	592	39.52	19.38	14.92	0.48	16
G29	341.80	30.98	507	37.08	26.9	14.46	0.56	9
G30	259.40	20.61	569	28.36	24.18	13.94	0.35	25
Mean	300.02	30.85	502	39.74	23.39	14.49		
Min	204.75	20.61	371	27.54	18.63	12.52		
Max	394.60	40.90	596	53.29	32.53	15.91		
LSD (%5)	109.59	9.34	138	9.17	4.4	1.79		
LSD (%1)	145.81	12.42	184	12.2	5.86	2.38		

Gyld: grain yield, HI: harvest index, NSPM: number of spikes per square meter, TGW: 1000-grain weight, NSPS: number of seeds per spike, GPC: Grain protein content, MSI: multiple selection index, Ranked: ranked of MSI values.

Among selected genotypes, the entries G9 (394.6 g m^{-2}) and G16 (388.9 g m^{-2}) showed higher grain yield. Also, the entry G7 had the highest level of grain protein (15.91%) in the flour and the entry G18 (40.9%) revealed highest harvest index in this experiment (Figure 2). Other researchers used the multiple selection index to identify superior genotypes in maize (GAZAL *et al.*, 2017), rice (SABOURI *et al.*, 2008), sugarcane (DE AZEREDO *et al.*, 2017), popcorn composites (VIEIRA *et al.*, 2017), papaya (VIVAS *et al.*, 2012) and in *Miscanthus* (SLAVOV *et al.*, 2019).

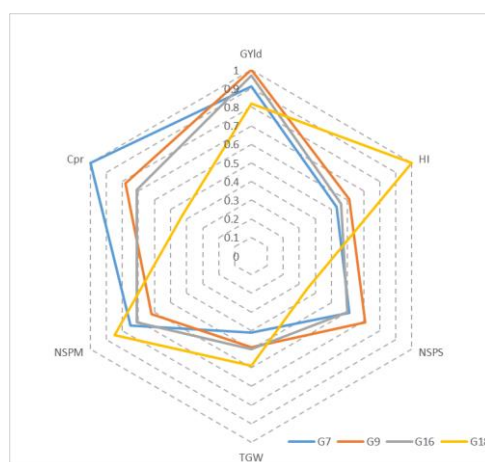


Figure 2. Standardized mean values of the superior wheat genotypes for six desired traits.

The GT-biplot (Figures 3 and 4) displayed 72.51% of total variation in the standardized data of the 30 genotypes for six traits, whose are presented in Table 2. The polygon view of the GT-biplot (Figure 3) could be used to identify genotypes that are particularly good in certain traits. The vertex genotype in each sector show the highest performance for all traits, which are in the same sector. Therefore, the superior genotypes can be selected for using in future breeding programs (YAN and RAJCAN, 2002). Based on given information, it seems that the entry G20 had the highest values of grain yield (GYld) and harvest index (HI) in the rain-fed conditions. Also, the entry G4 were the favorable genotype for 1000-grain weight (TGW) and the number of spikes per square meter (NSPM). The entries G5 and G6 was the most favorable genotype for grain protein content (GPC or CPr) and the number of seeds per spike (NSPS), respectively. No traits fell into the sector where the entries G12, G30, G17, G15 and G22 were the on the vertex, indicating that these genotypes showed inefficiency in some or all desired traits and were unfavorable to the groups of studied traits. Thus, they are not considered for breeding programs focused on increasing the expression of these traits (Figure 3). Figure 4 represents interrelationship among traits. The angle between the vectors of two traits is associated with the correlation coefficient between them. A highly positive correlation is shown with acute angle

between the vectors of the traits while those with obtuse angle are negatively correlated (YAN and FRÉGEAU-REID, 2008).

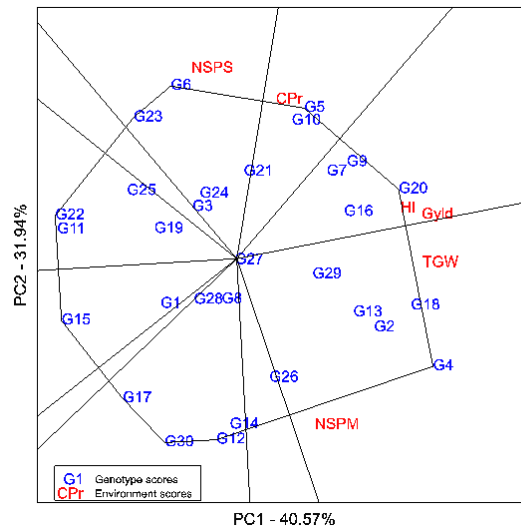


Figure 3. Wheat genotype-by-trait biplot, showing which cultivar had the highest values for which traits. PC, principal component.

Figure 3 shows (i) a significant positive correlation (acute angle) between the grain yield (GYld), the harvest index (HI) and thousand grain weight (TGW), (ii) a strong negative correlation (obtuse angle) between the number of seeds per spike (NSPS) and the number of spikes per square meter (NSPM), and (iii) non-significant correlation between grain protein content (GPC or CPr) and other agronomic traits. From the viewpoint of developing grain yield, negative correlation between the number of seeds per spike and the number of spikes per square meter are undesirable and constitute a challenge to wheat breeding for rain-fed conditions. In this situation, any increase in one of them will reduce another one. Therefore, it should be considered as an optimal point for the both. Similar relationships among yield components were reported for multi-location wheat yield trials (QUINTERO *et al.*, 2018; BUSTOS *et al.*, 2013; GARCÍA *et al.*, 2013; ACRECHE and SLAFER, 2006). Lack of association between grain protein content and other agronomic traits, suggested that high yielding genotypes do not always have high protein in flour. MAICH *et al.* (2017) stated that flour protein content was negatively associated with all the agronomic variables. The “ideal” genotype defined as a genotype that combines several suitable traits in its genetic composition. The “ideal” genotype defined as a genotype that combines several suitable traits in its genetic composition. The vector length of a genotype from the GT-biplot origin measures the genotype’s peculiarity which differs from an “average” genotype (i.e. a genotype located at the origin of the biplot). Hypothetically, superior genotype is a genotype which shows high performance for all traits. Therefore, genotypes with long vectors are those that have extreme levels for one or more traits (YAN and FRÉGEAU-REID, 2008). Based on the above-mentioned concepts, the entries G20, G9, G7 and G16 with long vectors were those that showed

extreme values for one or more traits. Such genotypes may (or may not) be superior, but they may be useful in future breeding programs for some useful traits (Figure 4). Similar results reported by other researchers in wheat (MISHRA *et al.*, 2015), in rice (SHARIFI and EBADI, 2018), in green beans (OLIVEIRA *et al.*, 2018) and in Oat (YAN and FRÉGEAU-REID, 2008).

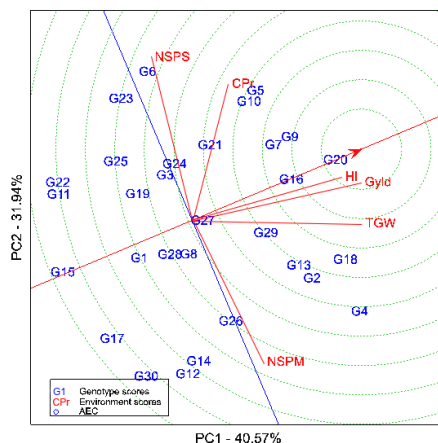


Figure 4. Genotype-by-trait biplot, showing the interrelationships among traits. PC, principal component.

CONCLUSION

Three genotypes (G7, G9 and G16) were selected with proven high performance in all desired traits by the both methodologies. These genotypes could be used for further improvement and selection as pure lines or as parental lines for the development of new wheat cultivars. In addition, the results also verified that it would be possible to determine contrasting genotypes based on the trait(s) for improving genetic materials in wheat breeding programs. In summary, The GT-biplot analysis for graphical selection of genotypes based on multiple traits can be useful but similar results may be achieved based on the multiple selection index of SMITH (1936) by applying the appropriate weights to their component trait. Nearly identical superior genotypes were selected in each methodology. The multiple selection index methodology is a very simple and fast method. Therefore, the use of the multiple selection index is recommended to identify superior genotypes for simultaneous improvement of several traits.

Supplementary data

Multiple Selection Index Toolbox is a single executable program which can be requested from M. H. Romena (m.h.romena@gmail.com). It runs on Windows 7/8/8.1/10. Supplementary materials including a manual and some application examples are available.

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REFERENCES

- ACRECHE, M. and G. AFER (2006): Grain weight response to increases in number of grains in wheat in a Mediterranean area. *Field Crops Res.*, 98: 52–59.
- BAKER, R.J. (1986): Selection indices in plant breeding. CRC Press, Inc.
- BATTENFIELD, S.D., C. GUZMÁN, R.C. GAYNOR, R.P. SINGH, R.J. PEÑA, S. DREISIGACKER, A.K. FRITZ, J.A. POLAND (2016): Genomic selection for processing and end-use quality traits in the CIMMYT spring bread wheat breeding program. *Plant genome-US.*, 9(2): 1-12.
- BUSTOS, D.V., A.K. HASAN, M.P. REYNOLDS, D.F. CALDERINI (2013): Combining high grain number and weight through a DH-population to improve grain yield potential of wheat in high-yielding environments. *Field Crops Res.*, 145: 106–115.
- DE AZEREDO, A.A.C., L.L. BHERING, B.P. BRASILEIRO, C.D. CRUZ, L.C.I. SILVEIRA, R.A. OLIVEIRA, J.C. BESPALHOK FILHO, E. DAROS (2017): Comparison between different selection indices in energy cane breeding. *Gen. Mol. Res. GMR.*, 16(1): 1-12.
- DEGHANI, H., H. OMIDI, N. SABAGHNI (2008): Graphic analysis of trait relations of canola (*Brassica napus* L.) using biplot method. *Agr. J.*, 100: 760-764.
- GARCÍA, G.A., A.K. HASAN, L.E. PUHL, M.P. REYNOLDS, D.F. CALDERINI D.J. MIRALLES (2013): Grain yield potential strategies in an elite wheat double-haploid population grown in contrasting environments. *Crop Sci.*, 53: 2577–2587.
- GAZAL, A., F.A. NEHVI, A.A. LONE, Z.A. DAR, M.A. WANI (2017): Smith Hazel Selection Index for the Improvement of Maize Inbred Lines under Water Stress Conditions. *Int. J. Pure App. Biosci.*, 5(1): 72-81.
- GERLAND, P., A.E. RAFTERY, H. ŠEVČÍKOVÁ, N. LI, D. GU, T. SPOORENBERG, L. ALKEMA, B.K. FOSDICK, J. CHUNN, N. LALIC, G. BAY, T. BUETTNER, G.K. HEILING J. WILMOTH (2014): World population stabilization unlikely this century. *Sci.*, 346: 234–237.
- GRAVOIS, K.A. and R.W. MCNEW (1993): Genetic relationships among and selection for rice yield and yield components. *Crop Sci.*, 33(2): 249-252.
- HACH, C.C., S.V. BRAYTON, A.B. KOPELOVE (1985): A powerful Kjeldahl nitrogen method using peroxymonosulfuric acid. *J. Agric. Food Chem.*, 33(6): 1117-1123.
- HEINZ, R., L.H. DE SOUSA MOTA, M.C. GONÇALVES, A.L.V. NETO, A. CARLESSO (2012): Seleção de progênies de meio-irmãos de milho para eficiência no uso de nitrogênio. *Revista Ciência Agronômica.*, 43(4): 731-739.
- JANNINK, J.L., J.H. ORF, N.R. JORDAN, R.W. SHAW (2000): Index selection for weed suppressive ability in soybean. *Crop Sci.*, 40(4): 1087-1094.
- MAICH, R.H., M.E. STEFFOLANI, J.E. DI RIENZO, A.E. LEÓN (2017): Association between grain yield, grain quality and morpho-physiological traits along ten cycles of recurrent selection in bread wheat (*Triticum aestivum* L.). *Cereal Res. Comm.*, 45(1): 146-153.
- MISHRA, C.N., V. TIWARI, V.G. SATISH-KUMAR, V. GUPTA, A. KUMAR, I. SHARMA (2015): Genetic diversity and genotype by trait analysis for agromorphological and physiological traits of wheat (*Triticum aestivum* L.). *Sabroa J. Breed. Gen.*, 47(1): 40-48.
- MOHAMMADI, R., A. AMRI (2011): Graphic analysis of trait relations and genotype evaluation in durum wheat. *J. Crop Improv.*, 25(6): 680-696.
- NAWAZ, H., N. HUSSAIN, M. JAMIL, A. YASMEEN, S.A.H. BUKHARI, M. AURANGZAIB, M. USMAN (2020): Seed biopriming mitigates terminal drought stress at reproductive stage of maize by enhancing gas exchange attributes and nutrient uptake. *Turk. J. Agric. For.*, 44 (3): 250-261.

- OBER, E.S., M.I. BLOA, C.J.A. CLARK, A.K. ROYAL, W. JAGGARD, K.W. PIDGEON (2005): Evaluation of physiological traits as indirect selection criteria for drought tolerance in sugar beet. *Field Crop Res.*, *91*: 231-249.
- OLIVEIRA, T.R.A.D., G.D.A. GRAVINA, G.H.F.D. OLIVEIRA, K.C. ARAÚJO, L.C.D. ARAÚJO, R.F. DAHER, M. VIVAS, M.L. GRAVINA, D.P.D. CRUZ (2018): The GT biplot analysis of green bean traits. *Ciência Rural.*, *48*(6): 1-6.
- POSPISIL, A., M. POSIPISL, M. BRCIC (2020) Agronomic traits of einkorn and emmer under different seedling rates and topdressing with organic fertilizers. *Turk. J. Agric. For.*, *44* (1): 95-102.
- QUINTERO, A., G. MOLERO, M.P. REYNOLDS, D.F. CALDERINI (2018): Trade-off between grain weight and grain number in wheat depends on GxE interaction: A case study of an elite CIMMYT panel (CIMCOG). *Eur. J. Agron.*, *92*: 17-29.
- RENCHER, A. (2002): *Methods of Multivariate Analysis* (2nd ed.). Brigham Young University: John Wiley & Sons, Inc.
- SABAGHNI, N. and M. JANMOHAMMADI (2014): Interrelationships among some morphological traits of wheat (*Triticum aestivum* L.) cultivars using biplot. *Bot. Lith.*, *20*(1): 19-26.
- SABOURI, H., B. RABIEI M. FAZLALIPOUR (2008): Use of selection indices based on multivariate analysis for improving grain yield in rice. *Rice Sci.*, *15*(4): 303–310.
- SAFARI DOLATABAD, S., R. CHOUKAN, E. MAJIDI HERVAN, H. DEGHANI (2010): Multienvironment analysis of traits relation and hybrids comparison of maize based on the genotype by trait Biplot. *Americ. J. Agric. Biol. Sci.*, *5*(1): 107-113.
- SAMONTE, S., R. TABIAN, L.T. WILSON (2013): Parental selection in rice cultivar improvement. *Rice Sci.*, *20*(1): 45-51.
- SAS INSTITUTE (2003): Release 9.1. SAS Institute, Inc., Cary NC USA.
- SHARIFI, P. and A.A., EBADI (2018): Relationships of rice yield and quality based on genotype by trait (GT) biplot. *Anais da Academia Brasileira de Ciências.*, *90*(1): 343-356.
- SLAVOV, G., C. DAVEY, M. BOSCH, P. ROBSON, I. DONNISON, I. MACKAY (2019): Genomic index selection provides a pragmatic framework for setting and refining multi-objective breeding targets in *Miscanthus*. *Ann. Bot.*, *124*: 521-529.
- SMITH, H.F. (1936): A discriminant function for plant selection. *Ann. Eugen.*, *7*(3): 240-250.
- ŠRAMKOVÁ, Z., E. GREGOVÁ, E. ŠTURDÍK (2009): Chemical composition and nutritional quality of wheat grain. *Acta Chimica Slovaca.*, *2*(1): 115-138.
- TADESSE, W., M.M. NACHIT, O. ABDALLA, S. RAJARAM (2017): Wheat Breeding at ICARDA: Achievements and Prospects in the CWANA Region. *Tec & Doc Lavoisier*.
- VIEIRA, R.A., R.D. ROCHA, C.A. SCAPIM, A.T.D. AMARAL JUNIOR (2017): Recurrent selection of popcorn composites UEM-CO1 and UEM-CO2 based on selection indices. *Crop Breed. Appl. Biotech.*, *17*(3): 266-272.
- VIVAS, M., S.F.D. SILVEIRA, M.G.D. PEREIRA (2012): Prediction of genetic gain from selection indices for disease resistance in papaya hybrids. *Revista Ceres.*, *59*(6): 781-786.
- XU, N., M., FOK, J. LI, X. YANG, W. YAN (2017): Optimization of cotton variety registration criteria aided with a genotype-by-trait biplot analysis. *Sci. Rep.*, *7*(1): 17237.
- YAN, J., N., ZHANG, X. WANG, S. ZHANG, S.Q. ZHANG, S.Q. ZHANG, S.Q. ZHANG (2018): Selection of yield-related traits for wheat breeding in semi-arid region. *Int. J. Agric. Biol.*, *20*: 569–574.
- YAN, W. and J. FRÉGEAU-REID (2008): Breeding line selection based on multiple traits. *Crop Sci.*, *48*(2): 417-423.
- YAN, W. and J. FRÉGEAU-REID (2018): Genotype by Yield x Trait (GYT) Biplot: a novel approach for genotype selection based on multiple traits. *Sci. Rep.*, *8*: 1-10.
- YAN, W. and I. RAJCAN (2002): Biplot analysis of test sites and trait relations of soybean in Ontario. *Crop Sci.*, *42*(1): 11-20.

IDENTIFIKACIJA SUPERIORNIH GENOTIPOVA PŠENICE NA OSNOVU AGRONOMSKIH KARAKTERISTIKA I SADRŽAJA PROTEINA U ZRNU U OPTIMALNIM USLOVIMA

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Izvod

Nekoliko metoda oplemenjivanja biljaka uspešno je korišćeno za poboljšanje genetičkih resursa u mnogim kulturama kao što je pšenica. Međutim, izbor genotipova na osnovu više osobina je složen zadatak za oplemenjivače. Odabrani genotipovi treba da pokazuju visoke performanse u nizu željenih osobina. GT-biplot i indeks višestruke selekcije su predloženi za identifikaciju superiornog genotipa na osnovu različitih željenih osobina. U ovoj studiji, trideset genotipova pšenice je ocenjeno korišćenjem randomizovanog kompletnog blok dizajna sa tri ponavljanja u optimalnim uslovima da bi se procenili genotipovi korišćenjem dve različite metode selekcije višestrukih osobina (tj. GT-biplot i indeks višestruke selekcije) za agronomske osobine i sadržaj proteina u zrnu. Rezultati su pokazali da su gotovo isti genotipovi (G7, G9 i G16) odabrani kao superiorni prema obe metodologije. Među superiorno odabranim genotipovima, G9 (394,6 gr/m²) i G16 (388,9 gr/m²) su pokazali veći prinos zrna. Nadalje, unos G7 je imao najveći nivo proteina u zrnu (15,91%), a G18 (40,9%) je pokazao najveći žetveni indeks. Pored toga, obe metode su bile prikladne za identifikaciju superiornih genotipova pšenice na osnovu više osobina, ali bi indeks višestruke selekcije mogao biti jednostavniji i brži.

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