$\mathscr{R}$esearch Article

Diversity analysis and structural modeling of some traits in wheat genotypes

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ABSTRACT

This investigation was carried out during 2018/2019 season in three locations (Homs, Al-Swaida and Tartous) belongs to the General Commission for Scientific Agricultural Research in Syria, using 17 Italian, Syrian and Ethiopian wheat genotypes to estimate the potential diversity by principle component and cluster analysis, and to study the structural modeling between grain yield and other traits to define best traits as predictors and selection indexes of grain yield, and to determine the superior genotypes in grain yield. Results indicated a remarkable variation of 74% due only to the first four principle components with Eigen value more than 1. PC Biplot showed that Tartous was the best location, and the genotype SD09 was superior in grain yield per plant followed by SH5 and IP39. Structural modeling results revealed that the total and fertile tillers number per plant were the best predictors for grain yield per plant, while fertile tillers per plant with grains weight per spike could be used as selection indexes of wheat grain yield because they had positive strong direct effect on grain yield per plant. Cluster analysis results confirmed the need to assess more various genotypes from different origins.

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KEYWORDS: Wheat, diversity, structural modeling, PCA, biplot, cluster

INTRODUCTION

Wheat is the most important grain crop in the world which provide people with almost 50% of the required calories [1]. Breeding programs aim to increase the selection efficiency by assessing more genetic variations among wheat genotypes [2], this can be studied through different methods of multivariate analysis such as principle component and cluster analysis. Principle component analysis is used to reduce the large number of traits to a limited number which represents the majority of the existent variation [3]. Al-Otayk [4] applied principle component analysis to study the variation in wheat germplasm, their results showed remarkable variation among them. Categorize germplasm in many groups depending on their variation is applied by Cluster analysis [5]. Cluster analysis was applied by Devesh et al. [1] depending on the agronomic traits of various wheat trait. Poudel et al. [6] estimated the diversity between wheat genotypes, their results showed that wheat genotypes were clustered in various main and sub main clusters. Sahu et al. [7] declared that correlation is used to just to illustrate relation between traits, but

not for prediction of any trait, whereas path analysis considers as an efficient method for confirming the correlation depending on the effects and reasons of these effects and to eliminate any false effect. Abd El-Mohsen [8] mentioned that prediction of grain yield via other traits can be applied by regression analysis. The objectives of this investigation were to: (i) evaluate the magnitude of potential diversity between exotic and local wheat genotypes by using principal component analysis and cluster analysis, (ii) study the nature of structural modeling between grain yield and other traits via Regression and path analysis, (iii) define the superior genotypes regarding grain yield in various locations to be used in breeding programs.

MATERIAL AND METHODS

Plant Materials

Seventeen genetic resources of primitive wheat originated from different countries (Italy, Ethiopia and Syria) were used

in this study (Table 1). They were kindly provided by the International Centre for Agricultural Research in the Dry Areas (ICARDA), and by the genetic resources department in the General Commission for Scientific Agricultural Research (GCSAR), Syria.

Field Experiments

The investigation was carried out at three research centers (Homs, Al-Swaida and Tartous) in the General Commission for Scientific Agricultural Research (GCSAR), Syria during the season 2018/2019. The experiment was arranged in a randomized complete block design (RCBD), with three replicates. Each replicate consisted of four rows, each row of 1meter long, with 20cm between rows and 5cm between plants, depth of planting was 3-5 cm. Recommended cultural practices like irrigation and pesticide control were applied according to Agricultural ministry guides. Days to flowering, days to heading, plant height(cm), awn length(cm), total tillers number per plant, fertile tillers number per plant, spike length(cm), spike peduncle length(cm), grain number per spike, granis weight per spike, 1000-grain weight(g) and grain yield per plant(g) were all measured on ten randomly selected plants (Table 2).

Statistical Analysis

Summary statistics were analyzed by SPSS.12 software. Principal component analyses to assess level of variance in traits between genotypes was conducted by Minitap.12 software. Cluster analysis was also analyzed via Minitap.12 software depending on single linkage method with Euclidean distance measure. Correlation and simple linear regression SLR between grain yield per plant as the dependent variable and each of the studied traits as independent variables and Biplot were all analyzed via Genstat.12 software. Path coefficients analysis to identify the direct and indirect effects of studied traits on grain yield was done according to Singh and Chudhary [9] using Genstat.12 software, the strength of direct and indirect effects value was scaled according to [10] as follows: More than 1: very strong,

(0.3 - 0.9): strong, (0.2 - 0.29): medium, (0.1 – 0.19) weak, less than 0.1: neglected.

RESULTS AND DISCUSSION

Summary statistics for studied traits revealed that the mean of (days to heading and days to flowering) was (132.95, 136.03) day respectively, with a range of (56.00, 62.00) day respectively. Mean of (plant height, awn length, spike length and spike peduncle length) was (124.33, 10.25, 11.23, 40.18) cm respectively with a range of (156.20, 14.30, 16.70, 44.63) cm respectively. The range of total and fertile tillers number per plant was (52.60, 34.30) respectively, with a mean of (16.73, 11.86) tiller respectively. The mean and range of grains number per spike were (11.23 and 84.60) grain respectively.

Results also indicated that the mean of (granis weight per spike, 1000-grain weight and grain yield per plant) was (1.50, 35.37 and 13.55) g respectively with a range of (4.70, 73.70, 50.71) g respectively. Grain yield per plant was the main source of the explored variations between wheat genotypes since its coefficient of variation reached 61.9%, followed by grain weight per spike 46% (Table 3). Other traits such as fertile tillers number per plant and grains number per spike also were sources of remarkable variation (39.7, 35.8) respectively.

Principle Component Analysis

Twelve principal components were obtained for the studied traits, but only the first four principal components (PC1, PC2, PC3 and PC4) present the variability between wheat genotypes relating to studied traits as they revealed Eigen value larger than 1.0(3.85, 2.49, 1.51 and1.10) respectively (Figure 1), while other components were neglected as they resulted an Eigen value less than one. The maximum variability was 74% divided to (32.1, 20.7, 12.6 and 9.2) % revealed by the first four principle components (PC1, PC2, PC3 and PC4) respectively (Table 4). The first principal component PC1consisted of plant height and spike peduncle length (-0.347 and -0.386) respectively. The second principal component PC2 contained four traits: days to flowering and days to heading, fertile tillers number per plant and grain yield per plant (0.476, 0.527, -0.349, -0.373) respectively. Also the third principal component PC3 enclosed four traits: awn length, total tillers number per plant, grains weight per spike and 1000-grain weight (0.396, -0.506, 0.370 and 0.320) respectively. Spike length and grains number per spike

Table 1: List of wheat genotypes used in this study

No	Genotype	Origin	Species
1	IP39	Italy	*Triticum polonicum*
2	IP40	Italy	*Triticum polonicum*
3	IP45	Italy	*Triticum polonicum*
4	IP46	Italy	*Triticum polonicum*
5	IP47	Italy	*Triticum polonicum*
6	IP49	Italy	*Triticum polonicum*
7	IP50	Italy	*Triticum polonicum*
8	IP52	Italy	*Triticum polonicum*
9	IC80	Italy	*Triticum carthlicum*
10	IC81	Italy	*Triticum carthlicum*
11	IC83	Italy	*Triticum carthlicum*
12	IC89	Italy	*Triticum carthlicum*
13	ED04	Ethiopia	*Triticum dicoccum*
14	SD09	Syria	*Triticum dicoccum*
15	SD11	Syria	*Triticum dicoccum*
16	SH3	Syria	*Triticum durum*
17	SH5	Syria	*Triticum durum*

Table 2: List of Traits abbreviations used in this study

Trait	abbreviation	Trait	abbreviation
FD	Days to flowering	GWS	Grains weight per spike
HD	Days to heading	TGW	1000- grain weight
PH	Plant height	GYP	Grain yield per plant
AL	Awn length	Tar	Tartous location
TT	Total tillers number	Sw	Al-Swaida location
FT	Fertile tillers number	Ho	Homs location
SL	Spike length	CV	Coefficient of Variation
SPL	Spike peduncle length	SD	Standard Deviation
GNS	Grains number per spike		

Table 3 : Means and content of variations of 17 studied genotypes

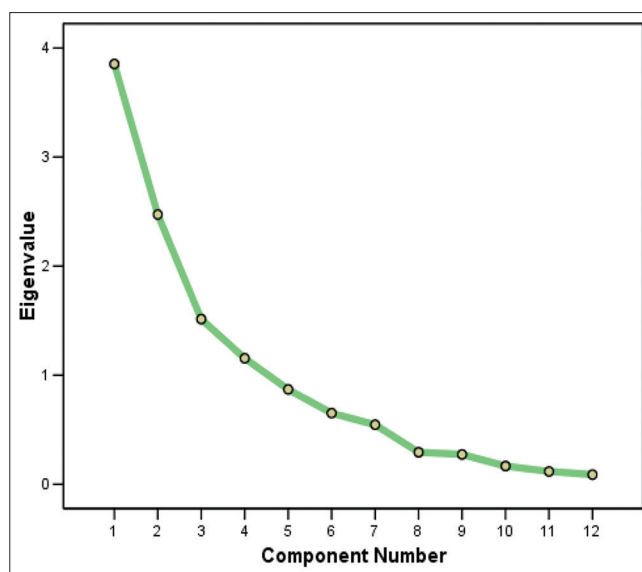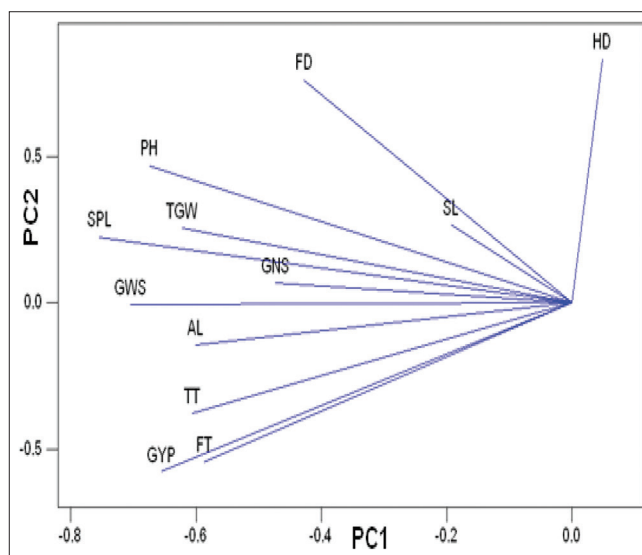| Trait	Mean	Sum	Range	CV%	SD
Hd	132.95	20342.00	56.00	1.8	11.02
Fd	136.03	20813.00	62.00	3.4	11.09
PH	124.33	19021.97	156.20	14.2	33.08
AL	10.25	1568.70	14.30	17.7	3.08
TT	16.73	2559.00	52.60	33.1	8.74
FT	11.86	1813.81	34.30	39.7	6.41
SL	11.23	1717.85	16.70	19.5	3.15
SPL	40.18	6147.84	44.63	17.0	10.60
GNS	11.23	1717.85	84.60	35.8	3.15
GWS	1.50	230.24	4.70	46	0.89
TGW	35.37	5411.45	73.70	17.6	12.07
GYP	13.55	2073.65	50.71	61.9	12.02

Table 4: Eigen value, proportion and cumulative variation of analyzed components

Principal components	Eigen value	Proportion of variation%	Cumulative variation%
PC1	3.85	0.321	0.321
PC2	2.49	0.207	0.528
PC3	1.51	0.126	0.654
PC4	1.10	0.092	0.746
PC5	0.91	0.075	0.822
PC6	0.65	0.054	0.875
PC7	0.55	0.045	0.921
PC8	0.31	0.025	0.946
PC9	0.27	0.023	0.969
PC10	0.17	0.014	0.983
PC11	0.20	0.010	0.993
PC12	0.09	0.007	1.000

Figure 1: Scree plot showing eigen value variation

Figure 2: Loading plot of studied traits in the first two Components

were related to the fourth principle component PC4 (-0.750, 0.408) respectively (Table 5). Loading plot of the studied traits relating to the first two principle components indicated that all traits were negatively connected to PC1 (except days to heading), while five traits: Grains weight per spike, awn length, total tillers per plant, fertile tillers per plant and grain yield per plant were negatively connected to PC2 (Figure 2). Principle components Biplot distribution of genotypes and locations for the final grain yield indicated that Tartous was the best location followed by Homs, and the genotype SD09 was superior in grain yield per plant followed by SH5 and IP39 comparing to all other genotypes (Figure 3).

Correlation Analysis

Results showed significant positive correlation between days to flowering and days to heading (0.749**), plant height (0.581**), total tillers number per plant (0.173*), spike peduncle length (0.472**), grains number per spike (0.173*), grain weight per spike (0.195*) and 1000-grain weight (0.359**). Correlation was positive and significant between days to heading and plant height (0.244**), while negative and significant with each of awn length (-0.251**), fertile tillers number per plant (-0.275**) and grain yield per plant (-0.456**). Plant height had a positive significant correlation with awn length (0.314**), total tillers number per plant (0.269**), fertile tillers number per plant (0.185*), spike length (0.379**), spike peduncle length (0.630**), grains number per spike (0.287**), grain weight

per spike (0.320**) and 1000-grain weight (0.395**). Positive significant correlation was found between total tillers number per plant and fertile tillers number per plant (0.859**), spike peduncle length (0.347**), grains number per spike (0.168*) and grain yield per plant (0.571**). Also fertile tillers number per plant had a positive significant correlation with spike peduncle length (0.279**), grains weight per spike (0.170*) and grain yield per plant (0.649**). Spike length correlated significantly and positively with spike peduncle length (0.174*). Results also indicated significant positive correlation between spike peduncle length and grains number per spike, grains weight per spike, 1000-grain weight and grain yield per plant (0.229**, 0.438**, 0.472**, 0.350**) respectively. Grains number per spike exhibited a positive and significant correlation with each of grain weight per spike and grain yield per plant (0.476**, 0.173*) respectively, and also between grains weight per spike and each of 1000-grain weight and grain yield per plant (0.531**,

Table 5: The first four principle components for the studied traits

Trait	PC1	PC2	PC3	PC4
FD	-0.222	0.476	-0.278	0.161
HD	0.019	0.527	-0.249	0.280
PH	-0.347	0.291	-0.099	-0.246
AL	-0.305	-0.092	0.396	-0.150
TT	-0.307	-0.246	-0.506	0.033
FT	-0.297	-0.349	-0.404	-0.006
SL	-0.104	0.186	-0.000	-0.750
SPL	-0.386	0.134	-0.052	-0.104
GNS	-0.240	0.068	0.176	0.408
GWS	-0.357	-0.009	0.370	0.255
TGW	-0.318	0.154	0.320	-0.017
GYP	-0.329	-0.373	-0.032	0.081

0.557**) respectively, and finally between 1000-grain weight and grain yield per plant (0.244**) (Table 6). All correlations between studied traits were plotted (Figure 4).

Regression Analysis

Results of simple linear regression SLR to predict grain yield per plant as a dependent trait by each of other studied traits as independent traits reveled that only six traits can be used as predictors of grain yield per plant (days to heading, awn length, total tillers per plant, fertile tillers per plant, spike peduncle length and grains weight per spike) as they had a significant regression with grain yield per plant (Table 7). The coefficient of determination R^2 between grain yield and days to heading was 0.208 which means that the late heading genotypes will have a reduction in grain yield in rate of 20.8% because of the negative correlation between days to heading and grain yield per plant. The coefficient of determination R^2 between grain yield and other traits like awn length, total tillers number per plant, fertile tillers number per plant, spike peduncle length and grain weight per plant were (0.096, 0.326, 0.421, 0.122 and 0.310) respectively, indicated that each of these traits can predict separately the variation in grain yield per plant at in a rate of (9.6, 32.6, 42.1, 1.2 and 3.10) % respectively (Figure 5). Regression equation is listed in Table. 8.

Path Analysis

Results of path analysis showed that the direct effects on grain yield per plant for fertile tillers number per plant and grains weight per spike were strong and positive (0.33807 and 0.53401) respectively, while strong but negative for days to heading (-0.44066), positive and medium for days to flowering (0.23038), weak and negative for plant height and grains number per spike (-0.11706 and -0.11170) respectively, while weak and positive for total tillers number per spike (0.17852). The direct effect of awn length, spike length, spike peduncle length and 1000- grain weight was neglected (-0.05714, -0.02154, 0.00307 and -0.03707).

Results also revealed that the indirect effect of days to flowering via days to heading was strong and negative (-0.33017), while positive but weak via grains weight per spike (0.10403), other
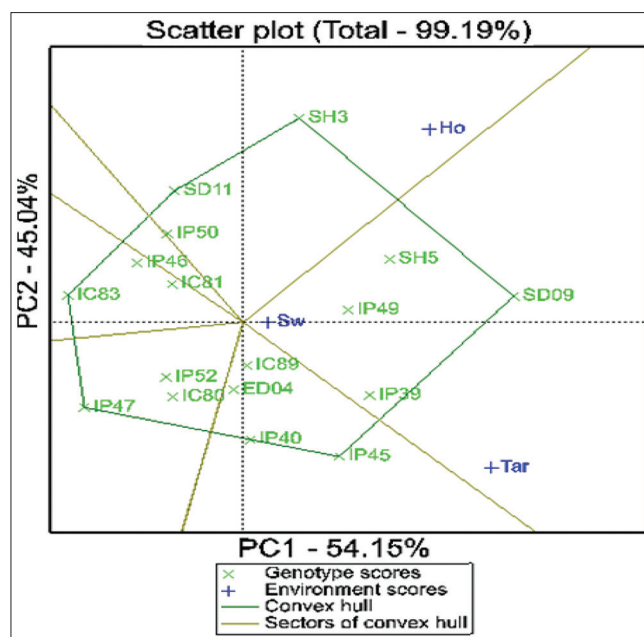

Figure 3: Principle Component Biplot of Genotypes and locations for grain yield trait

Figure 4: Loading plots of correlations between studied traits

indirect effects were neglected. The indirect effects of days to heading via other traits were all neglected except its weak and positive indirect effect via days to flowering (0.17262). Plant height had weak and positive indirect effects via days to flowering and grains weight per spike (0.13375, 0.17091) respectively, while weak but negative via days to heading (-0.10734), and neglected indirect effects via other traits. The indirect effect of awn length was positive medium via grains

Table 6: Correlation matrix between studied traits

Trait	FD	HD	PH	AL	TT	FT	SL	SPL	GNS	GWS	TGW	GYP
FD	1											
HD	0.749**	1										
PH	0.581**	0.244**	1									
AL	-0.020	-0.251**	0.314**	1								
TT	0.173*	-0.130	0.269**	0.166*	1							
FT	-0.005	-0.275**	0.185*	0.267**	0.859**	1						
SL	0.158	0.073	0.379**	0.183	0.001	-0.017	1					
SPL	0.472**	0.033	0.630**	0.306**	0.347**	0.279**	0.174*	1				
GNS	0.173*	0.118	0.287**	0.335**	0.168*	0.138	0.013	0.229**	1			
GWS	0.195*	-0.075	0.320**	0.441**	0.126	0.170*	0.035	0.438**	0.476**	1		
TGW	0.359**	0.069	0.395**	0.449**	0.084	0.061	0.096	0.472**	0.138	0.531**	1	
GYP	-0.068	-0.456**	0.120	0.309**	0.571**	0.649**	-0.040	0.350**	0.173*	0.557**	0.244**	1

**Correlation is significant at the 0.01 level.   *Correlation is significant at the 0.05 level

Table 7: Summary of S.L.R. between grain yield and each of other studied traits

Trait	Source	d. f.	M.S	R	R^2
FD	Regression	1	102.2^{NS}	-0.068	0.005
	Residual	151	144.7		
	Total	152	144.4		
HD	Regression	1	4562.6^S	-0.456	0.208
	Residual	151	115.2		
	Total	152	144.4		
PH	Regression	1	316.2^{NS}	0.120	0.014
	Residual	151	143.3		
	Total	152	144.4		
AL	Regression	1	2102.1^S	0.309	0.096
	Residual	151	131.5		
	Total	152	144.4		
TT	Regression	1	7166.75^S	0.571	0.326
	Residual	151	97.93		
	Total	152	144.4		
FT	Regression	1	9248.28^S	0.649	0.421
	Residual	151	84.14		
	Total	152	144.4		
SL	Regression	1	80.2^{NS}	0.040	0.002
	Residual	151	144.9		
	Total	152	144.4		
SPL	Regression	1	2688.3^S	0.350	0.122
	Residual	151	127.6		
	Total	152	144.4		
GNS	Regression	1	490.6^{NS}	0.173	0.030
	Residual	151	142.1		
	Total	152	144.4		
GWS	Regression	1	6814.6^S	0.557	0.310
	Residual	151	100.3		
	Total	152	144.4		
TGW	Regression	1	1301.9^{NS}	0.244	0.059
	Residual	151	136.8		
	Total	152	144.4		

^{S}Regression is significant

Table 8: Regression equations between grain yield and predictors traits

No	Regression Equation
1	GYP = 79.9 − 0.4972 HD
2	GYP = 1.16 + 1.209 AL
3	GYP = 0.42 + 0.7853 TT
4	GYP = − 0.87 1.217 FT
5	GYP = − 2.38 + 0.3966 SPL
6	GYP = 2.19 + 7.552 GWS

weight per spike (0.23531), and positive weak via days to heading (0.11052), whereas neglected via other traits. Total tillers had only a positive medium indirect effect via fertile tillers per plant (0.29040), while other indirect effects were all neglected. The indirect effects of fertile tillers per plant were positive but weak via days to heading and total tillers per plant (0.12139, 0.15335) respectively, and all other indirect effects were neglected. Spike length had neglected indirect effects on grain yield per plant via all traits. Spike peduncle length had a positive and weak indirect effect via days to flowering (0.10873) and positive and medium via grains weight per spike (0.23409), other indirect effects were all neglected. All indirect effects of grains number per spike were neglected except via grains weight per spike which was medium and positive (0.25396). All indirect effects of grains weight per spike on plant grain yield via other traits were neglected. The same result for 1000-grain weight which all its indirect effects via other traits were neglected except its positive and weak indirect effect via total tillers number per spike (0.01498) and its positive and medium indirect effect via grains weight per spike (0.28364) (Table 9).

Cluster Analysis

Results of cluster analysis depending on studied field traits revealed that the similarity coefficient ranged from 43.50% to 100%, and three main groups of genotypes were clustered together, each of contained sub clusters. The first main group included nine genotypes, which seven originated from Italy (IC80, IC81, IC83, IC89, IP46, IP47, IP49) and one originated from Ethiopia (ED04) and another one originated from Syria (SD11). The second main group contained five genotypes originated all from Italy (IP39, IP50, IP40, IP45, IP52). The third main group consisted of three Syrian originated genotypes (SD09, SH3 and SH5) (Figure. 6).

DISCUSSION

According to our results, the coefficient of variation for grain yield was the highest in representing variation between wheat genotypes, this could be explained due the complex nature of yield trait which affected by most of the quantitative traits. Our results agree with the findings of Grzesiak et al. [11] who found that the coefficient of variation for wheat grain yield was
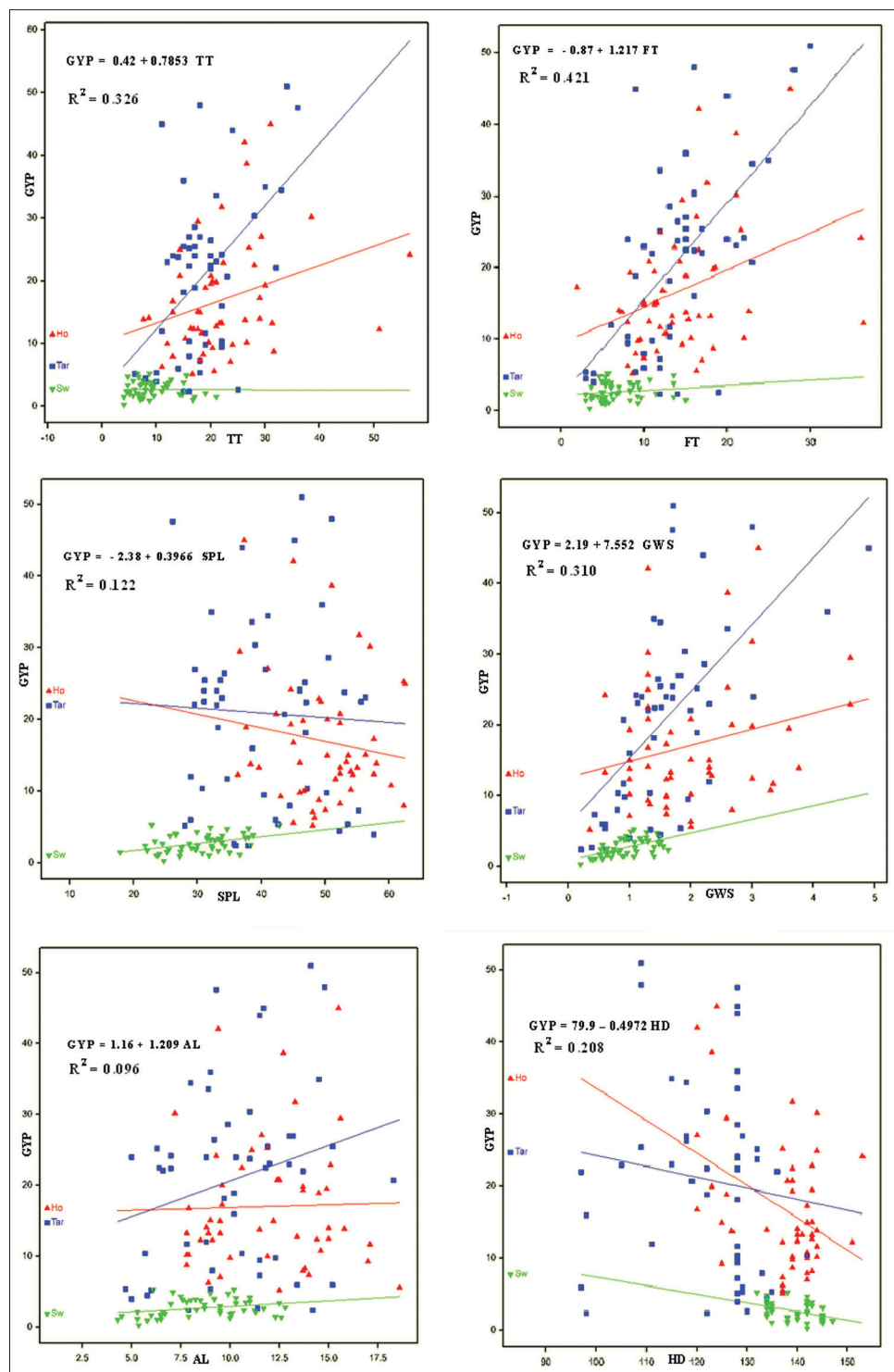
Figure 5: Loading plots of significant S.L.R between grain yield and predictors traits

high (63.7). Correlation between days to heading and grain yield was negative which means that late heading plants are accompanied with low yield and vice versa. Quantitative traits were mainly correlated positively with each other and with grain yield since they are affecting the final grain yield. These results were reported also by Marzougui et al. [12] who found that grain yield had significant and negative correlation with days to heading, while positive with spike peduncle length, and

also positive between spike peduncle length and grains weight per spike, these were also approved [13,14]. Regarding Principle component analysis, the first four components represented about three quarter of variation which refer to the importance of the studied traits in providing wide variability to be explored, this agrees with the finding of Sisodia and Rai [15] who declared that the first principle components explain the main variability in various wheat genotypes. In addition, our results

Table 9: Direct (underlined bold diagonal) and indirect effects of studied traits on grain yield per plant of wheat genotypes

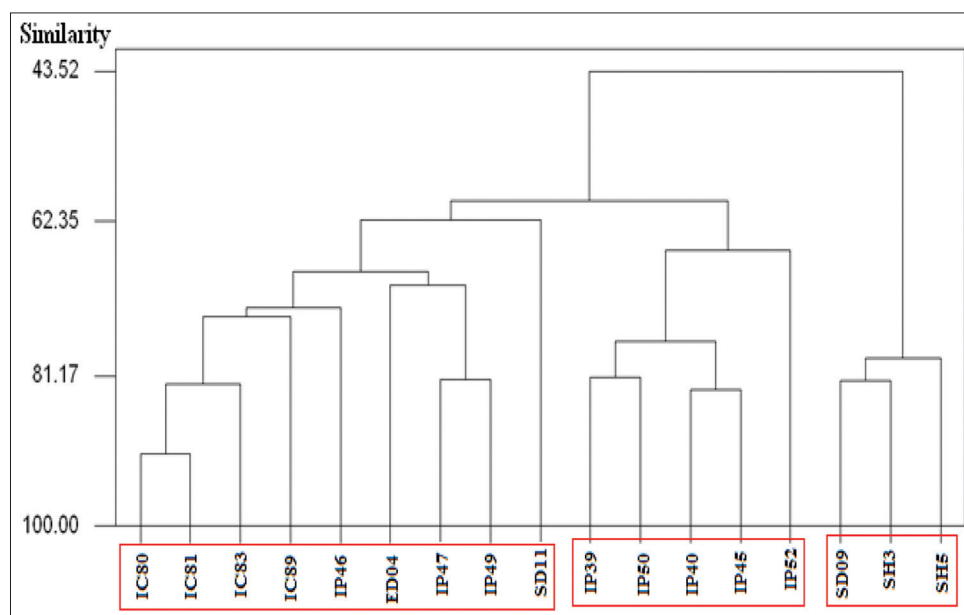| Trait	FD	HD	PH	AL	TT	FT	SL	SPL	GNS	GWS	TGW	R
FD	**0.23038**	-0.33017	-0.06796	0.00112	0.03080	-0.00182	-0.00340	0.00145	-0.01935	0.10403	-0.01331	-0.0682
HD	0.17262	**-0.44066**	-0.02852	0.01433	-0.02319	-0.09313	-0.00157	0.00010	-0.01317	-0.04012	-0.00258	-0.4559
PH	0.13375	-0.10734	**-0.11706**	-0.01791	0.04807	0.06246	-0.00817	0.00193	-0.03200	0.17091	-0.01463	0.1200
AL	-0.00451	0.11052	-0.03670	**-0.05714**	0.02956	0.09038	-0.00297	0.00094	-0.03746	0.23531	-0.01849	0.3094
TT	0.03974	0.05723	-0.03152	-0.00946	**0.17852**	0.29040	-0.00003	0.00106	-0.01876	0.06728	-0.00311	0.5714
FT	-0.00124	0.12139	-0.02163	-0.01528	0.15335	**0.33807**	0.00036	0.00086	-0.01543	0.09086	-0.00226	0.6490
SL	0.03642	-0.03208	-0.04442	-0.00787	0.00024	-0.00558	**-0.02154**	0.00053	-0.00140	0.01881	-0.00356	-0.0605
SPL	0.10873	-0.01433	-0.07376	-0.01747	0.06192	0.09447	-0.00374	**0.00307**	-0.02555	0.23409	-0.01750	0.3499
GNS	0.03990	-0.05197	-0.03354	-0.01917	0.02998	0.04669	-0.00027	0.00070	**-0.11170**	0.25396	-0.00511	0.1495
GWS	0.04488	0.03311	-0.03747	-0.02518	0.02249	0.05752	-0.00076	0.00135	-0.05312	**0.53401**	-0.01969	0.5571
TGW	0.08271	-0.03062	-0.04620	-0.02850	0.01498	0.02060	-0.00207	0.00145	-0.01540	0.28364	**-0.03707**	0.2435

Figure 6: Dendrogram of studied wheat genotypes based on studied traits

are in agreement with results of Devesh et al. [1] who indicated that the PC1 in wheat contained spike peduncle length and plant height, and PC3 contained tillers number per plant, and in general most of yield traits were located in the first three components. It was noticed that the Syrian originated genotype SD09 was the superior in grain yield per plant and this could be explained to its adaptability to local environments comparing with the exotic genotypes. Regression study between grain yield and days to heading revealed that the late heading genotypes will suffer from a grain yield reduction in rate of 20.8%, while any raise in awn length, total tillers number per plant, fertile tillers number per plant, spike peduncle length and grains weight per plant will cause an increasing of grain yield in a rate of (9.6, 32.6, 42.1, 1.2 and 3.10) % respectively, and these results sounds logic since these traits are related to yield as it is well-known, so these traits can be used as significant predictors for grain yield. Our findings are in agreement with many researchers' results [16-18]. Our results of cluster analysis concluded that most genotypes that obtained from the same origin gathered in the same cluster like the majority of Italian genotypes in the first cluster, as well as in the third cluster regarding the Syrian genotypes. Our results also insured that genotypes from the same species were clustered together like all *Triticum polonicum*

genotypes in the second clusters. Wide variation was obvious between different cluster which make our results valuable for breeders to determine the method of choosing which genotypes to be used as parents for wheat improvement, This agrees with Mutwali et al. [19] who declared that related wheat genotypes were clustered together, and with [20] who reported that each cluster contains very close genotypes, and also with Jaiswal et al. [21]. According to path analysis results, both traits fertile tillers number per plant and grains weight per spike had positive strong direct effect on grain yield per plant and their correlation with grain yield were positive also, which means that both traits could be used effectively as selection indexes for grain yield, other scientists reported similar results [22, 23, 24, 25].

CONCLUSIONS

Valuable variation was confirmed according to our results between studied genotypes, caused by grain yield and most of the studied traits which be a sign of their importance. It was concluded also that the total and fertile tillers number per plant were the best predictors of the final grain yield per plant, and fertile tillers per plant with grains weight per spike could be used as selection indexes of wheat grain yield. Our results confirmed

the necessity to evaluate different genotypes originated from many sources to get benefit of their variability and to emphasize on the Syrian genotype SD09 in wheat breeding program for yield improvement.

CONFLICT OF INTEREST

The authors declared that there is no conflict of interest.

AUTHOR CONTRIBUTIONS

Contribution were equal for all authors.

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