Assessment of protein yield criteria through correlation, regression and path analysis in bread wheat (Triticum aestivum L.) cultivars

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ABSTRACT: Study on relationship among some morphological and agronomic attributes with protein yield of bread wheat cultivars was done in randomized complete block design. Relationship among measured traits were assessed by phenotypic correlation coefficient, step-wise regression and path analysis. Correlation analysis showed the significant reltaion of seed and protein yield with all the traits except correlation of grain filling duration and peduncle length with seed yield as well as spike yield and peduncle length with protein yield. Regression analysis by using step-wise method revealed that 83.8 percent of total variation exist in protein yield accounted for by traits entered to regression model namely; grain filling rate, grain filling duration, peduncle length and spike harvest index. Grain filling rate accounted for the highest amount of variation about 46.5%. Other traits accounted for 20, 11.3 and 6 percent of variation of protein yield, respectively. Because of that, these traits are recommended as the main componenets of protein yield in bread wheat cultivars. Path analysis showed the traits grain filling rate and grain filling duration had the highest and positive direct effects on protein yield. On the other hand, peduncle length and spike harvest index showed low positive and negative direct effect on protein yield. Overall, grain filling rate and grain filling duration were recognized as the best indirect selection criteria to improve protein yield in bread wheat cultivars via seletion especially from preliminary generations of breeding programs.

Keywords: Hexaploid wheat, step-wise regression, path analysis, protein yield, indirect selection

INTRODUCTION

Wheat (Triticum aestivum L.), being the most important food grain of Iran and valuable staple food, invites the attention of breeders, researchers and growers to raise the level of production to over come the food challenge due to increasing population. To overcome food shortage and to feed the ever-increasing population, it is important to increase per unit yield through the development of high yielding and relatively stable wheat genotypes for diverse environments. (Ansari , 2002) reported that wheat crop sown in mid November produces more tillers plant[-1] and more grain yield compared to that planted in mid and late December. A considerable yield improvement in spring wheat is still possible through the use of better breeding techniques and advance agronomic practices.

Manifestation of wheat protein yield fluctuates widely as a result of its interaction with environment because yield is a complicated quantitative parameter and is the product of several contributing factors affecting yield directly or indirectly. Wheat production can be increased through development of productive genotypes/varieties for various agro-climatic conditions and stresses. Selection for protein yield improvement can only be effective if

sufficient genetic variability is present in the genetic material (Ali et al., 2008). Phenotypic correlations are important in determining the degree of association of various yield contributing parameters with protein yield so knowledge of their direct positive and negative effects in new genotypes for adopting suitable selection strategy.

(Singh and Dewivedi , 2002) have reported significant positive association of protein yield plant[-1] with number of spikes bearing tillers plant-1 both at genotypic and phenotypic levels. (Tammam et al .,2000) reported that grain yield plant-1 had a positive genetic correlation with number of spikes plant-1 and 1000-kernel weight. (Shahid et al .,2002) observed that spike length had significant positive genotypic correlation with grain yield.(Kashif and Khaliq .,2004) reported that plant height, spike length, spikelets spike[-1] and 1000-grain weight were positively and significantly correlated with grain yield at genotypic level.

(Ahmad et al .,2010) reported the efficacy of grain filling rate, harvest index and biological yield to increase protein and seed yield in winter wheat genotypes. In other study the results of genetic correlation analysis between yield and the traits remained in ridge regression model showed that 1000-grain weight had the highest direct effect on yield, but the highest indirect effect of this trait was applied through plant total weight, although 1000-grain weight showed the highest direct effect in phenotypic correlation analysis, too. Moreover, fertile tiller number had the strongest negative direct effect on yield (Khayatnejad et al., 2010).

Therefore, the objective of this study was to assertion the phenotypic correlations among measured attributes as well as step-wise regression and path analysis of protein yield in order to determine the best indirect selection criteria in bread wheat cultivars.

MATERIALS AND METHODS

Eighteen bread wheat lines along with Parsi and Sivand cultivars as check (totally twenty winter wheat genotypes) were planted at the beginning of November 2012 at the Research field of Jehad-Agriculture Institute of Isfahan, Isfahan, Iran. Each plots comprise six rows with 2m long and 0.2m apart. In spring 2013 the trial was irrigated every 8 days. Amount of precipitation was 142 mm.

Sixtheen traits viz; seed yield (Kg/ha), spike weight (g), spike harvest index (%), plant harvest index (%), number of seed/spike, biological yield (Kg/ha), number of spikelet/spike, spike yield (g), 1000-seed weight (g), spike length (cm), plant height (cm), peduncle length (cm), grain filling duration, grain filling rate (Kg/ha/day), protein percentage (%) and protein yield (Kg/ha) were measured on 25 normal plants randomly selected from each plot after border effect eliminating.

Traits have been investigated for relation by using pearson's correlation coefficients. Then it is assumed that each of the variables measured depends upon the underlying factors but is also subject to random errors. Step-wise regression was achieved to determine the main components of protein yield as traits entered to the best regression model, which accounted for variation exist in protein yield as dependent variable and other traits as independents. Direct and indirect effects of traits entered to regression model were determined by using path coefficient analysis. In this study, path analysis was carried out based on method given by (Dewey and Lu ,1959). Correlation and step-wise regression was done by SPSS while path analysis was performed using $PATH_2$ software for all the traits entered to regression model.

RESULTS AND DISCUSSION

Relationship among all the studied traits were investigated using phenotypic correlation coefficients. Results for correlation coefficient analysis are presented in Tables 1. The results revealed that protein yield showed highly significant correlation with all the traits except with spike yield and peduncle length. On the other hand, seed yield positively correlated with all the traits except peduncle length and grain filling duration. Correlation of spike yield with seed yield, grain filling rate, protein yield, number of seed/spike and number of spikelet/spike were positive and highly significant while with others non-singificant relationship were observed (Table 1).

Step-wise regression dictated on the importance of the traits grain filling rate, grain filling duration, peduncle length and spike harvest index as the main components of protein yield. These traits entered to regression model and accounted for totally 83.8 percent of variation exist in protein yield (Table 2). The highest portion of these model belongs to grain filling rate about 46.5%. Other traits accounted for 20, 11.3 and 6 percent of variation of protein yield, respectively (Table 2). Hence, grain filling rate and grain filling duration are the main components of protein yield in bread wheat cultivars.

Path analysis for protein yield as dependent variable based on the traits entered to regression model indicated that trait grain filling rate has the highest and positive direct effect on protein yield (Table 3). Grain filling duration also has direct and positive effect on protein yield. Because of that, the traits grain filling rate and grain filling duration are the best indirect selelction criteria to improve protein yield of bread wheat genotypes as well as found transgressive segregation especially from preliminary segreation generations.

On the other hand, these traits correlated positively and significantly with protein yield. Therefore, positive indirect effect of this trait on oil yield via other traits on protein yield must be considered, simultaneously (Akram et al., 2008; Anwar et al., 2009).

Traits peduncle length and spike harvest index showed low positive and negative direct effects on protein yield, recpectively. Also, indirect effects of these traits via grain filling rate and grain filling duration on protein yield were negligible (Table 3). Thus, indirect selection for protein yield improvement through peduncle length and spike harvest index and consider their direct and indirect effects on protein yield can't be efficient in wheat breeding programs. These results are in accordance with the earlier findings (Akram et al., 2008; Golparvar et al., 2006).

Assessment of relationship using correlation coefficient analyses help breeders to distinguish significant relation between traits. Step-wise regression can reduce effect of non-important traits in regression model, in this way traits accounted for considerable variations of dependent variable are determined (Aycecik and Yildirim, 2006). Path analyses that present by (Li ,1956) have been extensively used for segregating correlation between protein yield and its components in wheat. Path analysis is used to determine the amount of direct and indirect effects of the variables on the dependent variable (Li, 1956; Usman et al., 2006).

Genetic enhancement of grain filling ability must be done by selection via traits grain filling rate and grain filling duration. Increasing plant yield could enable breeders to better realize the desired increment in drought stress resistance of bread wheat genotypes and yield stability. Increasing in traits plant height and peduncle length can improve photosynthetic reservoir in bread wheat genotypes (USDA, 2009).

In conclusion, it can be suggested from results of present study that indirect selection in preliminary breeding generations through traits that have the highest direct effect on dependent variables. These traits usually determine by means of statistical procedure like correlation, regression and path analysis. In this research, revealed that traits grain filling rate and grain filling duration are the best indirect selection criteria to improve protein yield in wheat cultivars specifically in early generations.

Table 2. Step-wise regression for protein yield (dependent variable) in bread wheat cultivars

Variable	$b_{(1)}$	Partial R^2	Model R^2	F
Grain filling rate	6.41	46.50	46.5	**
Grain filling duration	88.64	20.00	66.5	**
Peduncle length	156.36	11.30	77.8	**
Spike harvest index	-9.39	6.00	83.8	*
Intercept	-3993.25			**

(1): b values have been tested relative to zero.

Table 3. Path analysis for protein yield in bread wheat cultivars

Variable	(1)	(2)	(3)	(4)	Sum of effects
(1) Grain filling rate	<u>1.17</u>	-0.66	-0.02	0.03	0.514
(2) Grain filling duration	-0.81	<u>0.95</u>	-0.01	-0.04	0.098
(3) Peduncle length	-0.20	-0.09	<u>0.10</u>	0.07	-0.116
(4) Spike harvest index	-0.14	0.14	-0.03	<u>-0.24</u>	-0.271
Residual	0.26				

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