Correlation, Path-coefficient, Normal and Stepwise Regression Analyses Via Two Cycles of Pedigree Selection in Bread Wheat (*Triticum aestivum* L).

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Abstract

Correlation, path- coefficient and regression analyses are important statistical tools which can help breeders to characterized the crop populations during the selection program and select the desirable genotypes of high yield. The current study was aimed to assess these analyses during three successive seasons i.e., 2012/2013, 2013/2014 and 2014/2015 at Fac. Agric. Farm, Assiut University, Egypt. The genetic materials were two segregating bread wheat populations i.e. Debeira x Sahel and Giza 165 x Sakha 93. Grain yield/plant revealed positive and high phenotypic correlation with each of number of spikes/plant, biological yield/plant and weight of spikes/ plant in base and the two cycles of pedigree selection for grain yield/plant in both populations, respectively. It is clear that the strong correlation occurred between grain yield/plant and weight of spikes/plant in all cases. The partitioning of phenotypic correlation into direct and indirect effects by path analysis revealed that the highest direct effect on grain yield/plant was exerted by weight of spikes/plant in base and the two cycles of pedigree selection for grain yield in both populations. Simple regression analysis revealed that the weight of spikes/plant (WS/P) (model no. 6) was superior to other traits and its relative contributions (more than 0.920) in grain yield in both populations across all generations. Multiple regression analysis revealed that, in both populations, the highest contribution in grain yield as more than 96% in base and the two cycles of selection were obtained as done from the model no. 9 which included only two traits i.e. WS/P and threshing index (TI). Meanwhile, those two traits were the main predominant elements in both populations. The stepwise regression analysis revealed to three fitted models for each of base and cycle one as well as two superior models for cycle two of selection in population I. Meanwhile, two fitted models were exhibited for each of base and cycle one and four efficient models released from cycle two of selection in population II. The model no. 1 in all cases included only the WS/P in both populations. It is remark results that the relative contribution of WS/P in grain yield/plant was decreased from 0.921, to 0.843 and to 0.782 and from 0.965, to 0.922 and to 0.840 for base, cycle one and cycle two of selection in population I and II, respectively. Moreover, the model no. 2 in all cases, also, included two traits of WS/P and TI in both populations, which increased the relative contribution for grain yield/plant from 0.921 to 0.988 in base, from 0.843 to 0.969 in cycle one and from 0.782 to 0.993 in cycle two of pedigree selection in population I. As well as from 0.965 to 0.994 in base, from 0.922 to 0.989 in cycle one and from 0.840 to 0.997 in cycle two of selection in population II.

Introduction

Wheat is the most important cereal crop both in area and production over Worlds, thereby providing about 20.0% of total food calories for the people of the world (Vamshikrishna *et al.*, 2013). Moreover, wheat (*Triticum aestivum* L.) is the strategic cereal crop not only in Egypt, but also all over the world. Egypt produces about 8.2 M tons and consumes 17.9 M tons. The gap between total production and consumption is met by imports (USDA, 2014). Also, demand of wheat is increasing with increasing population. Consequently, the maximum crop yield is an important objective in most breeding program and the major emphasis in wheat breeding is on the development of improved varieties (Fellahi *et al.*, 2013). The success of selection procedure depends on the choice of selection criteria for improving grain yield (Samonte *et al.*, 1998).

Correlation coefficient is an important statistical tool which can help wheat's breeders to select the genotypes of high yield. Some of the researchers indicated the positive correlation between grain yield and its components in wheat such as spikes number/plant (Mondal and Hhajura, 2001 and Abdel-Mohsen and Abd El-Shafi, 2014), grains number/spike (Kashif and Khaliq, 2004 and Hannachi *et al.* 2013), biological yield (Naderi *et al.*, 2000 and Fellahi *et al.*, 2013) and harvest index (Ali and Shakor, 2012 and Nasri *et al.*, 2014). Moreover, the positive or negative correlations of grain yield with plant height, seed index and spike length of wheat were also reported (Chaudhary, 1995 and Tammam *et al.*, 2000).

Breeding decisions based only on correlation coefficients may not always be effective since they provide only one-dimensional information while neglecting important and complex interrelationship among plant traits (Kang, 1994).

Path coefficient analysis is an excellent means that can be used by plant breeder to assist in identifying traits that are useful as selection criteria to improve crop yield (Kang *et al.*, 1989 and Milligan *et al.*, 1990).

Path coefficient analysis divides the correlation coefficients into direct and indirect effects (Dixet and Dubey, 1984). Consequently, correlation studies along with path analysis provide a better understanding of the association of different traits with grain yield.

Stepwise multiple linear regression aims to construct a regression equation that includes the traits accounting for the majority of the total yield variation. Spikes number, spike length, seed index, plant height, biological yield, harvest index and weight of spikes were the most important variables contributing the total variability of grain yield (Mohamed, 2009; Ashmawy *et al.*, 2010 and Abd El-Mohsen and Abd El-Shafi, 2014). Moreover, Soleymanfard *et al.* (2012) reported that 75% variation in grain yield was due to spikes/m^2, seed index and plant height. Meanwhile, Nasri *et al.* (2014) found that stepwise regression showed a model included biological yield, harvest index and weight spikes/unit had R^2 of 0.984. The objectives of the current study were:

1- Study the correlation between yield and some of its compo-

nents across base and two cycles of pedigree selection in two segregating populations of bread wheat.

2- Assess the contributions of highest correlated traits with yield via path coefficient analysis in base population and two cycles of selection in both populations.

3- Determine the better models had the significance of the yield components affecting the grain yield via the normal regression and stepwise regression analyses through selection cycles in both populations.

Materials and Methods

The current study was carried out during the three successive seasons i.e., 2012/2013, 2013/2014 and 2014/2015 at Fac. Agric. Farm, Assiut University, Egypt.

I- Genetic materials: The genetic materials in the current investigation were two F_4 segregating bread wheat populations i.e. Debeira x Sahel and Giza165 x Sakha 93.

II- Field procedures:

The F_4-plants for replicated trials were 497 and 210 for population I and II, respectively. Both populations along with their respective parents as well as unselected bulk sample were sown on Nov. 25th, 2013 in randomized complete block design (RCBD) of three replications. The unselected bulk sample was consisted of a mixture of equal number of grains from each family for each population. The plot size was one row, 1.5 m long, 30 cm apart and 5 cm between grains within the row. At harvest, the following traits were measured on 10 random guarded plants in each plot (row)/replicate:

1-Plant height (PH), cm; the distance from ground surface to the base of the main spike.

2-Spike length (SL), cm; measured from the base of the main spike to its tip excluding awns.

3-Number of spikes/plant (NS/P); number of spikes of the plant.

4-Number of spikelets/spike (NSe/S); number of spikelets of the main spike/plant.

5-Weight of spikes/plant (WS/P) in g.; weight of spikes of the plant.

6-Biological yield/plant (BY/P) in g.; the air dry weight of the up ground growth/plant.

7-Grain yield/plant (GY/P) in g.; was recorded as the weight of grains of each guarded plant.

8-Harvest index % (HI); the ratio of GY/P to BY/P.

9-Threshing index % (TI); the ratio of GY/P to WS/P.

The analysis of variance for each population was done as outlined by Steel and Torrie, 1980; and the family means provided the basis of the pedigree line selection. Furthermore, the simple and multiple regression analyses between grain yield/plant and each of the other traits were performed to determine the R^2 values for each case. Moreover, the path-analysis was done for grain yield/plant as resultant variable with the three traits as causal variables which had the highest values of correlation; i.e. no. of spikes/plant, weight of spikes/plant and biological yield/plant; with yield in base population to divide the correlation values to direct and indirect effects on yield. Also, the stepwise regression was done for finding the relationship between the causal, effected and signif-

icant independent yield components on grain yield.

Single trait selection was practiced based on grain yield/plant. The best 20% of the families (100 and 50 families for population I and II, respectively) were marked for grain yield/plant based on the family means.

All the selected families, respective parents and bulk sample for each population were sown in separate trail on Nov. 25th 2014. The same procedures and experimental design of the previous season were followed for each trail.

The twenty and ten superior families out of previous selections for population I and II were saved for evaluation in the F_6 generation. The predicted genetic advances were calculated from these superior families for each population.

III- Statistical analysis

1- Simple, multiple and step wise regression analyses

The Ver. 10 of SPSS-PC program of Nie *et al.* (1975) was used to estimate simple and multiple regression, coefficient of determination (R^2) and stepwise multiple regression in the base and selected families of both populations. Path-analysis was done as outlined by Dewey and Lu (1959).

**2-The phenotypic (r_{pij}) correlations**

The phenotypic (r_{pij}) correlations via base population and the two cycles of selection were calculated among the studied traits as outlined by Walker (1960) as:

$$rp_{ij} = Cov.\ p_{ij}/\sigma_{pi} \times \sigma_{pj}$$

Where: Cov. pij: the phenotypic covariance between i and j traits. σ_{pi} and σ_{pj} are the phenotypic standard deviation of the traits i and j, respectively.

3- Path coefficient analysis:

Simple phenotypic correlation coefficient between each pairs of studied traits was estimated for grain yield/plant criterion in the base population and the two cycles of selection for both studied populations. Path coefficient analysis was done according to the procedure followed by Dewey and Lu (1959). The contribution of number of spikes/plant (NS/P), biological yield/plant (BY/P) and weight of spikes/plant (WS/P), who possessed the highest correlation values with grain yield/plant (GY/P) across all generation in both populations as well as residual factors (X) were included in the path coefficient analysis as shown in the following diagram:
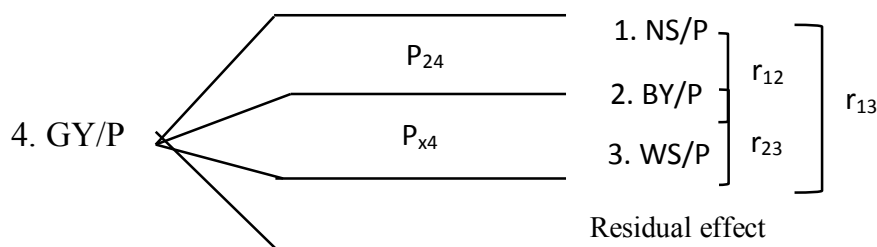
Fig. 1: Direct and indirect of NS/P, BY/P and WS/P on GY/P.

$r_{14} = p_{14} + r_{12}\ p_{24} + r_{13}\ p_{34}$
$r_{24} = p_{24} + r_{12}\ p_{14} + r_{23}\ p_{34}$
$r_{34} = p_{34} + r_{13}\ p_{14} + r_{23}\ p_{24}$
$1 = p_{xy}^2 + p_{14}^2 + p_{24}^2 + p_{34}^2 + 2p_{14}r_{12}p_{24} + 2p_{14}r_{13}p_{34} + 2p_{24}r_{23}p_{34}$

4 - Stepwise regression analysis

The stepwise regression analysis was carried out for the data obtained to test the significance of the independent variables affecting the grain yield in the base population and the two cycles of selection for both studied populations. Stepwise multiple linear regressions proved to be more efficient than the full model regression to determine the predictive equation for yield (Naser and Leilah, 1993 and Mohamed, 1999).

Results and Discussion

I- Description of the base population

The two base populations were presented by 497 and 210 F_4 replicated families for population 1 and 2, respectively along with their parents and the unselected bulk sample.

The values of phenotypic correlations between grain yield/plant and each of number of spikes/plant, biological yield/plant and weight of spikes/plant were high and accounted 0.652, 0.891 and 0.960 in population I and 0.786, 0.959 and 0.982 in population II, respectively. Also, weight of spikes/ plant possessed high phenotypic correlations with each of number of spikes/plant (0.751) and biological yield/plant (0.968) in population I, as well as (0.819) and (0.975) in population II, respectively (Table 1).

Weight of spikes/plant was superior trait for its contribution (0.920 and 0.965) in grain yield/plant, followed by (in rank) biological yield/plant (0.794 and 0.920) and numbers of spikes/plant (0.425 and 0.617) in populations I and II, respectively (Table 2). Moreover, the R^2 values for all traits together on grain yield/plant were 0.987 and 0.995 in populations I and II, respectively. The path coefficient analyses revealed that about 95 and 97% of variance in grain yield/plant could be explained by these three traits in populations I and II, respectively. Also, weight of spikes/plant out of them had the major direct and indirect effects on grain yield/plant (Tables 5 & 6).

II- Pedigree line selection in the F_4 and F_5-generations for grain yield/plant, g.

The observed direct responses of pedigree line selection for grain yield/plant (selection criterion) in population I were 15.98 and 33.18, 13.68 and 12.57, and 26.94 and 28.39% over one and two cycles of selection as accounted from unselected bulk sample, better parent and mid parents. These direct responses were 8.89 and 32.35, 8.33 and 24.45, and 17.21 and 36.58% for same respective items in population II. It is clear that the direct response for grain yield/plant in cycle two (F_6) was larger than cycle one (F_5) in both populations indicating to the effectiveness of direct pedigree selection for grain yield in those studied populations of bread wheat. Moreover, the three traits i.e. number of spikes/plant, biological yield/plant and weight of spikes/plant had the highest positive values of correlated response in cycle one (F_5) and cycle two (F_6) in both populations.

III. Phenotypic correlation in one (F_5) and two (F_6) cycles of pedigree selection for grain yield/plant.

Grain yield/plant had positive and high phenotypic correlation with each of number of spikes/plant (0.582 and 0.305), biological yield/plant

(0.807 and 0.708) and weight of spikes/ plant (0.918 and 0.884) in one and two cycles of selection for grain yield/plant in population I, respectively. It is clear that the greatest correlation occurred between grain yield/plant and weight of spikes/plant in one and two cycles of selection (Table 3).

Weight of spikes/plant was correlated in high and positive values with each of spike length (0.539 and 0.650); number of spikes/plant (0.752 and 0.345) and biological yield/plant (0.953 and 0.866) in one and two cycles of selection for grain yield/plant in population I, respectively. Moreover, high and positive phenotypic correlation coefficients were recorded between biological yield/plant and each of spike length (0.636 and 0.640), number of spikes/plant (0.832 and 0.527), and number of spikelets/spike (0.390 and 0.541) in one and two cycles of selection for grain yield/plant. Also, the phenotypic correlation between harvest index and threshing index (0.881 and 0.680) was in same picture. Also, the values between number of spikelets and spike length were 0.651 and 0.545 in respective cycles. It is clear that the obtained values of correlation in one and two cycles of selection had the same trend as in base population with a little decrease in values with the cycles of selection. The same view of correlation results could be found in population II. These results could be expressed as change in genetic makeup from generation to other (Table 4).

Consequently, the results of correlation indicate that the most effective components in grain yield of wheat would be number of spikes/plant, biological yield and weight of spikes/plant in major issue and also spike length and number of spikelets/spike in minor role. It is concluded that these traits could be selected for wheat improvement and would be beneficial for the grain yield (Tables 3 & 4).

Positive genotypic correlation was recorded between yield and each of number of spikes/plant (Anawar *et al.,* 2009 and Kotal *et al.,* 2010), biological yield/plant (Ajmal *et al.,* 2009; Ferdeous *et al.,* 2010; Khan *et al.,* 2010 and Mostafa 2015). Also, the obtained correlations are accordance with those obtained by Abdel El-Kareem and El-Saidy (2011), Khan and Naqvi (2012), Mahdy *et al.* (2012a), Vamshikrishna *et al.* (2013), Ahmed *et al.* (2014) and Nasri *et al.* (2014).

IV. **Path analysis in base, one (F_5) and two (F_6) cycles of pedigree selection for grain yield/plant**

The partitioning of phenotypic correlation into direct and indirect effects by path analysis revealed that the highest direct effect on grain yield/plant was exerted by weight of spikes/plant in base population, cycle one and cycle two of pedigree selection for grain yield in both studied populations (Tables 5 & 6). The values of these direct effects accounted 1.5185, 1.5870 and 1.1181 in population I and 0.9460, 0.7508 and 1.4333 in population II relative to base population (F4), cycle one (F5) and cycle two (F6) of pedigree selection for grain yield/plant, respectively.

Moreover, the highest indirect effects were correlated also with the weight of spikes/plant across the base

population, cycle one and cycle two of selection in both studied populations. The estimates of these indirect effects were larger via biological yield/plant than number of spikes/plant across all generations in both populations. Their values were 1.4700, 1.5124 and 0.9683 via biological yield/plant followed by 1.404, 1.1934 and 0.3857 via number of spikes/plant in population I and 0.9223, 0.7088 and 1.3831 via biological yield/plant followed by 0.7748, 0.6254 and 0.5547 via number of spikes/plant in population II across their base population, cycle one and cycle two of pedigree selection for grain yield/ plant. The values over the unity could be due to the negative effect of other traits.

These results provided that the weight of spikes/plant has exhibited to be powerful trait as a yield component and must be given preference in selection to superior genotypes of wheat. It is remark and clear conclusion that the path coefficient analysis revealed that about 95, 89 and 80% of phenotypic variance $(1-R^2)$ in grain yield/plant could be explained by the selected traits of path analysis in base population, cycle one and cycle two of selection for grain yield/plant in population I, respectively. Also, about 97, 93 and 87% of phenotypic variance in grain yield/plant could be exerted by these selected traits for path analysis in base, cycle one and two of selection in grain yield/plant in population II, respectively. Meanwhile, most of these phenotypic direct and indirect effects were explained by weight of spikes/plant as revealed by path analysis.

Also, there are two remarks showed be taken an interest issue i.e. a) the direct and indirect effects of weight of spikes/plant were decreased from base population to cycle two of selection in both populations. This result was coupled with b) decreasing of variances $(1-R^2)$ exhibited from the path analysis. Otherwise, the residual factors were increased from base population to cycle one and cycle two of selection. The values were 0.2327, 0.3245 and 0.4485 in population I and 0.1851, 0.2707 and 0.3792 in population II across the base, cycle one and cycle two, respectively. These results are indicating that the genes controlling the weight of spikes/plant and other traits in the current path analysis tend to the maximum genetic expression. Consequently, the selection should be directed to other traits in next generations.

Different estimates of direct and indirect effects of yield components on grain yield of wheat revealed by many studies according the studied populations such as Kashif and Khaliq (2004), Gulmezoglu *et al.* (2010), Khan and Naqvi (2012), Fellahi *et al.* (2013), Hannachi *et al.* (2013), Vamshikrishna *et al.* (2013), Abd El-Mohsen and Abd El-Shafi (2014) and Nasri *et al.* (2014).

V. Simple, multiple and stepwise multiple regression analyses

Simple regression: Simple regression analysis revealed that the weight of spikes/plant (WS/P) (model no. 6) was superior to other traits and its relative contributions in grain yield were 0.921, 0.843 and 0.782 in population I and 0.956, 0.922 and 0.840 in population II for base (F4),

cycle one (F5) and cycle two (F6) of pedigree selection for grain yield/plant, respectively. Biological yield/plant (BY/P) (model no. 5) and number of spikes/plant (NS/P) (model no. 3) were in the second and third order, respectively, after WS/P for their contributions in grain yield of both populations.

Also, it is clear results that the value of each contribution of the three traits i.e. WS/P, BY/P and NS/P was decreased from the base population to cycle one and cycle two of selection in remark trend for both populations. These results are in line with correlation values, direct and indirect effects as revealed by path analysis of those traits on grain yield/plant, also, in both populations. The obtained results indicated that the genetic expression of these traits closed to the maximum values and the next cycles of selection should be directed to different traits as a tandem selection.

Spike length in both populations and plant height and number of spikelets/spike in population II exhibited to may be having an importance in the next cycles of selection due to their contribution in grain yield increased from base population to cycle one and cycle two of selection. For example, the spike length which contributed by 0.036 and 0.067 in base population, increased to 0.123 and 0.108 in cycle two in population I and II, respectively. Also, number of spikelets/spike recorded value of 0.100 in base increased to 0.299 in cycle two of selection in population II.

Multiple regressions: Multiple regression analysis revealed that, in population I, the highest contribution

in grain yield as more than 98% in base, 97% in cycle one and 99% in cycle two of selection were obtained via seven models nos. 9, 10, 13, 14, 17, 19 and 20. The model no. 9 included only two traits i.e. WS/P and TI. Meanwhile, those two traits were the main predominant elements in previous seven models. Also, in population II, ten models nos. 9, 10, 11, 13, 14, 16, 17, 18, 19 and 20 had contributed in grain yield by 99% or more in base, cycle one and cycles two of selection. All these models included mainly WS/P and TI as revealed in seven models as in pop. I and the other three models, namely 11, 16 and 18, the HI was found instead of TI. Consequently, the WS/P and TI had justified being more harmonized with grain yield variations. It is remark results that the model no. 9 which included only the WS/P and TI in both populations is superior to other combinations and preferred by wheat breeders.

It could be concluded that the coefficient of regression for weight of spikes/plant (WS/P) showed decreased linear relationship from base population to cycle two of selection in both of simple and multiple regression analyses, except models no. 19 and 20 in both populations and models nos. 15, 16, and 18 in population II, revealing that the other traits in multiple regression analysis could be change the trend of the coefficient of regression for WS/P according the relationship with these traits across the different generations via cycles of selection.

Stepwise regression: The stepwise regression analysis revealed to three fitted models for each of base

and cycle one as well as two superior models for cycle two of selection in population I. Meanwhile, two fitted models were exhibited for each of base and cycle one and four efficient models released from cycle two of selection in population II. The model no. 1 in all cases included only the WS/P in both populations. It is remark results that the relative contribution of WS/P in grain yield/plant was decreased from 0.921, to 0.843 and to 0.782 and from 0.965, to 0.922 and to 0.840 for base, cycle one and cycle two of selection in population I and II, respectively. Moreover, the model no. 2 in all cases, also, included two traits of WS/P and TI in both populations. It is remark results that the insertion of TI with WS/P in this model (no. 2) were increased the relative contribution for grain yield/plant from 0.921 to 0.988 in base, from 0.843 to 0.969 in cycle one and from 0.782 to 0.993 in cycle two of pedigree selection in population I. As well as from 0.965 to 0.994 in base, from 0.922 to 0.989 in cycle one and from 0.840 to 0.997 in cycle two of selection in population II.

It is clear finding what the relative contribution in this model (no.2) does not decrease but still staple from base population to cycle two of selection in opposite resulting as in model 1 in both populations. This means that the WS/P with TI increased the efficiency of this model which includes only two the traits to give excellent relative contribution close to 99% in grain yield. Consequently, it will be more suitable and preferable for indirect selection for grain yield in wheat.

Also, the insertion of third trait as found by Model 3 in base population (BY/G) and in cycle one (NSe/S) in population I and in cycle two (PH) of pedigree selection in population II increased the relative contribution for grain yield, as independent variable (predictor) from 0.921 to 0.988, from 0.843 to 0.971 and from 0.840 to 0.999, respectively.

It is obvious and remark result that the obtained Model no. 4 in cycle two of selection for grain yield which includes four traits i.e. WS/P, TI, PH and NSe/S gave relative contribution in grain yield equal to unity (1.000) in population II. Consequently, this Model is fit and superior to use in selection for grain yield. It is be noted that the relative contributions in grain yield were increased gradually in cycle two of selection in population II and accounted 0.840 (Model 1), 0.997 (Model 2), 0.997 (Model 3) and 1.000 (Model 4).

Finally, it could be concluded that the regression analysis showed the superiority contribution for weight of spikes/plant in grain yield in all studied models which included it. These results are in line with the values of coefficient of correlation between both of them.

Many researchers have used the stepwise on wheat such as Mohamed (1999), Pržulj and Momcilovic (2011), Soleymanifard et al. (2012), Hannachi et al. (2013); Abd El-Mohsen and Abd El-Shafi (2014) and Nasri et al. (2014). Also, Stepwise regression was used to remove the effects of ineffective or low impact on yield traits in the regression model. Moreover, stepwise multiple linear regressions proved to be more effi-

cient than the full model regression to determine the predictive equation for yield in wheat [Naser and Leilah (1993), Mohamed (1999) and Nasri *et al.* (2014)].

Actual and expected yields

The insignificant values of χ2 between the actual and expected yields exerted high homogeneity between them of all studied models in cycle two (F6) of selection for both populations (Tables 10 & 11). Moreover, the coefficients of correlation between actual and expected yield were extremely high and significant for Models 5 & 6 out of simple, Models of stepwise and all proposed Models of multiple regression analyses in both populations. According to the values of R2 resulted from these models, χ2 values and coefficients of correlation for actual and expected yields, it could be concluded that the high R2 values resulted high homogeneity between actual and expected yield as in their respective regression models.

It is remark result that the Model no. 2 of stepwise regression which be equal to Model no. 9 of multiple regression included only two traits of WS/P and IT possessed χ2 equal to zero as well as coefficients of correlation and reliability equal to unity in both populations, indicating that completely the variance of GY/P can be accounted for by the linear combination of WS/P and TI scores can use their regression equations ($\hat{Y}$= -15.792 + 0.679 WS/P + 0.233 TI in population I and $\hat{Y}$= -18.146 + 0.681 WS/P + 0.266 TI in population II) for predicating GY/P.

The results revealed that the rates (F_6/F_5) of actual grain yield/plant were ranged from 69.83 to 97.96 with an average of 83.91% in population I, and ranged from 72.19 to 107.13 with an average of 86.75% in population II, indicating that the average of yield in F6 was lower than F5 and represented more than 80% of it. This result could be extending to all families except the family no. 249 of population II which appeared F6/F5 of 107.13% and stated as promised family before (Tables 12 & 13).

In the final finding, the stepwise multiple regression analysis is a multiple statistical method that can screen or select the most important variables (traits) through a dependent variable (grain yield). Based on this method, weight of spikes/plant (WS/P) was the most important trait and had the strongest variation in grain yield/plant in the current studied populations of wheat. Moreover, the threshing index (TI) with WS/P were presented powerful model to predict grain yield/plant, this was remark finding.

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الإرتباط ومعامل المرور والإنحدار العادى والمتدرج خلال دورتين من الإنتخاب المُنسب فى عشيرتين من قمح الخبز

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الملخص

تعتبر تحليلات الإرتباط ومعامل المرور والإنحدار أدوات إحصائية مهمة تساعد مربـى النبات لتوصيف العشائر النباتية خلال برامج الإنتخاب وإنتخاب التراكيب الوراثيـة المرغوبـة ذات المحصول العالى. وتهدف الدراسة الحالية إلى تقدير تلك التحليلات خـلال ثلاثـة مواسـم متتابعة هى ٢٠١٣/٢٠١٢ و ٢٠١٤/٢٠١٣ و ٢٠١٥/٢٠١٤ بمزرعة كلية الزراعة جلمعـة أسيوط. وقد أستخدمت عشيرتين إنعزالتين هما دييبيرا * ساحل و جيزة ١٦٥ * سخا ٩٣. لقـد أرتبط محصول حبوب/النبات بقيم عالية و موجبـة بصـفات عـدد سـنابل/النبـات والـوزن البيولوجى/نبات ووزن سنابل/النبات فى العشيرة الأساسية ودورتـين مـن الإنتخـاب المنسـب لمحصول حبوب/النبات فى العشيرتين تحت الدراسة. وقد أوضحت النتائج أن أعلى قيم الإرتباط سجلت بين محصول حبوب /النبات ووزن سنابل النبات فى جميع الحالات. كما أوضـح تقسـيم الإرتباط إلى تأثير مباشر وغير مباشر من خلال تحليل معامل المرور أن وزن سـنابل النبـات كان لها التأثير المباشر وغير المباشر الأعلى على محصول حبوب/النبات فى العشرة الأساسـية ودورتى الإنتخاب المنسب فى العشيرتين. كمـا أوضـح الإنحدار البسـيط أن أيضـا وزن سنابل/النبات (الموديل رقم ٦) كانت الأعلى فى مساهمتها فى محصول حبوب النبات (أكثر مـن ٠.٩٢٠) فى العشيرتين فى جميع الحالات. وأشار الإنحدار المتعدد أن أعلـى مسـاهمة فـى محصول حبوب/النبات كانت أعلى من ٩٦% فى العشيرة الأساسية ودورتـى الإنتخـاب مـن الموديل رقم ٩ والذى يشمل صفتين فقط هما وزن سنابل/النبات ومعامل التقريط فى العشيرتين وأن هاتين الصفتين كانتا فى أغلب موديلات الإنحدار تحت الدراسة. وأوضح الإنحدار المتـدرج أن هناك ثلاثة موديلات متفوقة فى العشيرة الأساسية والدورة الأولى من الإنتخاب وموديلين فى الدورة الثانية من الإنتخاب فى العشيرة الأولى وأن هناك موديلين متفوقين فى العشيرة الأساسـية والدورة الأولى من الإنتخاب وأربعة موديلات فى الدورة الثانية مـن الإنتخـاب فـى العشـيرة الثانية. ولقد أشتمل الموديل الأول فى جميـع حـالات الإنحـدار المتـدرج علـى صـفة وزن سنابل/النبات فقط فى العشيرتين. وقد أظهرت النتائج أن مساهمة وزن سنابل/النبات قد أنفضـت من ٠.٩٢١ إلى ٠.٨٤٣ وإلى ٠.٧٨٢ ومن ٠.٩٦٥ إلى ٠.٩٢٢ والى ٠.٨٤٠ فـى العشـيرة الأساسية إلى الدورة الأولى والثانية من الإنتخاب فى العشيرة الأولى والثانية على الترتيب. كمـا أن الموديل رقم ٢ فى جميع الحالات من الإنحدار المتدرج أشتمل عل صفتين فقـط همـا وزن سنابل/النبات ومعامل التقريط فى العشيرتين والذى زاد من المساهمة النسبية فـى محصـول حبوب/النبات من ٠.٩٢١ إلى ٠.٩٨٨ فى العشيرة الأساسية ومـن ٠.٨٤٠ إلـى ٠.٩٦٩ فـى الدورة الأولى ومن ٠.٧٨٢ إلى ٠.٩٩٣ فى الدورة الثانية من الإنتخاب المنسب فـى العشـيرة الأولى. وبالمثل من ٠.٩٦٥ إلى ٠.٩٩٤ فى العشير الأساسية ومن ٠.٩٢٢ إلـى ٠.٩٨٩ فـى الدورة الأولى ومن ٠.٨٤٠ إلى ٠.٩٩٧ فى الدورة الثانية من الإنتخاب فى العشيرة الثانية.

Table 1. Phenotypic correlations among studied traits for the F_4-generatin of population I (above diagonal) and II (below diagonal).

	PH	SL	NS/P	NSe/S	BY/P	WS/P	GY/P	HI	TI
PH		0.330	0.210	0.446	0.391	0.319	0.282	-0.205	-0.089
SL	0.136		0.363	0.619	0.449	0.351	0.189	-0.535	-0.569
NS/P	0.198	0.092		0.296	0.811	0.751	0.652	-0.317	-0.335
NSe/S	0.383	0.538	0.168		0.399	0.308	0.183	-0.462	-0.438
BY/P	0.363	0.323	0.844	0.410		0.968	0.891	-0.189	-0.237
WS/P	0.320	0.313	0.819	0.339	0.975		0.960	0.019	-0.110
GY/P	0.321	0.260	0.786	0.316	0.959	0.982		0.250	0.152
HI	-0.137	-0.202	-0.226	-0.303	-0.147	0.019	0.127		0.864
TI	-0.152	-0.344	-0.488	-0.247	-0.445	-0.461	-0.301	0.522	

Table 2. Coefficient of determination (R^2) for grain yield/plant by studied traits for families in both populations in the F_4-generation.

	PH	SL	NS/P	NSe/S	BY/P	WS/P	HI	TI	All traits
Pop. I	0.079	0.035	0.425	0.033	0.794	0.920	0.062	0.022	0.987
Pop. II	0.103	0.067	0.617	0.100	0.920	0.965	0.016	0.090	0.995

Table 3. Estimation of phenotypic correlation coefficients for studied traits in the cycle one (F$_5$) (above diagonal) and cycle two (F$_6$) (blew diagonal) of pedigree line selection for grain yield/ plant in population I.

	PH	SL	NS/P	NSe/S	BY/P	WS/P	GY/P	HI	TI
PH		0.366	0.208	0.274	0.373	0.260	0.176	-0.324	-0.215
SL	0.340		0.506	0.651	0.636	0.539	0.308	-0.585	-0.652
NS/P	0.204	0.054		0.234	0.832	0.752	0.582	-0.656	-0.660
NSe/S	0.475	0.545	0.377		0.390	0.308	0.105	-0.457	-0.501
BY/P	0.362	0.640	0.527	0.541		0.953	0.807	-0.574	-0.602
WS/P	0.050	0.650	0.345	0.344	0.866		0.918	-0.351	-0.478
GY/P	-0.173	0.351	0.305	0.093	0.708	0.884		-0.025	-0.127
HI	-0.685	-0.531	-0.356	-0.678	-0.658	-0.296	0.047		0.881
TI	-0.384	-0.728	-0.182	-0.543	-0.560	-0.568	-0.124	0.680	

Table 4. Estimation of phenotypic correlation coefficients for studied traits in the cycle one (F$_5$) (above diagonal) and cycle two (F$_6$) (blew diagonal) of pedigree line selection for grain yield/ plant in population II.

	PH	SL	NS/P	NSe/S	BY/P	WS/P	GY/P	HI	TI
PH		0.193	0.060	0.446	0.398	0.246	0.234	-0.553	-0.207
SL	0.155		0.185	0.400	0.397	0.384	0.282	-0.417	-0.425
NS/P	-0.146	-0.211		0.012	0.838	0.833	0.825	-0.373	-0.412
NSe/S	-0.099	0.708	0.081		0.185	0.014	-0.025	-0.533	-0.133
BY/P	0.088	0.279	0.515	0.642		0.944	0.928	-0.551	-0.470
WS/P	0.191	0.461	0.387	0.741	0.965		0.960	-0.339	-0.554
GY/P	0.398	0.330	0.299	0.545	0.850	0.916		-0.215	-0.316
HI	0.366	-0.006	-0.531	-0.347	-0.620	-0.446	-0.116		0.562
TI	0.317	-0.408	-0.533	-0.616	-0.562	-0.499	-0.111	0.876	

Table 5. Partitioning of phenotypic correlation coefficients into direct and indirect effects by path coefficient analysis for base, cycle one and cycle two of pedigree selection for grain yield /plant in population I.

Correlation			Phenotypic correlation		
Generation			Base pop. (F$_4$)	Cycle one (F$_5$)	Cycle two (F$_6$)
1-Number of spikes/plant vs. Grain yield/plant	**r**	=	**0.6520**	**0.5820**	**0.3050**
Direct effect	P$_{14}$	=	-0.0552	-0.0797	0.0781
Indirect effects via biological yield/plant	r$_{12}$p$_{24}$	=	-0.4332	-0.5317	-0.1589
Indirect effects via weight of spikes/plant	r$_{13}$p$_{34}$	=	1.1404	1.1934	0.3857
	Total	=	**0.6520**	**0.5820**	**0.3050**
2-Biological yield/plant vs. Grain yield/plant	**r**	=	**0.8910**	**0.8070**	**0.7080**
Direct effect	P$_{24}$	=	-0.5342	-0.6391	-0.3014
Indirect effects via number of spikes/plant	r$_{12}$p$_{14}$	=	-0.0448	-0.0663	0.0412
Indirect effects via weight of spikes/plant	r$_{23}$p$_{34}$	=	1.4700	1.5124	0.9683
	Total	=	**0.8910**	**0.8070**	**0.7080**
3-Weight of spikes/plant vs. Grain yield/plant	**r**	=	**0.9600**	**0.9180**	**0.8840**
Direct effect	P$_{34}$	=	1.5185	1.5870	1.1181
Indirect effects via number of spikes/plant	r$_{13}$p$_{14}$	=	-0.0415	-0.0599	0.0269
Indirect effects via biological yield/plant	r$_{23}$p$_{24}$	=	-0.5171	-0.6091	-0.2610
	Total	=	**0.9600**	**0.9180**	**0.8840**
	1-R^2	=	**0.9459**	**0.8947**	**0.7988**
	Residual factor	=	**0.2327**	**0.3245**	**0.4485**

Table 6. Partitioning of phenotypic correlation coefficients into direct and indirect effects by path coefficient analysis for base, cycle one and cycle two of pedigree selection for grain yield /plant in population II.

Correlation			Phenotypic correlation		
Generation			Base pop. (F$_4$)	Cycle one (F$_5$)	Cycle two (F$_6$)
1-Number of spikes/plant vs. Grain yield/plant	**r**	=	**0.7860**	**0.8250**	**0.2990**
Direct effect	P$_{14}$	=	-0.0685	0.0533	0.0257
Indirect effects via biological yield/plant	r$_{12}$p$_{24}$	=	0.0797	0.1463	-0.2814
Indirect effects via weight of spikes/plant	r$_{13}$p$_{34}$	=	0.7748	0.6254	0.5547
	Total	=	**0.7860**	**0.8250**	**0.2990**
2-Biological yield/plant vs. Grain yield/plant	**r**	=	**0.9590**	**0.9280**	**0.8500**
Direct effect	P$_{24}$	=	0.0945	0.1746	-0.5464
Indirect effects via number of spikes/plant	r$_{12}$p$_{14}$	=	-0.0578	0.0446	0.0132
Indirect effects via weight of spikes/plant	r$_{23}$p$_{34}$	=	0.9223	0.7088	1.3831
	Total	=	**0.9590**	**0.9280**	**0.8500**
3-Weight of spikes/plant vs. Grain yield/plant	**r**	=	**0.9820**	**0.9600**	**0.9160**
Direct effect	P$_{34}$	=	0.9460	0.7508	1.4333
Indirect effects via number of spikes/plant	r$_{13}$p$_{14}$	=	-0.0561	0.0444	0.0099
Indirect effects via biological yield/plant	r$_{23}$p$_{24}$	=	0.0921	0.1648	-0.5272
	Total	=	**0.9820**	**0.9600**	**0.9160**
	1-R^2	=	**0.9657**	**0.9267**	**0.8562**
	Residual factor	=	**0.1851**	**0.2707**	**0.3792**

Table 7. Regression analysis in different models for base, cycle one and cycle two of pedigree selection for grain yield/plant in population I

Model No.	Independent trait/s	Generation	R²	Regression equation
1	PH	Base (F4)	0.080	$\hat{Y} = 2.064 + 0.175\ \dot{X}$
		Cycle one (F5)	0.031	$\hat{Y} = 13.797 + 0.088\ \dot{X}$
		Cycle two (F6)	0.030	$\hat{Y} = 21.248 - 0.050\ \square$
2	SL	Base (F4)	0.036	$\hat{Y} = 9.253 + 0.758\ \dot{X}$
		Cycle one (F5)	0.095	$\hat{Y} = 13.441 + 0.747\ \dot{X}$
		Cycle two (F6)	0.123	$\hat{Y} = 11.484 + 0.558\ \dot{X}$
3	NS/P	Base (F4)	0.425	$\hat{Y} = 5.089 + 1.397\ \dot{X}$
		Cycle one (F5)	0.339	$\hat{Y} = 11.869 + 0.966\ \dot{X}$
		Cycle two (F6)	0.093	$\hat{Y} = 14.603 + 0.280\ \dot{X}$
4	NSe/S	Base (F4)	0.034	$\hat{Y} = 2.323 + 0.674\ \dot{X}$
		Cycle one (F5)	0.011	$\hat{Y} = 15.625 + 0.269\ \dot{X}$
		Cycle two (F6)	0.009	$\hat{Y} = 15.581 + 0.105\ \dot{X}$
5	BY/P	Base (F4)	0.794	$\hat{Y} = 1.924 + 0.373\ \square$
		Cycle one (F5)	0.651	$\hat{Y} = 8.046 + 0.268\ \dot{X}$
		Cycle two (F6)	0.502	$\hat{Y} = 8.969 + 0.196\ \dot{X}$
6	WS/P	Base (F4)	0.921	$\hat{Y} = 0.748 + 0.693\ \dot{X}$
		Cycle one (F5)	0.843	$\hat{Y} = 4.807 + 0.567\ \dot{X}$
		Cycle two (F6)	0.782	$\hat{Y} = 5.037 + 0.500\ \dot{X}$
7	HI	Base (F4)	0.062	$\hat{Y} = 7.237 + 0.244\ \square$
		Cycle one (F5)	0.001	$\hat{Y} = 22.540 - 0.018\ \square$
		Cycle two (F6)	0.002	$\hat{Y} = 17.005 + 0.020\ \dot{X}$
8	TI	Base (F4)	0.023	$\hat{Y} = 7.680 + 0.136\ \dot{X}$
		Cycle one (F5)	0.016	$\hat{Y} = 27.825 - 0.083\ \square$
		Cycle two (F6)	0.015	$\hat{Y} = 21.426 - 0.052\ \square$
9	WS/P , TI	Base (F4)	0.988	$\hat{Y} = -16.655 + 0.713\ \square_1 + 0.232\ \square_2$
		Cycle one (F5)	0.969	$\hat{Y} = -18.093 + 0.687\ \square_1 + 0.264\ \square_2$
		Cycle two (F6)	0.993	$\hat{Y} = -15.792 + 0.679\ \square_1 + 0.233\ \square_2$
10	BY/P, WS/P, TI	Base (F4)	0.988	$\hat{Y} = -15.872 - 0.035\ \square_1 + 0.770\ \square_2 + 0.223\ \square_3$
		Cycle one (F5)	0.970	$\hat{Y} = -16.767 - 0.043\ \square_1 + 0.756\ \square_2 + 0.248\ \square_3$
		Cycle two (F6)	0.994	$\hat{Y} = -15.512 - 0.021\ \square_1 + 0.714\ \square_2 + 0.229\ \square_3$

Table 7. Counted.

Model No.	Independent traits	Generation	R^2	Regression equation
11	BY/P, WS/P, HI	Base (F4)	0.980	$\hat{Y} = -13.497 + 0.219\,X_1 + 0.322\,X_2 + 0.333\,X_3$
		Cycle one (F5)	0.951	$\hat{Y} = -13.052 + 0.171\,X_1 + 0.369\,X_2 + 0.351\,X_3$
		Cycle two (F6)	0.971	$\hat{Y} = -12.691 + 0.295\,X_1 + 0.113\,X_2 + 0.361\,X_3$
12	NS/P, BY/P, WS/P	Base (F4)	0.944	$\hat{Y} = 1.375 - 0.115\,X_1 - 0.220\,X_2 + 1.090\,X_3$
		Cycle one (F5)	0.895	$\hat{Y} = 4.679 - 0.135\,X_1 - 0.211\,X_2 + 0.978\,X_3$
		Cycle two (F6)	0.798	$\hat{Y} = 4.596 + 0.072\,\dot{X}_1 - 0.082\,X_2 + 0.629\,X_3$
13	NSe/S, WS/P, TI	Base (F4)	0.988	$\hat{Y} = -15.726 - 0.033\,X_1 + 0.715\,X_2 + 0.229\,X_3$
		Cycle one (F5)	0.971	$\hat{Y} = -14.453 - 0.118\,X_1 + 0.689\,X_2 + 0.251\,X_3$
		Cycle two (F6)	0.993	$\hat{Y} = -14.915 - 0.026\,X_1 + 0.680\,X_2 + 0.228\,X_3$
14	SL, WS/P, TI	Base (F4)	0.988	$\hat{Y} = -15.431 - 0.067\,X_1 + 0.717\,X_2 + 0.224\,X_3$
		Cycle one (F5)	0.971	$\hat{Y} = -15.569 - 0.133\,X_1 + 0.697\,X_2 + 0.246\,X_3$
		Cycle two (F6)	0.994	$\hat{Y} = -14.087 - 0.095\,X_1 + 0.691\,X_2 + 0.219\,X_3$
15	SL, NS/P, BY/P, WS/P	Base (F4)	0.955	$\hat{Y} = 6.026 - 0.449\,X_1 - 0.155\,X_2 - 0.120\,X_3 + 0.963\,X_4$
		Cycle one (F5)	0.914	$\hat{Y} = 8.189 - 0.459\,X_1 - 0.191\,X_2 - 0.114\,X_3 + 0.885\,X_4$
		Cycle two (F6)	0.873	$\hat{Y} = 8.868 - 0.637\,X_1 - 0.060\,X_2 - 0.011\,X_3 + 0.680\,X_4$
16	NS/P, BY/P, WS/P, HI	Base (F4)	0.980	$\hat{Y} = -13.509 + 0.002\,X_1 + 0.219\,X_2 + 0.322\,X_3 + 0.333\,X_4$
		Cycle one (F5)	0.952	$\hat{Y} = -14.428 + 0.133\,X_1 + 0.163\,X_2 + 0.352\,X_3 + 0.373\,X_4$
		Cycle two (F6)	0.972	$\hat{Y} = -12.913 - 0.057\,X_1 + 0.322\,X_2 + 0.081\,X_3 + 0.373\,X_4$
17	NS/P, BY/P, WS/P, TI	Base (F4)	0.988	$\hat{Y} = -15.943 + 0.012\,X_1 - 0.037\,X_2 + 0.772\,X_3 + 0.223\,X_4$
		Cycle one (F5)	0.972	$\hat{Y} = -18.022 + 0.130\,X_1 - 0.067\,X_2 + 0.766\,X_3 + 0.259\,X_4$
		Cycle two (F6)	0.994	$\hat{Y} = -15.532 + 0.014\,X_1 - 0.025\,X_2 + 0.717\,X_3 + 0.229\,X_4$
18	PH, NS/P, BY/P, WS/P, HI	Base (F4)	0.980	$\hat{Y} = -13.855 + 0.005\,X_1 + 0.009\,X_2 + 0.212\,X_3 + 0.330\,X_4 + 0.332\,X_5$
		Cycle one (F5)	0.952	$\hat{Y} = -14.115 - 0.005\,X_1 + 0.127\,X_2 + 0.170\,X_3 + 0.342\,X_4 + 0.374\,X_5$
		Cycle two (F6)	0.973	$\hat{Y} = -11.760 - 0.010\,X_1 - 0.059\,X_2 + 0.326\,X_3 + 0.072\,X_4 + 0.374\,X_5$
19	PH, NS/P, BY/P, WS/P, HI, TI	Base (F4)	0.988	$\hat{Y} = -15.735 - 0.002\,X_1 + 0.008\,X_2 - 0.550\,X_3 + 0.805\,X_4 - 0.025\,X_5 + 0.237\,X_6$
		Cycle one (F5)	0.972	$\hat{Y} = -17.789 + 0.0001\,X_1 + 0.122\,X_2 - 0.102\,X_3 + 0.828\,X_4 - 0.050\,X_5 + 0.286\,X_6$
		Cycle two (F6)	0.996	$\hat{Y} = -16.457 + 0.005\,X_1 + 0.048\,X_2 - 0.180\,X_3 + 0.996\,X_4 - 0.158\,X_5 + 0.320\,X_6$
20	PH, SL, NS/P, NSe/S, BY/P, WS/P, HI, TI	Base (F4)	0.988	$\hat{Y} = -15.112 - 0.020\,X_1 - 0.046\,X_2 + 0.003\,X_3 + 0.004\,X_4 - 0.051\,X_5 + 0.801\,X_6 - 0.024\,X_7 + 0.232\,X_8$
		Cycle one (F5)	0.973	$\hat{Y} = -15.336 + 0.001\,X_1 - 0.043\,X_2 + 0.093\,X_3 - 0.055\,X_4 - 0.081\,X_5 + 0.803\,X_6 - 0.037\,X_7 + 0.266\,X_8$
		Cycle two (F6)	0.997	$\hat{Y} = -15.172 + 0.006\,X_1 - 0.064\,X_2 + 0.037\,X_3 - 0.010\,X_4 - 0.168\,X_5 + 0.986\,X_6 - 0.151\,X_7 + 0.307\,X_8$

Table 8. Regression analysis in different models for base, cycle one and cycle two of pedigree selection for grain yield/plant in population II

Model No.	Independent trait/s	Generation	R^2	Regression equation
1	PH	Base (F4)	0.103	$\hat{Y} = 4.134 + 0.132\,\dot{X}$
		Cycle one (F5)	0.055	$\hat{Y} = 9.809 + 0.108\,\dot{X}$
		Cycle two (F6)	0.158	$\hat{Y} = 8.952 + 0.126\,\dot{X}$
2	SL	Base (F4)	0.067	$\hat{Y} = 1.124 + 1.443\,\dot{X}$
		Cycle one (F5)	0.080	$\hat{Y} = 7.788 + 1.154\,\dot{X}$
		Cycle two (F6)	0.108	$\hat{Y} = 10.652 + 0.723\,\dot{X}$
3	NS/P	Base (F4)	0.618	$\hat{Y} = 0.127 + 2.112\,\dot{X}$
		Cycle one (F5)	0.680	$\hat{Y} = 5.622 + 1.681\,\dot{X}$
		Cycle two (F6)	0.090	$\hat{Y} = 14.668 + 0.326\,\dot{X}$
4	NSe/S	Base (F4)	0.100	$\hat{Y} = -5.738 + 0.991\,\square$
		Cycle one (F5)	0.001	$\hat{Y} = 22.473 - 0.056\,\square$
		Cycle two (F6)	0.299	$\hat{Y} = -4.840 + 1.112\,\square$
5	BY/P	Base (F4)	0.920	$\hat{Y} = 0.845 + 0.410\,\dot{X}$
		Cycle one (F5)	0.862	$\hat{Y} = 4.645 + 0.339\,\dot{X}$
		Cycle two (F6)	0.723	$\hat{Y} = 6.161 + 0.266\,\dot{X}$
6	WS/P	Base (F4)	0.965	$\hat{Y} = 1.452 + 0.720\,\dot{X}$
		Cycle one (F5)	0.922	$\hat{Y} = 3.400 + 0.654\,\square$
		Cycle two (F6)	0.840	$\hat{Y} = 3.979 + 0.546\,\dot{X}$
7	HI	Base (F4)	0.016	$\hat{Y} = 10.085 + 0.175\,\dot{X}$
		Cycle one (F5)	0.046	$\hat{Y} = 30.935 - 0.224\,\square$
		Cycle two (F6)	0.014	$\hat{Y} = 22.095 - 0.083\,\square$
8	TI	Base (F4)	0.091	$\hat{Y} = 42.512 - 0.312\,\square$
		Cycle one (F5)	0.100	$\hat{Y} = 40.338 - 0.243\,\square$
		Cycle two (F6)	0.013	$\hat{Y} = 23.320 - 0.065\,\square$
9	WS/P , TI	Base (F4)	0.994	$\hat{Y} = -15.903 + 0.785\,\square_1 + 0.200\,\square_2$
		Cycle one (F5)	0.989	$\hat{Y} = -18.705 + 0.772\,\square_1 + 0.240\,\square_2$
		Cycle two (F6)	0.997	$\hat{Y} = -18.146 + 0.681\,\square_1 + 0.266\,\square_2$
10	BY/P, WS/P, TI	Base (F4)	0.994	$\hat{Y} = -15.910 + 0.003\,\square_1 + 0.779\,\square_2 + 0.200\,\square_3$
		Cycle one (F5)	0.989	$\hat{Y} = -18.458 + 0.017\,\square_1 + 0.739\,\square_2 + 0.237\,\square_3$
		Cycle two (F6)	0.998	$\hat{Y} = -18.422 + 0.019\,\square_1 + 0.648\,\square_2 + 0.269\,\square_3$

Table 8. Counted.

Model No.	Independent traits	Generation	R^2	Regression equation
11	BY/P, WS/P, HI	Base (F4)	0.994	$\hat{Y} = -14.993 + 0.379\,X_1 + 0.082\,X_2 + 0.351\,X_3$
		Cycle one (F5)	0.989	$\hat{Y} = -17.618 + 0.384\,X_1 + 0.070\,X_2 + 0.415\,X_3$
		Cycle two (F6)	0.995	$\hat{Y} = -19.624 + 0.439\,X_1 - 0.076\,X_2 + 0.493\,X_3$
12	NS/P, BY/P, WS/P	Base (F4)	0.967	$\hat{Y} = 1.936 - 0.187\,X_1 + 0.038\,X_2 + 0.698\,X_3$
		Cycle one (F5)	0.927	$\hat{Y} = 3.170 + 0.104\,\dot{X}_1 + 0.064\,X_2 + 0.511\,X_3$
		Cycle two (F6)	0.856	$\hat{Y} = 3.389 + 0.029\,\dot{X}_1 - 0.167\,X_2 + 0.847\,X_3$
13	NSe/S, WS/P, TI	Base (F4)	0.994	$\hat{Y} = -15.906 + 0.0001\,X_1 + 0.785\,X_2 + 0.200\,X_3$
		Cycle one (F5)	0.989	$\hat{Y} = -18.706 + 0.0002\,X_1 + 0.772\,X_2 + 0.240\,X_3$
		Cycle two (F6)	0.999	$\hat{Y} = -15.544 - 0.113\,X_1 + 0.700\,X_2 + 0.255\,X_3$
14	SL, WS/P, TI	Base (F4)	0.994	$\hat{Y} = -15.049 - 0.058\,X_1 + 0.786\,X_2 + 0.197\,X_3$
		Cycle one (F5)	0.990	$\hat{Y} = -17.094 - 0.107\,X_1 + 0.775\,X_2 + 0.233\,X_3$
		Cycle two (F6)	0.998	$\hat{Y} = -17.726 - 0.032\,X_1 + 0.684\,X_2 + 0.264\,X_3$
15	SL, NS/P, BY/P, WS/P	Base (F4)	0.971	$\hat{Y} = 6.777 - 0.429\,X_1 - 0.317\,X_2 + 0.069\,X_3 + 0.692\,X_4$
		Cycle one (F5)	0.936	$\hat{Y} = 7.841 - 0.457\,X_1 - 0.018\,X_2 + 0.087\,X_3 + 0.534\,X_4$
		Cycle two (F6)	0.932	$\hat{Y} = 10.559 - 0.964\,X_1 - 0.015\,X_2 - 0.467\,X_3 + 1.526\,X_4$
16	NS/P, BY/P, WS/P, HI	Base (F4)	0.994	$\hat{Y} = -15.208 + 0.028\,X_1 + 0.378\,X_2 + 0.078\,X_3 + 0.354\,X_4$
		Cycle one (F5)	0.989	$\hat{Y} = -17.645 + 0.055\,X_1 + 0.378\,X_2 + 0.064\,X_3 + 0.414\,X_4$
		Cycle two (F6)	0.995	$\hat{Y} = -19.576 - 0.009\,X_1 + 0.445\,X_2 - 0.085\,X_3 + 0.493\,X_4$
17	NS/P, BY/P, WS/P, TI	Base (F4)	0.994	$\hat{Y} = -16.063 + 0.020\,X_1 + 0.001\,X_2 + 0.780\,X_3 + 0.201\,X_4$
		Cycle one (F5)	0.989	$\hat{Y} = -18.473 + 0.049\,X_1 + 0.013\,X_2 + 0.732\,X_3 + 0.236\,X_4$
		Cycle two (F6)	0.998	$\hat{Y} = -18.463 + 0.006\,X_1 - 0.015\,X_2 + 0.654\,X_3 + 0.269\,X_4$
18	PH, NS/P, BY/P, WS/P, HI	Base (F4)	0.994	$\hat{Y} = -15.173 + 0.000\,X_1 + 0.027\,X_2 + 0.379\,X_3 + 0.077\,X_4 + 0.354\,X_5$
		Cycle one (F5)	0.989	$\hat{Y} = -19.723 + 0.016\,X_1 + 0.110\,X_2 + 0.361\,X_3 + 0.075\,X_4 + 0.425\,X_5$
		Cycle two (F6)	0.998	$\hat{Y} = -19.507 + 0.020\,X_1 - 0.004\,X_2 + 0.434\,X_3 - 0.083\,X_4 + 0.464\,X_5$
19	PH, NS/P, BY/P, WS/P, HI, TI	Base (F4)	0.994	$\hat{Y} = -16.621 + 0.002\,X_1 + 0.038\,X_2 + 0.174\,X_3 + 0.455\,X_4 + 0.167\,X_5 + 0.115\,X_6$
		Cycle one (F5)	0.991	$\hat{Y} = -20.831 + 0.017\,X_1 + 0.109\,X_2 + 0.162\,X_3 + 0.442\,X_4 + 0.200\,X_5 + 0.133\,X_6$
		Cycle two (F6)	1.000	$\hat{Y} = -18.139 + 0.017\,X_1 + 0.013\,X_2 - 0.062\,X_3 + 0.772\,X_4 - 0.102\,X_5 + 0.310\,X_6$
20	PH, SL, NS/P, NSe/S, BY/P, WS/P, HI, TI	Base (F4)	0.995	$\hat{Y} = -15.826 + 0.020\,X_1 - 0.044\,X_2 + 0.021\,X_3 + 0.000\,X_4 + 0.176\,X_5 + 0.457\,X_6 + 0.165\,X_7 + 0.113\,X_8$
		Cycle one (F5)	0.991	$\hat{Y} = -19.642 + 0.017\,X_1 - 0.023\,X_2 + 0.098\,X_3 - 0.025\,X_4 + 0.162\,X_5 + 0.446\,X_6 + 0.190\,X_7 + 0.135\,X_8$
		Cycle two (F6)	1.000	$\hat{Y} = -16.943 + 0.015\,X_1 - 0.001\,X_2 + 0.010\,X_3 - 0.046\,X_4 - 0.056\,X_5 + 0.771\,X_6 - 0.081\,X_7 + 0.294\,X_8$

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Table 9. Stepwise regression analysis for base, cycle one and cycle two of pedigree selection for grain yield/plant in the population I & II.

Generation	Model No.	Independent trait	R^2	Regression equation
Population I				
	1	WS/P	0.921	$\hat{Y} = 0.748 + 0.693\ \dot{X}_1$
Base (F_4)	2	WS/P, TI	0.988	$\hat{Y} = -16.655 + 0.713\ X_1 + 0.232\ X_2$
	3	WS/P, TI, BY/P	0.988	$\hat{Y} = -15.872 + 0.770\ X_1 + 0.223\ X_2 - 0.035\ X_3$
Cycle one (F_5)	1	WS/P	0.843	$\hat{Y} = 4.807 + 0.567\ \dot{X}_1$
	2	WS/P, TI	0.969	$\hat{Y} = -18.093 + 0.687\ X_1 + 0.264\ X_2$
	3	WS/P, TI, NSe/S	0.971	$\hat{Y} = -14.453 + 0.689\ X_1 + 0.251\ X_2 - 0.118\ X_3$
Cycle two (F_6)	1	WS/P	0.782	$\hat{Y} = 5.037 + 0.500\ X_1$
	2	WS/P, TI	0.993	$\hat{Y} = -15.792 + 0.679\ X_1 + 0.233\ X_2$
Population II				
Base (F_4)	1	WS/P	0.965	$\hat{Y} = 1.452 + 0.720\ \dot{X}_1$
	2	WS/P, TI	0.994	$\hat{Y} = -15.903 + 0.785\ X_1 + 0.200\ X_2$
Cycle one (F_5)	1	WS/P	0.922	$\hat{Y} = 3.400 + 0.654\ \dot{X}_1$
	2	WS/P, TI	0.989	$\hat{Y} = -18.705 + 0.772\ X_1 + 0.240\ X_2$
	1	WS/P	0.840	$\hat{Y} = 3.979 + 0.546\ \dot{X}_1$
Cycle two (F_6)	2	WS/P, TI	0.997	$\hat{Y} = -18.146 + 0.681\ X_1 + 0.266\ X_2$
	3	WS/P, TI, PH	0.999	$\hat{Y} = -17.921 + 0.669\ X_1 + 0.251\ X_2 + 0.014\ X_3$
	4	WS/P, TI, PH, NSe/S	1.000	$\hat{Y} = -15.881 + 0.686\ X_1 + 0.245\ X_2 + 0.012\ X_3 - 0.090\ X_4$

Table 10. Actual and expected (F6) grain yield/ plant, g. from different models of simple, multiple and stepwise regression analyses and their Chi², correlation and reliability coefficients in population I.

Fam. No.	Actual grains/ plant, g. (F6)	Expected Grain yields/ plant, g. for F6									
		Simple regression analysis								Stepwise analysis	
		Mod. 1	Mod. 2	Mod.3	Mod. 4	Mod. 5	Mod. 6	Mod. 7	Mod. 8	Mod. 1	Mod. 2
28	18.26	17.65	18.51	17.44	18.07	18.55	18.97	17.75	18.02	18.97	18.38
34	17.18	17.57	17.21	17.65	17.70	17.45	17.19	17.79	17.76	17.19	17.15
36	16.96	17.74	17.47	17.53	17.69	17.28	16.96	17.81	17.70	16.96	17.08
41	18.88	17.54	18.11	18.82	18.00	19.30	19.26	17.73	17.98	19.26	18.98
108	18.20	17.87	17.81	17.74	17.69	17.32	17.78	17.86	17.72	17.78	18.14
141	16.53	17.78	17.81	17.57	17.79	16.91	16.69	17.82	17.74	16.69	16.54
258	17.53	17.80	17.88	17.53	17.76	17.02	17.46	17.86	17.75	17.46	17.55
261	17.74	17.77	18.11	17.74	17.83	18.26	17.68	17.76	17.73	17.68	17.91
289	16.39	17.99	17.47	17.68	17.80	17.13	16.61	17.78	17.74	16.61	16.45
291	17.06	17.59	17.81	18.39	17.91	18.07	17.30	17.74	17.82	17.30	17.04
296	19.31	17.96	17.81	17.74	17.83	18.04	18.27	17.84	17.61	18.27	19.29
313	17.40	17.48	17.66	17.87	17.93	17.91	17.02	17.77	17.65	17.02	17.41
321	17.55	18.11	17.06	17.66	17.79	16.84	16.86	17.87	17.58	16.86	17.51
401	18.06	17.52	18.18	17.63	17.81	18.64	18.51	17.74	17.95	18.51	18.08
441	16.86	17.87	17.99	17.59	17.77	16.75	17.20	17.85	17.82	17.20	16.88
460	19.32	17.95	17.92	17.78	17.83	18.35	19.30	17.79	17.97	19.30	19.05
466	16.42	17.87	18.03	17.66	17.83	17.65	17.38	17.75	17.98	17.38	16.43
474	17.10	17.89	17.47	18.19	17.86	17.48	17.36	17.80	17.82	17.36	17.13
518	19.65	18.14	17.45	18.01	17.66	18.10	18.64	17.87	17.62	18.64	19.71
536	19.92	17.82	18.51	18.02	17.84	19.43	19.90	17.76	17.94	19.90	20.03
Chi ² =		1.24	1.13	1.16	1.27	0.64	0.28	1.28	1.27	0.28	0.01
r =		0.173	0.351	0.305	0.093	0.708	0.884	0.047	0.124	0.884	0.996
Reliability coefficient		0.030	0.123	0.093	0.009	0.505	0.784	0.002	0.016	0.784	0.994

Table 10. Continued.

Fam. No.	Actual grains/ plant, g. (F6)	Expected Grain yields/ plant, g. for F6											
		Multiple regression analysis											
		Mod. 9	Mod. 10	Mod. 11	Mod. 12	Mod. 13	Mod. 14	Mod. 15	Mod. 16	Mod. 17	Mod. 18	Mod. 19	Mod. 20
28	18.26	18.38	18.34	18.33	18.85	18.34	18.30	18.65	18.40	18.35	18.80	18.40	18.32
34	17.18	17.15	17.09	17.06	17.11	17.17	17.18	17.72	17.08	17.12	17.47	17.19	17.21
36	16.96	17.08	17.02	17.03	16.87	17.10	17.05	17.15	17.07	17.04	17.50	17.07	17.04
41	18.88	18.98	18.89	19.17	19.26	18.96	18.97	19.17	19.04	18.95	19.41	18.98	18.93
108	18.20	18.14	18.13	18.15	17.94	18.16	18.07	17.84	18.13	18.17	18.57	18.23	18.16
141	16.53	16.54	16.50	16.64	16.70	16.54	16.46	16.42	16.66	16.54	17.09	16.54	16.46
258	17.53	17.55	17.55	17.66	17.61	17.56	17.47	17.38	17.67	17.59	18.09	17.61	17.53
261	17.74	17.91	17.80	17.74	17.42	17.90	17.80	17.31	17.80	17.82	18.24	17.84	17.76
289	16.39	16.45	16.38	16.20	16.53	16.45	16.42	16.65	16.20	16.42	16.68	16.53	16.48
291	17.06	17.04	16.92	16.97	17.19	17.02	16.99	17.01	16.88	16.98	17.28	17.07	17.00
296	19.31	19.29	19.23	18.98	18.26	19.27	19.21	18.47	19.02	19.26	19.49	19.36	19.28
313	17.40	17.41	17.28	17.22	16.77	17.37	17.34	16.92	17.25	17.31	17.63	17.37	17.30
321	17.55	17.51	17.48	17.50	16.96	17.50	17.52	17.48	17.50	17.53	18.00	17.54	17.50
401	18.06	18.08	18.00	18.09	18.28	18.10	18.03	18.36	18.16	18.01	18.54	18.01	17.98
441	16.86	16.88	16.90	17.05	17.41	16.89	16.80	16.90	17.02	16.94	17.46	16.97	16.88
460	19.32	19.05	19.05	18.86	19.43	19.06	19.07	19.71	18.84	19.09	19.29	19.24	19.21
466	16.42	16.43	16.38	16.58	17.28	16.44	16.38	17.04	16.59	16.41	17.04	16.38	16.33
474	17.10	17.13	17.08	17.30	17.46	17.12	17.14	17.55	17.22	17.14	17.66	17.15	17.11
518	19.65	19.71	19.67	19.83	18.76	19.74	19.70	19.32	19.83	19.72	20.32	19.66	19.64
536	19.92	20.03	19.96	19.99	19.80	20.04	19.96	19.74	20.01	19.99	20.44	20.01	19.94
Chi ² =		0.01	0.01	0.04	0.26	0.01	0.01	0.16	0.03	0.01	0.24	0.01	0.00
r =		0.996	0.997	0.985	0.894	0.997	0.997	0.935	0.986	0.997	0.986	0.998	0.999
Reliability coefficient		0.994	0.997	0.974	0.797	0.995	0.997	0.878	0.975	0.995	0.978	0.999	1.000

Table 11. Actual and expected grain yield/ plant (F6), g. from different models of simple, multiple and stepwise regression analyses and their Chi², correlation and reliability coefficients in population II.

Fam. No.	Actual grains/ Plant (F6)	Expected Grain yields/ plant, g. for F6											
		Simple regression analysis								Stepwise regression analysis			
		Mod. 1	Mod. 2	Mod. 3	Mod. 4	Mod. 5	Mod. 6	Mod. 7	Mod. 8	Mod. 1	Mod. 2	Mod. 3	Mod. 4
1	20.06	17.87	19.23	18.51	20.14	20.73	20.84	19.05	19.09	20.84	20.20	20.07	20.08
59	16.85	18.80	19.23	18.71	18.88	17.90	17.99	18.91	19.06	17.99	16.78	16.81	16.82
70	20.01	20.22	18.75	18.09	18.07	18.55	18.92	18.54	18.57	18.92	19.92	19.97	20.00
154	17.51	18.28	18.27	18.78	18.07	17.12	17.22	18.55	18.61	17.22	17.64	17.53	17.54
192	18.57	18.70	18.07	19.69	18.07	19.87	19.06	19.12	18.97	19.06	18.48	18.46	18.56
226	18.33	18.99	18.32	18.54	18.81	18.55	18.32	18.83	18.78	18.32	18.34	18.32	18.31
236	18.16	18.18	18.07	18.93	18.07	18.15	17.74	18.74	18.64	17.74	18.17	18.04	18.07
249	22.03	19.32	19.47	19.41	20.59	21.07	21.73	18.80	18.90	21.73	22.06	22.03	21.99
279	16.66	18.52	19.23	18.19	18.88	16.87	16.93	18.64	18.74	16.93	16.76	16.71	16.65
289	19.60	18.93	19.14	18.99	18.29	19.02	19.15	18.73	18.72	19.15	19.61	19.55	19.61
Chi ² =		1.12	1.15	1.20	0.93	0.36	0.21	1.30	1.30	0.21	0.00	0.00	0.00
r =		0.398	0.330	0.299	0.545	0.850	0.916	0.116	0.111	0.916	0.999	0.999	1.000
Reliability coefficient		0.159	0.108	0.090	0.299	0.725	0.844	0.014	0.013	0.844	0.999	0.000	0.000

Table 11. Continued.

Fam. No.	Actual grains/ plant,g. (F6)	Expected Grain yields/ plant, g.											
		Multiple regression analysis											
		Mod. 9	Mod. 10	Mod. 11	Mod. 12	Mod. 13	Mod. 14	Mod. 15	Mod. 16	Mod. 17	Mod. 18	Mod. 19	Mod. 20
1	**20.06**	20.20	20.14	20.19	20.74	20.13	20.20	20.48	20.18	18.49	20.12	20.09	20.09
59	**16.85**	16.78	16.70	16.72	18.12	16.74	16.77	17.48	16.69	15.38	16.83	16.85	16.86
70	**20.01**	19.92	19.84	19.88	19.09	19.91	19.92	19.60	19.87	18.45	20.08	20.02	20.03
154	**17.51**	17.64	17.57	17.69	17.41	17.58	17.65	17.98	17.65	16.35	17.62	17.55	17.57
192	**18.57**	18.48	18.48	18.59	18.62	18.55	18.53	18.52	18.56	16.94	18.70	18.61	18.61
226	**18.33**	18.34	18.29	18.26	18.20	18.27	18.36	18.49	18.24	16.90	18.36	18.42	18.39
236	**18.16**	18.17	18.13	18.16	17.59	18.13	18.19	17.89	18.13	16.79	18.12	18.14	18.13
249	**22.03**	22.06	21.98	22.08	21.99	21.95	22.06	22.02	22.04	20.32	22.12	22.08	22.06
279	**16.66**	16.76	16.68	16.79	17.08	16.63	16.73	16.36	16.77	15.47	16.80	16.71	16.70
289	**19.60**	19.61	19.55	19.49	19.23	19.61	19.60	18.87	19.46	18.11	19.53	19.64	19.65
Chi ² =		0.00	0.00	0.01	0.19	0.00	0.00	0.09	0.01	1.23	0.00	0.00	0.00
r =		0.999	0.999	0.998	0.925	0.999	0.999	0.965	0.998	0.997	0.999	1.000	1.000
Reliability coefficient		0.999	0.999	0.996	0.863	1.000	0.999	0.935	0.996	0.845	1.002	1.007	1.004

Table 12. Homogeneity of actual and expected grain yield/plant between cycle one and cycle two as F6/F5 of pedigree selection in population I.

Fam. No.	Actual grains yield/plant, g	Expected grain yield/plant, g											
		Simple regression analysis								Multiple regression analysis			
		Mod. 1	Mod. 2	Mod. 3	Mod. 4	Mod. 5	Mod. 6	Mod. 7	Mod. 8	Mod. 9	Mod. 10	Mod. 1 1	Mod. 1 2
28	89.30	80.90	81.91	82.99	81.42	85.96	89.35	81.35	81.73	91.11	90.76	90.10	89.42
34	85.26	81.60	80.59	79.12	82.10	82.59	84.10	81.60	81.17	86.74	86.51	86.17	86.09
36	83.72	81.63	80.49	77.06	81.63	80.55	80.15	81.59	80.30	84.96	84.44	84.88	81.09
41	92.76	81.39	80.63	79.35	82.33	84.21	87.02	81.07	80.41	93.51	93.07	92.36	90.80
108	93.10	81.53	80.69	79.25	80.99	78.19	85.14	81.60	79.89	93.72	94.02	94.60	90.45
141	72.37	79.06	80.74	80.89	82.01	74.50	75.15	81.80	81.99	72.96	73.11	74.56	76.65
258	86.67	80.45	84.51	87.18	82.09	84.15	87.55	82.14	82.26	87.25	87.23	87.72	87.86
261	83.13	82.18	84.42	84.09	82.38	88.19	86.97	81.75	83.04	84.17	83.88	84.24	86.25
289	75.53	85.02	81.81	78.78	83.11	76.54	74.42	81.63	81.33	73.92	73.62	72.75	74.74
291	74.34	81.34	79.66	77.33	82.39	78.91	75.39	81.27	80.90	76.25	75.63	76.28	76.02
296	73.27	82.93	77.75	77.31	81.13	75.03	72.37	82.05	80.99	74.12	73.68	72.77	70.77
313	74.38	78.98	76.94	73.49	81.96	72.81	69.17	81.29	79.21	73.98	73.40	72.49	69.70
321	87.53	85.90	78.61	82.79	81.54	82.84	82.61	82.14	80.95	86.47	85.99	86.82	82.36
401	83.93	82.42	84.38	86.19	81.89	89.30	86.26	81.61	82.80	83.59	82.80	83.28	82.69
441	69.83	80.16	76.84	72.45	80.05	65.57	68.13	81.75	80.58	67.97	68.31	67.85	71.28
460	96.93	82.06	84.89	88.96	82.89	92.96	99.17	81.91	83.94	94.94	94.99	94.81	99.07
466	79.47	80.41	80.12	81.32	80.56	76.60	75.93	81.39	82.24	72.06	71.92	73.41	76.16
474	80.79	80.83	80.68	88.17	82.47	84.09	82.89	81.87	82.14	81.63	81.17	82.03	82.14
518	97.96	85.92	82.83	86.25	82.58	90.00	93.30	82.18	81.63	97.98	97.62	99.53	93.43
536	97.91	81.94	87.02	86.37	82.82	97.12	98.04	81.77	82.79	98.83	97.99	96.30	95.52
Min.	69.83	78.98	76.84	72.45	80.05	65.57	68.13	81.07	79.21	67.97	68.31	67.85	69.70
Max.	97.96	85.92	87.02	88.96	83.11	97.12	99.17	82.18	83.94	98.83	97.99	99.53	99.07
Mean	83.91	81.83	81.28	81.47	81.92	82.00	82.66	81.69	81.51	83.81	83.51	83.65	83.12

Table 12. Continued.

Fam. No.	Actual grains yield/plant, g	Expected grain yield/plant, g								Stepwise regression analysis	
		Multiple regression analysis									
		Mod. 13	Mod. 14	Mod. 15	Mod. 16	Mod. 17	Mod. 18	Mod. 19	Mod. 20	Mod. 1	Mod. 2
28	89.30	83.94	91.06	90.38	91.06	91.63	93.46	91.55	91.80	89.35	91.11
34	85.26	80.77	86.47	88.22	85.86	86.49	88.19	86.65	86.80	84.10	86.74
36	83.72	79.30	84.44	82.55	84.67	84.32	87.23	84.08	84.16	80.15	84.96
41	92.76	87.37	93.29	91.16	91.24	93.21	93.39	93.28	93.24	87.02	93.51
108	93.10	86.98	93.16	89.63	94.68	94.59	97.44	94.45	94.28	85.14	93.72
141	72.37	68.35	72.73	75.04	74.81	73.64	77.18	73.41	73.23	75.15	72.96
258	86.67	80.46	86.61	85.78	88.12	88.03	90.77	87.91	87.63	87.55	87.25
261	83.13	78.40	83.76	85.31	84.34	84.06	86.76	83.99	83.96	86.97	84.17
289	75.53	69.33	73.39	74.11	72.57	73.82	74.92	74.15	73.85	74.42	73.92
291	74.34	71.84	76.04	76.07	75.37	75.53	77.47	75.67	75.70	75.39	76.25
296	73.27	70.25	74.14	73.03	72.83	73.89	74.88	74.13	74.31	72.37	74.12
313	74.38	69.87	73.73	71.22	72.37	73.47	74.34	73.59	73.54	69.17	73.98
321	87.53	80.14	86.48	85.83	86.64	86.19	89.40	85.88	86.27	82.61	86.47
401	83.93	77.61	83.21	83.27	83.95	83.40	86.01	83.12	83.27	86.26	83.59
441	69.83	64.63	67.99	70.23	67.58	68.58	69.63	68.72	68.76	68.13	67.97
460	96.93	87.62	94.92	99.71	94.95	95.64	97.71	96.09	96.15	99.17	94.94
466	79.47	67.48	72.08	75.66	73.81	72.57	76.19	72.17	72.39	75.93	72.06
474	80.79	75.59	81.62	82.86	81.86	81.92	84.48	81.74	81.73	82.89	81.63
518	97.96	90.81	97.54	95.31	99.41	97.99	102.23	97.32	97.25	93.30	97.98
536	97.91	91.52	98.14	95.41	96.18	98.24	98.75	98.30	98.11	98.04	98.83
Min.	69.83	64.63	67.99	70.23	67.58	68.58	69.63	68.72	68.76	68.13	67.97
Max.	97.96	91.52	98.14	99.71	99.41	98.24	102.23	98.30	98.11	99.17	98.83
Mean	83.91	78.11	83.54	83.54	83.61	83.86	86.02	83.81	83.82	82.66	83.81

Table 13. Homogeneity of actual and expected grain yield/plant between cycle one (F5) and cycle two (F6) of pedigree selection in population II.

Fam. No.	Actual grains yield/plant, g	Expected grain yield/plant, g											
		Simple regression analysis								Multiple regression analysis			
		Mod. 1	Mod. 2	Mod. 3	Mod. 4	Mod. 5	Mod. 6	Mod. 7	Mod. 8	Mod. 9	Mod. 10	Mod. 11	Mod. 12
1	88.78	86.27	88.26	86.88	95.11	95.81	91.74	91.63	88.56	89.19	89.35	89.72	92.41
59	84.82	88.61	92.85	90.66	88.94	90.90	90.70	90.39	91.23	84.30	84.15	84.67	91.57
70	73.17	95.07	85.44	72.34	85.28	70.49	70.32	86.75	85.52	72.62	72.56	73.17	71.16
154	79.94	87.40	88.85	91.47	85.39	83.46	80.10	91.32	89.55	80.31	80.37	80.51	82.04
192	93.81	90.98	87.59	90.95	85.52	99.95	94.01	91.03	87.50	94.09	94.39	93.66	92.11
226	94.04	91.31	88.76	95.52	88.92	95.41	93.80	91.00	90.72	92.93	93.00	91.90	93.71
236	91.77	88.31	88.08	92.84	85.63	89.34	89.83	88.72	89.82	91.13	91.11	90.55	88.78
249	107.13	89.38	91.38	96.11	97.50	103.68	106.16	90.44	90.30	107.07	107.03	106.31	107.95
279	81.88	86.68	88.26	89.10	89.38	80.57	78.15	88.26	85.51	79.60	79.52	79.99	79.66
289	72.19	86.40	89.40	75.27	86.67	69.92	70.95	85.88	84.66	72.25	72.12	71.22	71.04
Min.	72.19	86.27	85.44	72.34	85.28	69.92	70.32	85.88	84.66	72.25	72.12	71.22	71.04
Max.	107.13	95.07	92.85	96.11	97.50	103.68	106.16	91.63	91.23	107.07	107.03	106.31	107.95
Mean	86.75	89.04	88.89	88.11	88.84	87.95	86.58	89.54	88.34	86.35	86.36	86.17	87.04

Table 13. Continued

Fam. No.	Actual grains yield/plant, g	Expected grain yield/plant, g									
		Multiple regression analysis								Stepwise regression analysis	
		Mod. 13	Mod. 14	Mod. 15	Mod. 16	Mod. 17	Mod. 18	Mod. 19	Mod. 20	Mod. 1	Mod. 2
1	88.78	88.89	89.76	92.02	89.84	82.20	89.47	89.61	89.42	91.74	89.19
59	84.82	84.07	84.54	88.10	84.51	77.57	84.75	85.00	84.63	90.70	84.30
70	73.17	72.57	72.96	73.21	73.22	67.54	73.90	73.60	73.44	70.32	72.62
154	79.94	80.01	80.55	83.74	80.46	74.93	80.01	80.21	80.10	80.10	80.31
192	93.81	94.38	94.49	91.36	93.37	86.48	93.87	94.64	94.45	94.01	94.09
226	94.04	92.55	93.37	94.43	91.97	86.08	92.42	93.63	93.23	93.80	92.93
236	91.77	90.92	91.52	89.39	90.49	84.46	90.52	91.43	91.17	89.83	91.13
249	107.13	106.50	107.67	108.51	106.28	99.11	105.93	106.78	106.51	106.16	107.07
279	81.88	78.95	79.97	77.05	80.05	73.96	79.89	79.84	79.63	78.15	79.60
289	72.19	72.24	72.38	69.14	71.21	66.90	71.27	72.24	72.11	70.95	72.25
Min.	72.19	72.24	72.38	69.14	71.21	66.90	71.27	72.24	72.11	70.32	72.25
Max.	107.13	106.50	107.67	108.51	106.28	99.11	105.93	106.78	106.51	106.16	107.07
Mean	86.75	86.11	86.72	86.70	86.14	79.92	86.20	86.70	86.47	86.58	86.35