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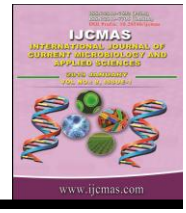


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# Estimates of Direct and Indirect Effects along with Correlation Coefficient Analysis in Bread Wheat (*Triticum aestivum* L.)

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**A B S T R A C T**

The present investigation entitled "Estimates of Direct & Indirect Effects along with Correlation Coefficient analysis in Bread Wheat (*Triticum aestivum* L.)" involving forty four genotypes was aim to study the correlation coefficient, path coefficient. All the forty four wheat genotypes were tested in randomized block design with three replications during *rabi* 2016-17 at Crop Research Centre, Chirori, SardarVallabhbhai Patel University of Agriculture and Technology, Meerut, (U.P.). The traits under study were days to 50% flowering, days to maturity, plant height, number of productive tillers per plant, spike length, total number of spikelets per spike, number of grains per spike, biological yield per plant, grain yield per plant, harvest index, 1000 seed weight and protein content. Correlation analysis indicated that in grain yield per plant was highly significant and positivity correlated with biological yield per plant and productive tillers per plant and significant and positivity correlated with harvest index. Genotypes from the same geographical region fell into different clusters and *vice-versa*. In the present investigation, grain yield was positively and directly affected by biological yield per plant, harvest index, total number of spikelets per spike, days to maturity, protein content and plant height, This suggested that selection of parents for hybridization should be on genetic diversity rather than on the geographical areas.

## Introduction

The majority of the cultivated wheat varieties belong to the species of the genus *Triticum*, is bread wheat (*Triticum aestivum* L.) which is hexaploid (2n=42). Second important wheat is *durum* wheat (*Triticum durum*) which is a tetraploid with 2n=28. Durum wheat is an economically important crop and widely grown in most parts of the world and Ethiopia. It is cultivated on 10 to 11% of the world wheat areas and accounting about 8% of the total wheat production (Ganeva *et al.*, 2011). The total area and production of durum wheat is about 20 million hectares and 30 million metric tons globally (Kahrizi *et al.*, 2010).

Globally, bread wheat (*Triticum aestivum* L.) is most important species which covers 90 per cent of the cultivated area under wheat. In India, wheat is grown on an area of 30.17 m ha with a production of 93.50 million tonnes, productivity of 3093 kg/ha. In Uttar Pradesh, wheat is grown on an area of 9.65 m ha with a production of 26.87 million tonnes and productivity of 2785 kg/ha (Agriculture Statistics at a Glance, 2016). In world, total production of wheat is around 737.83 m tonnes, an area about 223.11 m ha and productivity is 3.39 mt/ha (USDA, Report 2017).

Wheat is an ancient food grain crop which belongs to the family *poaceae*. It is a self-pollinated cereal crop with the 1-3% out crossing. After green revolution wheat occupied a prominent position among the world agricultural crops. It is known as high energy rich cereal and famous for high production and productivity at global level including India. Production of wheat ranked second in India after China, in the world. The consumption of wheat is increasing with increase in human population and food diversity in India as well as in Uttar Pradesh. It can be grown in varied environmental condition during *rabi* season.

Conventional analysis of variance and statistical parameters like phenotypic and genotypic coefficients of variability, heritability and genetic advance have been used to assess the nature and magnitude of variation in wheat breeding material. The result of a crop development programme depends upon the amount of genetic variability existing in the germplasm. Furthermore, heritability of a plant trait is very important in determining the response to selection because it implies the extent of transmissibility of traits into next generations (Surek *et al.,* 2003). In addition, high genetic advance coupled with high heritability estimate offers the most effective condition for selection for a trait (Larik *et al.,* 2000).

A great deal of research work has been done in the domain of wheat breeding through genetic manipulation. However, increasing population and the changing circumstances in the country necessitate the breeders for further breakthrough in this food crop. For bringing improvement in heritable characters, estimation of genetic parameters is of prime importance in any breeding programme. Heritability estimates provide the information about index of transmissibility of the quantitative characters of economic importance and are essential for an effective crop breeding strategy. The magnitude of heritability also helps in predicting the behaviour of succeeding generations by devising the appropriate selection criteria and assessing the level of genetic improvement (Hanson *et al.*, 1963). Similarly, genetic advance gives clear picture and precise view of segregating generations for possible selection. An estimate of genetic advance along with heritability is helpful in assessing the reliability of character for selection. Therefore, the study of phenotypic variability for various traits under investigation is of great importance (Kumar and Kerkhi, 2015). Grain yield, being a complex trait, depends upon component variables and their interaction. Degree and direction of relationship between two or more variables lead to estimation of correlation. Correlation studies provide better understanding of yield component which helps the plant breeder during selection (Robinson *et al.,* 1951 and Johnson *et al.,* 1955). Path coefficient analysis measures the direct and indirect contribution of independent variables on dependent variables and thus helps breeder in determining the yield component and understanding cause of association between two variables (Dewey and Lu, 1959). The information obtains by path coefficient analysis helps in indirect selection for genetic improvement of yield because direct selection is not effective for low heritable trait like yield. Thus, the estimation of heritability and genetic advance is essential for a breeder which helps in understanding the magnitude, nature and interaction of genotype and environmental variation of the trait. With the above reference, the present experiment was conducted to study the extent of genotypic and phenotypic variability among the genotypes and to estimate genetic advance, correlation coefficient among the selected characters, direct and indirect effects of component characters on yield of wheat to screen out the suitable parental groups for future breeding programme, to sustain the productivity of wheat (Rajpoot *et al.*, 2013).

## Materials and Methods

The present experiment was carried out during *rabi* 2016-17, at Crop Research Centre, Chirori, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut (U.P.), situated at an elevation of about 297 meters above mean sea level with 29.01˚'N latitude and 77.75˚E longitude, representing the North Western Plain Zone.

## Results and Discussion

In the present investigation, correlation coefficients at phenotypic and genotypic levels among the grain yield and its contributing traits and also among the contributing traits themselves have been worked out (Table 1 and 2). In general, genotype correlation coefficient was higher than corresponding phenotypic correlation coefficient. This indicates that due to the phenotypic expression of correlation was lessened. In the present investigation, grain yield per plant was highly significant and positivity correlated with biological yield per plant and productive tillers per plant and significant and positivity correlated with harvest index both at genotypic and phenotypic level of significance. The corroborate findings also was reported by Saxena *et al.,* (2007), Ali *et al.,* (2008), Singh *et al.,* (2010), Singh and Tiwari (2011), Baloch *et al.,* (2013), Rajpoot *et al.,* (2013), Parnaliya *et al.,* (2015), Bhutto *et al.,* (2016) and Ayer *et al.*, (2017).

Correlation among the component character themselves revealed that early flowering retains early maturity and late flowering had negative and significant association with total number of spikelets per spike both at genotypic and phenotypic levels of significance. It may be explained that early flowering will give maximum period for grain development and thereby increasing the total number of spikelets per spike and ultimately increased the grain yield per plant. On the other hand, late flowering gives very short period for grain development thereby the total number of spikelets per spike and decreased the grain yield per plant. It is therefore, preferable to select early flowering type so that maximum period for grain development may be made available to plants. The similar findings were also reported by Khaliq *et al.,* (2004), Prasad *et al.,* (2006), Atta *et al.,* (2008), Kolakar *et al.,* (2012) and Parnaliya *et al.,* (2015).

Results indicate that grain yield was positively and directly affected by biological yield per plant, harvest index, total number of spikelets per spike, protein content, days to maturity and plant height; all these traits had positive genotypic correlation with grain yield. The enormous influence of these traits reflected their importance for grain yield determination. The similar findings were also observed by Tsegaye *et al.,* (2012), Parnaliya *et al.,* (2015), Dabi *et al.,* (2016) and Ayer *et al.,* (2017). It could be understood that biological yield has direct positive and significant effect on grain yield.

Contribution of the traits via other traits on grain yield was examined. Here considerable indirect effects are discussed. Biological yield per plant contributed indirect positive effect on grain yield via productive tillers per plant, 1000 seed weight and protein content.

The less residual effect was of considerable magnitude 0.0015 and 0.0023 at genotypic and phenotypic level of significance respectively. Therefore, it is imperative, that other characters which have not studied in the present investigations, influencing the grain yield obviously, they could be physiological or biochemical traits like photosynthetic efficiency in terms of chlorophyll content, translocation efficiency, nitrate reductase activity and so on. It can be suggested that it would always be desirable to study the physiological and biochemical traits along with yield components for the improvement of yield potential in wheat.

Summary and conclusion of the study are as follows:

## Correlation coefficients

The information about relationship between the yield and yield components facilitate the choice of suitable breeding methods to be applied and selecting the parents for improving the crop. The phenotypic and genotypic correlations have their own importance in breeding programme for the efficiency of selection under the force of favorable combinations.

Plant height was observed positive and non-significant association with spike length at both genotypic and phenotypic levels. It could be understood that plant height would increase the spike length. It can be interned that plant height would increase the spike length would also increase the grain yield. Productive tillers per plant were observed highly significant and positive association with biological yield per plant at both genotypic and phenotypic levels. It could be understood that productive tillers per plant would increase the biological yield per plant and, ultimately increase the grain yield. The similar findings were also reported by Khaliq *et al.,* (2004), Ali *et al.,* (2008), Singh *et al.,* (2010), Iftikhar *et al.,* (2012), Yahaya (2014), Dutamo *et al.,* (2015) and Shara *et al.,* (2016).

Spike length was observed highly significant and positive correlation with number of grains per spike and total number of spikelets per spike at both genotypic and phenotypic levels. It could be understood that longer spikes had more number of grains per spike and more total number of spikelets per spike. Total number of spikelets per spike was observed highly significant and positive association with number of grains per spike at both genotypic and phenotypic levels. It could be understood that more total number of spikelets per spike would increase the number of grains per spike and ultimately increase the grain yield. The similar findings were also reported by Atta *et al.,* (2008), Ajmal *et al.,* (2009), Singh *et al.,* (2010) and Bhutto *et al.,* (2016).

Number of grains per spike was observed significant and positive correlation with 1000 seed weight and harvest index at both genotypic and phenotypic levels. It could be understood that an increase number of grains per spike results into an increase the harvest index. The similar findings were also obtained by Sen and Tom (2007) and Shara *et al.,* (2016). Biological yield per were obtained positive and non-significant correlation with 1000 seed weight and protein content at both genotypic and phenotypic levels of significance.

**Table.1** Estimation of correlation coefficient among different characters genotypic (G) level in wheat

| Characters | Days to 50% flowering | Days to maturity | Plant height (cm) | Productive tillers/plant | Spike length (cm) | Spikelets per spike | Number of grain /spike | Biological yield /plant (g) | Harvest index (%) | 1000 seed weight (g) | Protein content (%) | Grain yield per plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Days to 50% flowering** | **1.000** | 0.823** | -0.061 | -0.081 | 0.302** | 0.027 | 0.053 | -0.093 | -0.370** | 0.157 | -0.212* | **-0.196*** |
| **Days to maturity** | | **1.000** | -0.015 | -0.162 | 0.247** | 0.046 | 0.103 | -0.176* | -0.214* | 0.138 | -0.205* | **-0.233**** |
| **Plant height (cm)** | | | **1.000** | 0.051 | 0.108 | -0.204* | -0.180* | 0.046 | 0.084 | -0.327** | -0.318** | **0.071** |
| **Productive tillers/plant** | | | | **1.000** | -0.145 | -0.162 | -0.216* | 0.992** | -0.075 | 0.130 | 0.068 | **0.947**** |
| **Spike length (cm)** | | | | | **1.000** | 0.275** | 0.276** | -0.184* | -0.069 | -0.166 | -0.513** | **-0.208*** |
| **Spikelets per spike** | | | | | | **1.000** | 0.910** | -0.156 | 0.098 | 0.207* | -0.047 | **-0.131** |
| **Number of grain per spike** | | | | | | | **1.000** | -0.203* | 0.186* | 0.203* | -0.040 | **-0.154** |
| **Biological yield per plant (g)** | | | | | | | | **1.000** | -0.053 | 0.123 | 0.120 | **0.962**** |
| **Harvest index (%)** | | | | | | | | | **1.000** | -0.057 | 0.083 | **0.217*** |
| **1000 seed weight (g)** | | | | | | | | | | **1.000** | 0.018 | **0.092** |
| **Protein content (%)** | | | | | | | | | | | **1.000** | **0.151** |
| **Grain yield per plant (g)** | | | | | | | | | | | | **1.000** |

*,**Significant at 5% and 1% level, respectively

**Table.2** Estimation of correlation coefficient among different characters phenotypic (P) level in wheat

| **Characters** | **Days to 50% flowering** | **Days to maturity** | **Plant height (cm)** | **Productive tillers/ plant** | **Spike length (cm)** | **SPIKELETS per spike** | **Number of grain /spike** | **Biological yield /plant (g)** | **Harvest index (%)** | **1000 seed weight(g)** | **Protein content (%)** | **Grain yield per plant (g)** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Days to 50% flowering** | **1.000** | 0.764** | -0.054 | -0.073 | 0.264** | 0.035 | 0.051 | -0.084 | -0.275** | 0.141 | -0.195* | **-0.170** |
| **Days to maturity** | | **1.000** | -0.005 | -0.153 | 0.228** | 0.040 | 0.086 | -0.169 | -0.192* | 0.126 | -0.203* | **-0.225**** |
| **Plant height (cm)** | | | **1.000** | 0.051 | 0.099 | -0.197* | -0.160 | 0.045 | 0.057 | -0.316** | -0.308** | **0.065** |
| **Productive tillers/plant** | | | | **1.000** | -0.144 | -0.152 | -0.192* | 0.976** | -0.065 | 0.119 | 0.064 | **0.919**** |
| **Spike length (cm)** | | | | | **1.000** | 0.285** | 0.275** | -0.182* | -0.049 | -0.162 | -0.501** | **-0.199*** |
| **Spikelets per spike** | | | | | | **1.000** | 0.894** | -0.145 | 0.095 | 0.185* | -0.056 | **-0.113** |
| **Number of grain per spike** | | | | | | | **1.000** | -0.177* | 0.166 | 0.170 | -0.057 | **-0.124** |
| **Biological yield per plant (g)** | | | | | | | | **1.000** | -0.047 | 0.119 | 0.118 | **0.950**** |
| **Harvest index (%)** | | | | | | | | | **1.000** | -0.051 | 0.068 | **0.264**** |
| **1000 seed weight (g)** | | | | | | | | | | **1.000** | 0.015 | **0.086** |
| **Protein content (%)** | | | | | | | | | | | **1.000** | **0.147** |
| **Grain yield per plant (g)** | | | | | | | | | | | | **1.000** |

*,** Significant at 5% and 1% level, respectively

**Table.3** Path coefficient analysis showing the direct and indirect effect of 12 characters on the grain yield at genotypic level

| Characters | Days to 50% flowering | Days to maturity | Plant height (cm) | Productive tillers/ plant | Spike length (cm) | Spikelets per spike | Number of grain /spike | Biological yield /plant (g) | Harvest index (%) | 1000 seed weight (g) | Protein content (%) | Correlation with Grain yield /plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Days to 50% flowering** | **-0.0119** | 0.0102 | -0.0002 | 0.0102 | -0.0018 | 0.0004 | -0.0007 | -0.1025 | -0.0977 | -0.0020 | -0.0007 | **-0.196*** |
| **Days to maturity** | -0.0098 | **0.0124** | -0.0001 | 0.0205 | -0.0015 | 0.0006 | -0.0014 | -0.1945 | -0.0566 | -0.0017 | -0.0007 | **-0.233**** |
| **Plant height (cm)** | 0.0007 | -0.0002 | **0.0030** | -0.0065 | -0.0006 | -0.0028 | 0.0025 | 0.0504 | 0.0222 | 0.0041 | -0.0011 | **0.071** |
| **Productive tillers/plant** | 0.0010 | -0.0020 | 0.0002 | **-0.1266** | 0.0009 | -0.0022 | 0.0029 | 1.0949 | -0.0198 | -0.0016 | 0.0002 | **0.947**** |
| **Spike length (cm)** | -0.0036 | 0.0031 | 0.0003 | 0.0184 | **-0.0060** | 0.0037 | -0.0038 | -0.2026 | -0.0182 | 0.0021 | -0.0017 | **-0.208*** |
| **Spikelets per spike** | -0.0003 | 0.0006 | -0.0006 | 0.0205 | -0.0017 | **0.0136** | -0.0124 | -0.1727 | 0.0258 | -0.0026 | -0.0002 | **-0.131** |
| **Number of grain per spike** | -0.0006 | 0.0013 | -0.0005 | 0.0273 | -0.0017 | 0.0123 | **-0.0136** | -0.2243 | 0.0492 | -0.0026 | -0.0001 | **-0.154** |
| **Biological yield per plant (g)** | 0.0011 | -0.0022 | 0.0001 | -0.1257 | 0.0011 | -0.0021 | 0.0028 | **1.1033** | -0.0139 | -0.0016 | 0.0004 | **0.962**** |
| **Harvest index (%)** | 0.0044 | -0.0027 | 0.0003 | 0.0095 | 0.0004 | 0.0013 | -0.0025 | -0.0580 | **0.2639** | 0.0007 | 0.0003 | **0.217*** |
| **1000 seed weight (g)** | -0.0019 | 0.0017 | -0.0010 | -0.0164 | 0.0010 | 0.0028 | -0.0028 | 0.1361 | -0.0151 | **-0.0126** | 0.0001 | **0.092** |
| **Protein content (%)** | **0.0025** | **-0.0025** | **-0.0010** | **-0.0086** | **0.0031** | **-0.0006** | **0.0005** | **0.1320** | **0.0220** | **-0.0002** | **0.0034** | **0.151** |

Residual effect (G)= 0.0015; *,** Significant at 5% and 1% level, respectively

**Table.4** Path coefficient analysis showing the direct and indirect effect of 12 characters on the grain yield at phenotypic level

| Characters | Days to 50% flowering | Days to maturity | Plant height (cm) | Productive tillers/ plant | Spike length (cm) | Spikelets per spike | Number of grain /spike | Biological yield /plant (g) | Harves t index (%) | 1000 seed weight (g) | Protein content (%) | Correlation with Grain yield /plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Days to 50% flowering** | **-0.0020** | 0.0039 | -0.0002 | 0.0020 | -0.0023 | 0.0006 | -0.0007 | -0.0833 | -0.0846 | -0.0021 | -0.0016 | **-0.170** |
| **Days to maturity** | -0.0015 | **0.0046** | 0.0005 | 0.0041 | -0.0020 | 0.0007 | -0.0012 | -0.1675 | -0.0592 | -0.0019 | -0.0017 | **-0.225**** |
| **Plant height (cm)** | 0.0001 | 0.0002 | **0.0041** | -0.0014 | -0.0009 | -0.0034 | 0.0022 | 0.0449 | 0.0175 | 0.0048 | -0.0025 | **0.065** |
| **Productive tillers/plant** | 0.0001 | -0.0008 | 0.0002 | **-0.0268** | 0.0013 | -0.0026 | 0.0027 | 0.9668 | -0.0200 | -0.0018 | 0.0005 | **0.919**** |
| **Spike length (cm)** | -0.0005 | 0.0012 | 0.0004 | 0.0038 | **-0.0088** | 0.0049 | -0.0038 | -0.1799 | -0.0152 | 0.0024 | -0.0041 | **-0.199*** |
| **Spikelets per spike** | -0.0001 | 0.0002 | -0.0008 | 0.0041 | -0.0025 | **0.0171** | -0.0123 | -0.1435 | 0.0292 | -0.0028 | -0.0005 | **-0.113** |
| **Number of grain per spike** | -0.0001 | 0.0004 | -0.0007 | 0.0052 | -0.0024 | 0.0153 | **-0.0138** | -0.1758 | 0.0511 | -0.0026 | -0.0005 | **-0.124** |
| **Biological yield per plant (g)** | 0.0002 | -0.0009 | 0.0002 | -0.0261 | 0.0016 | -0.0025 | 0.0025 | **0.9910** | -0.0144 | -0.0018 | 0.0010 | **0.950**** |
| **Harvest index (%)** | 0.0005 | -0.0010 | 0.0002 | 0.0017 | 0.0004 | 0.0016 | -0.0023 | -0.0464 | **0.3080** | 0.0008 | 0.0006 | **0.264**** |
| **1000 seed weight (g)** | -0.0003 | 0.0006 | -0.0013 | -0.0032 | 0.0014 | 0.0032 | -0.0024 | 0.1183 | -0.0156 | **-0.0150** | 0.0001 | **0.086** |
| **Protein content (%)** | **0.0004** | **-0.0010** | **-0.0013** | **-0.0017** | **0.0044** | **-0.0010** | **0.0008** | **0.1172** | **0.0209** | **-0.0002** | **0.0082** | **0.147** |

Residual effect (G)= 0.0023; *,** Significant at 5% and 1% level, respectively

It could be understood that an increase the biological yield per plant would also increase the 1000 seed weight. Harvest index were obtained positive and non-significant association with protein content at both genotypic and phenotypic levels. 1000 seed weight was obtained positive and non-significant correlation with protein content at both genotypic and phenotypic levels. The similar findings were also reported by Prasad *et al.,* (2006), Ajmal *et al.,* (2009) and Kolakar *et al.,* (2012). Protein content was obtained positive and non-significant association with grain yield per plant at both genotypic and phenotypic levels. The similar finding was obtained by Saxena *et al.,* (2007).

## Path coefficient

Path analysis is one of the efficient methods to understand the direct and indirect effects of different component characters on yield. As correlation coefficient alone unable to provide sufficient information to decide the breeding procedure to be adopted or making simultaneous selection for crop improvement, path analysis proposed by Dewey and Lu (1959). Therefore, path coefficient analysis was used to determine the direct and indirect effect of all the character into the grain yield per plant and the estimates are furnished in Table 3 and 4.

## Genotypic path analysis

In the present investigation, grain yield was positively and directly affected by biological yield per plant, harvest index, total number of spikelets per spike, days to maturity, protein content and plant height. The corroborative findings were reported by Saxena *et al.,* (2007), Tsegaye *et al.,* (2012), Parnaliya *et al.,* (2015), Dabi *et al.,* (2016) and Ayer *et al.,* (2017). It could be understood that biological yield per has direct positive and significant effect on grain yield. Contribution of the traits via other traits on grain yield was examined. Here considerable indirect effects are discussed. Biological yield per plant contributed indirect positive effect on grain yield via productive tillers per plant, 1000 seed weight and protein content.

## Phenotypic path analysis

Results indicate that grain yield was positively and directly affected by biological yield per plant, harvest index, total number of spikelets per spike, protein content, days to maturity and plant height; all these traits had positive genotypic correlation with grain yield. The enormous influence of these traits reflected their importance for grain yield determination. The similar findings were also observed by Tsegaye *et al.,* (2012), Parnaliya *et al.,* (2015), Dabi *et al.,* (2016) and Ayer *et al.,* (2017). It could be understood that biological yield has direct positive and significant effect on grain yield.

Contribution of the traits via other traits on grain yield was examined. Here considerable indirect effects are discussed. Biological yield per plant contributed indirect positive effect on grain yield via productive tillers per plant, 1000 seed weight and protein content. The less residual effect was of considerable magnitude 0.0015 and 0.0023 at genotypic and phenotypic level of significance respectively. Therefore, it is imperative, that other characters which have not studied in the present investigations, influencing the grain yield obviously, they could be physiological or biochemical traits like photosynthetic efficiency in terms of chlorophyll content, translocation efficiency, nitrate reductase activity and so on. It can be suggested that it would always be desirable to study the physiological and biochemical traits along with yield components for the improvement of yield potential in wheat.

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