**Exploring Trait Relationships: Correlation and Path Analysis in Bread Wheat (*Triticum aestivum* L.)**

**Abstract**

Wheat is a vital food source and part of the Indian economy. It is the second most important food grain in India followed by rice. Thus, a field experiment comprised of 60 genotypes of wheat was carried out using the randomized block design with three replications at Wheat Research Station, Junagadh Agricultural University, Junagadh during *Rabi*, 2023-24. The findings revealed significant positive correlations between grain yield per plant and traits such as plant height, number of effective tillers per plant, number of spikelets per spike, biological yield per plant and harvest index (%). The highest correlation of grain yield was observed with biological yield followed by the number of effective tillers per plant at both genotypic and phenotypic levels. Path coefficient analysis indicated that days to maturity, biological yield, harvest index, number of effective tillers per plant, length of main spike, 100-grain weight, number of spikelets per main spike and chlorophyll content at anthesis had a direct positive impact on grain yield. These results highlighted the importance of emphasizing the traits like number of effective tillers per plant, biological yield per plant and harvest index in wheat breeding programs to enhance grain yield, which had true relationship with grain production as they have shown positive and significant correlations along with positive direct effects.

**Key Words:** Correlation, Association, Path analysis, Chlorophyll, *Triticum* *aestivum*

**Introduction**

Wheat is an important staple food crop grown in a wide range of environments and provides food to the majority of people in the world. The human population is expected to exceed 9 billion by 2050; thus, a significant improvement in the yield and productivity of main cereals is required to ensure the future of global food security (Li *et al*., 2020). Similarly, it is expected that by 2050, the demand for wheat will have to be increased by 50% from its current levels (CIMMYT, 2024). Wheat is the second leading cereal crop in the world after rice providing approximately 19% of daily calories as well as 21% of protein requirements to humans (Tadesse *et al*., 2019).

The centre of origin of wheat is said to be Asia for 2n = 14 type, the Mediterranean basin and Abyssinia for 2n = 28 type; and Afghanistan for 2n = 42 type (Vavilov, 1951). From the given centres, it had spread all over the Mediterranean, tropical and subtropical regions of the world. Wheat has been referred to as the 'King of cereals' due to its large area and prominent position in the international food grain trade, as well as its high productivity. Present-day wheat is the most widely grown crop in more than 115 countries.

Wheat belongs to the genus ‘*Triticum’* of the “*Poaceae*” (*Gramineae*) family. *Triticum aestivum* L. (Bread wheat), *Triticum dicoccum* Schulb. (Emmer wheat) and *Triticum durum* Desf. (Macaroni wheat) are the three species of wheat that are grown for commercial use in India. Among them, *Triticum aestivum* L. is also known as bread wheat, Mexican dwarf wheat and hexaploid wheat. Bread wheat belongs to allohexaploid species (2n=6x=42), produced from two separate hybridization events. First hybridization occurred between the two grass species *Triticum urartu* (2n=2x=14) (A genome donor) and unknown species (most probably *Aegilops speltoides*)(2n=2x=14) (B genome donor). This new species developed would have been tetraploid wheat (2n=4x=28) like *Triticum turgidum* var. durum (AABB genome). Then the second hybridization might have occurred between the new tetraploid and third diploid species (2n=2x=14) *Triticum tauschii* (D genome donor) resulted in the hexaploid wheat (AABBDD genome) (Pourkheirandish *et* *al*., 2020).

Out of the total area under wheat cultivation, approximately 95% area is occupied by bread wheat, which is used to make ‘Chapati’. Durum wheat, which is cultivated on around 4 to 5 per cent of the total wheat area and is primarily farmed in the Peninsular and Central Zones of India, is best suited for making products like semolina, macaroni, pasta, noodles, *etc*. Whole wheat grain products are also high in dietary fibre, healthy phytochemicals, vital minerals, vitamins and amino acids (Shewry, 2009).

Yield is a complex attribute comprised of multiple components. Some of these have an immediate impact on yield, while others have an indirect effect. Thus, understanding the relationship between yield and its components is required. Correlation coefficient analysis assesses the mutual link between numerous plant traits and identifies the component characters on which to base selection for genetic yield improvement. If there is a high association between a set of desirable features, we will select one character, and the other will be taken care of automatically. If there is an unfavourable connection between desirable and undesirable features, selection may cause genetic slippage, limiting genetic advancement. The direction and magnitude of the correlation between yield and yield contributing features must be considered when selecting superior genotypes from a diverse genetic population; nevertheless, correlation does not provide information about the direct and indirect effects of the independent variable on the dependent variable. Thus, the path coefficient analysis is necessary (Dewey and Lu, 1959).

In a path coefficient analysis, which is given by Wright (1921) is standardized as partial regression coefficient, which helps in partitioning the correlation coefficient into various direct and indirect effects of independent characters on dependent trait. One variable is measured by one's direct impact on another. Path coefficient analysis facilitates the selection process and enables breeders to select a genotype based on two or more traits simultaneously.

**Material and Methods**

The experimental material of the present investigation was comprised of 60 genotypes of wheat obtained from Wheat Research Station, Junagadh Agricultural University, Junagadh during 2023-24 in *Rabi* season. The experiment was conducted in Randomized Block Design (RBD) with three replications. Each genotype was planted in a single row, having a length of 2.0 m, also the between raw spacing was 22.5 cm, with a 10 cm plant-to-plant distance. To avoid damage and border effects, each experiment was surrounded by border rows. The crop was successfully raised using the prescribed agronomic and plant protection practices.

Observations were recorded from five random plants in the plot. The analysis was carried out over 13 characters *viz.*, days to anthesis, plant height, number of effective tillers per plant, length of main spike, days to maturity, number of spikelets per main spike, grain filling period, number of grains per main spike, 100-grain weight, biological yield per plant, harvest index (%), chlorophyll content at anthesis, chlorophyll content at 21 DAA and grain yield per plant to assess the correlations and path coefficients analysis in wheat. Harvest index (%) was calculated in percentage by using the following formulae (Donald and Hamblin,1976):

Harvest index (%) = $\frac{Grain yield per plant \left(g\right)}{Biological yield per plant \left(g\right)}$ × 100

The analysis of variance for randomized block design (RBD) was carried out for each character with the method suggested by Panse and Sukhatme (1995). Genotypic (rg) and phenotypic (rp) correlation coefficients were calculated by adopting the method explained by Al-Jibouri *et al.* (1958). The genotypic path coefficient analysis was done as per the method described by Dewey and Lu (1959).

**Results and Discussion**

The ANOVA results demonstrated that mean squares due to genotypes were highly significant for all of the features tested, showing that there is a lot of genetic diversity for different characteristics among the genotypes under consideration. Similar results were also obtained by Abdurezake *et al.* (2024), Santhosini *et al.* (2023) and Akbarzai *et al.* (2023).

**Correlation Coefficient Analysis**

In the present experiment genotypic (rg) and phenotypic (rp) correlation coefficients computed are presented in Table 1. Days to anthesisshowed a positive and significant correlation with plant height (rg = 0.278, rp = 0.237), days to maturity (rg= 0.946, rp = 0.928), number of spikelets per main spike (rg= 0.552, rp = 0.499), number of grains per main spike (rg= 0.428, rp = 0.399) at both genotypic and phenotypic level. While, biological yield per plant (rp = 0.147) and spike length (rp = 0.200) showed positive and significant at only phenotypic level. On the other hand, days to anthesis exhibited a significant negative correlation with the grain filling (rg = -0.459, rp = -0.414), 100-grain weight (rg = -0.507, rp = -0.487) and harvest index (rp = -0.198). Similar results were obtained for days to anthesis by Saini *et al.* (2024), Abdulrezake *et al.* (2024) and Santhoshini *et al.* (2023) with days to maturity and spike related traits; and also by Javed *et al.* (2024) and Santhoshini *et al.* (2023) with plant height.

Plant height was observed to possess positive and significant correlation with spike length (rg = 0.500, rp = 0.449), number of spikelets per main spike (rg = 0.404, rp = 0.359), number of grains per main spike (rg = 0.321, rp = 0.267), biological yield per plant (rg = 0.431, rp = 0.373) and grain yield per plant (rg = 0.349, rp = 0.301). On the other hand, plant height showed a significant negative correlation with the grain filling period (rg = -0.184, rp = -0.172). Javed *et al.* (2024), Abdulrezake *et al.* (2024) and Santhoshini *et al.* (2023) reported similar results of positive correlations between plant height and biological yield.

Number of effective tillers per plantwas noticed to have positive and significant correlation with biological yield per plant (rg = 0.474, rp = 0.369) and grain yield per plant both (rg = 0.512, rp = 0.400). On the other hand, it exhibited a significant negative correlation with spike length (rg = -0.317, rp = -0.222) and number of grains per main spike (rp = -0.197). Saini *et al.* (2024) and Santhoshini *et al.* (2023) have already reported the positive correlations between number of tillers per plant and biological yield.

Length of main spikemanifested positive and significant correlation with days to maturity (rp = 0.162), number of spikelets per main spike (rg = 0.281, rp = 0.242) and number of grains per main spike (rg = 0.477, rp = 0.397). On the other hand, it displayed a significant negative correlation with the harvest index (rp = -0.159). These results were similar with Santhoshini *et al.* (2023), Abdulrezake *et al.* (2024) and Saini *et al.* (2024).

Days to maturity showed significant positive correlation with spike length (rp = 0.162), number of spikelets per main spike (rg = 0.49, rp = 0.441), number of grains per main spike (rg = 0.339, rp = 0.309) and biological yield (rp = 0.162). Similarly, reports of positive correlations of days to maturity with number of grains per spike and number of spikelets per spike by Saini *et al.* (2024) and Abdulrezake *et al.* (2024) were discussed.

Number of spikelets per spikeshowed the strongest positive correlation with the number of grains per spike (rg = 0.769, rp = 0.728) and biological yield (rg = 0.277, rp = 0.245). On the other hand, number of spikelets per spike showed a highly significant negative correlation with grain-filling period (rg = -0.343, rp = -0.261) and 100-grain weight (rg = -0.369, rp = -0.344). Saini *et al.* (2024), Abdulrezake *et al.* (2024) and Santhoshini *et al.* (2023) also reported the positive relationships between number of grains per spike and number spikelets per spike. Grain filling periodshowed a significant positive correlation with harvest index (rg = 0.258, rp = 0.201). The strongest negative correlation was found between grain filling period and number of grains per spike (rg= -0.377, rp= -0.315).

Number of grains per main spikeshowed a significant negative correlation with 100-grain weight (rg = -0.298, rp = -0.283). Similar results were reported by Abdulrezake *et al.* (2024) and Santhoshini *et al.* (2023). While 100-grain weightshowed negative significant correlations with days to anthesis (rg = -0.507, rp = -0.487), days to maturity (rg = -0.519, rp = -0.283), number of spikelets per main spike (rg = -0.369, rp = -0.344) and number of grains per main spike (rg = -0.298, rp = -0.283). Biological yield per plantshowed a highly significant and positive correlation with grain yield (rg = 0.883, rp = 0.875). Biological yield per plant exhibited negative correlation with harvest index (rg = -0.144, rp = -0.172).

Harvest indexhad a significant positive correlation with grain yield (rg = 0.321, rp = 0.304) and a weak but significant positive correlation chlorophyll content at 21 DAA (rg = 0.278, rp = 0.166). Chlorophyll content at anthesis showed significant positive correlation with chlorophyll content at 21 DAA (rg = 0.490, rp = 0.307). Chlorophyll content at 21 DAAshowed a weak positive correlation with grain yield (rg = 0.147, rp = 0.114). The weak positive correlation between chlorophyll content at 21 DAA and grain yield (rg = 0.147, rp = 0.114).

Grain yield per plant showed highest significant correlation with biological yield (rg = 0.883, rp = 0.875), a significant correlation with number of tillers per plant (rg = 0.512, rp = 0.400), positive correlation with Plant height (rg = 0.349, rp = 0.301), a moderate but significant correlation with harvest index (rg = 0.321, rp = 0.304) and weak but significant correlation with number of spikelets per spike (rp = 0.157).

In most cases, the direction of phenotypic and genotypic association between distinct traits remained almost unchanged. The genotypic correlation coefficients were larger than the phenotypic correlation coefficients in the majority of characteristics. The findings suggested a narrow environmental effect and the presence of an intrinsic relationship among these characteristics. This is highly useful for plant breeders who want to practice selection based on the phenotypic manifestation of various characteristics to improve wheat grain yield. In a few cases, the phenotypic correlation coefficients were larger than the matching genotypic correlation coefficients, which may be attributed to non-genetic reasons, most likely an environment that inflated the value of phenotypic correlation.

**Path analysis**

Yield is a complex feature composed of various components, some of which are categorized as key components and have a direct influence on yield, while others have an indirect influence by altering the behaviour and growth of different characteristics. Correlation studies only provide information on the magnitude and direction of the relationship between yield and its components, as well as between distinct components. However, path coefficient analysis is required to determine the direct effects of each independent variable on yield as well as the indirect effects through other characteristics (Dewey and Lu, 1959).

The positive and direct effect on grain yield per plant was depicted by days to maturity (1.8653) followed by biological yield (0.9081), harvest index (0.4804), number of effective tillers per plant (0.0763), length of main spike (0.0549), 100-grain weight (0.0418), number of spikelets per main spike (0.0316) and chlorophyll content at anthesis (0.0230). The negative and direct effect on grain yield per plant was observed for days to anthesis (-2.0358) followed by grain filling period (-0.6816), number of grains per main spike (-0.0622), chlorophyll content at 21 DAA (-0.0326) and plant height (-0.0027).

Saini *et al.* (2024) also reported the highest positive direct effects on grain yield from biological yield per plant, followed by harvest index, number of spikelets per spike, spike length, days to 50% heading, 1000-grain weight, number of productive tillers per plant and chlorophyll content. While, Mishra *et al.* (2024) from number of grains per spike; Sharma *et al.* (2023) from number of productive tillers per plant, biological yield per plant, test weight, harvest index, numbers of grains per spike and numbers of spikelets per spike; Santhoshini *et al.* (2023) from biological yield per plant, harvest index, number of spikelets per spike, number of productive tillers per plant, days to 50% heading, test weight and days to maturity found positive direct effects on grain yield trait. Also, scientists like Joshi *et al.* (2024) studied the variations present in bread wheat and identified diverse genotypes by studying the important bread wheat traits similar to the present investigation.

In the present study, grain yield per plant was considered as the dependent variable and other characters were taken as independent variables. The direct and indirect effects of these independent variables on grain yield per plant are presented in Table 2 and Figure 1. The residual effect being 0.0056 suggested that characters under study were sufficient to explain the variability in grain yield per plant in bread wheat.

**Conclusion**

These findings of correlation revealed that emphasis should be given to the selection of plants with the higher number of effective tillers per plant, good plant height, greater number of spikelets per spike, significant biological yield and higher harvest index for improving grain yield. Path coefficient analysis suggested that high positive direct effects on grain yield per plant were observed from days to maturity, followed by biological yield, harvest index, number of effective tillers per plant, length of main spike, 100-grain weight, number of spikelets per main spike and chlorophyll content at anthesis which have direct impact on grain yield. Thus, the overall results obtained conclude that number of effective tillers per plant, number of spikelets per spike, biological yield and harvest index are the important traits to be emphasized during selection in the breeding programs for improving grain yield in bread wheat.

**Disclaimer (Artificial intelligence)**

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, *etc*.) and text-to-image generators have been used during the writing or editing of this manuscript.

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**Table 1: Genotypic and phenotypic correlation coefficients among different characters in bread wheat**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Traits** |  | **PH** | **NOT** | **SL** | **DM** | **NOS** | **GFP** | **NOG** | **100 GW** | **BY** | **HI** | **CH 1** | **CH 2** | **GY** |
| **DA** | rg | 0.278\* | 0.156 | 0.235 | 0.946\*\* | 0.552\*\* | -0.459\*\* | 0.428\*\* | -0.507\*\* | 0.154 | -0.210 | 0.129 | -0.047 | 0.078 |
|  | rp | 0.237\*\* | 0.113 | 0.200\*\* | 0.928\*\* | 0.499\*\* | -0.414\*\* | 0.399\*\* | -0.487\*\* | 0.147\* | -0.198\*\* | 0.103 | -0.025 | 0.069 |
| **PH** | rg |  | -0.046 | 0.500\*\* | 0.242 | 0.404\*\* | -0.184 | 0.321\* | 0.144 | 0.431\*\* | -0.159 | -0.045 | -0.145 | 0.349\*\* |
|  | rp |  | -0.025 | 0.449\*\* | 0.189\* | 0.359\*\* | -0.172\* | 0.267\*\* | 0.134 | 0.373\*\* | -0.127 | -0.046 | -0.110 | 0.301\*\* |
| **NOT** | rg |  |  | -0.317\* | 0.125 | 0.073 | -0.135 | -0.228 | -0.150 | 0.474\*\* | 0.011 | 0.029 | -0.005 | 0.512\*\* |
|  | rp |  |  | -0.222\*\* | 0.104 | 0.077 | -0.049 | -0.197\*\* | -0.129 | 0.369\*\* | 0.007 | -0.012 | -0.005 | 0.400\*\* |
| **SL** | rg |  |  |  | 0.187 | 0.281\* | -0.204 | 0.477\*\* | -0.114 | 0.070 | -0.199 | -0.118 | -0.075 | -0.019 |
|  | rp |  |  |  | 0.162\* | 0.242\*\* | -0.140 | 0.397\*\* | -0.100 | 0.070 | -0.159\* | -0.116 | -0.098 | -0.004 |
| **DM** | rg |  |  |  |  | 0.49\*\* | -0.146 | 0.339\*\* | -0.519\*\* | 0.174 | -0.139 | 0.117 | -0.029 | 0.125 |
|  | rp |  |  |  |  | 0.441\*\* | -0.044 | 0.309\*\* | -0.487\*\* | 0.162\* | -0.135 | 0.102 | -0.009 | 0.111 |
| **NOS** | rg |  |  |  |  |  | -0.343\*\* | 0.769\*\* | -0.369\*\* | 0.277\* | -0.159 | -0.099 | -0.179 | 0.189 |
|  | rp |  |  |  |  |  | -0.261\*\* | 0.728\*\* | -0.344\*\* | 0.245\*\* | -0.151\* | -0.086 | -0.156\* | 0.157\* |
| **GFP** | rg |  |  |  |  |  |  | -0.377\*\* | 0.125 | 0.007 | 0.258\* | -0.075 | 0.063 | 0.105 |
|  | rp |  |  |  |  |  |  | -0.315\*\* | 0.114 | 0.003 | 0.201\*\* | -0.027 | 0.043 | 0.085 |
| **NOG** | rg |  |  |  |  |  |  |  | -0.298\* | 0.109 | 0.009 | -0.083 | -0.148 | 0.082 |
|  | rp |  |  |  |  |  |  |  | -0.283\*\* | 0.094 | -0.007 | -0.051 | -0.119 | 0.061 |
| **100 GW** | rg |  |  |  |  |  |  |  |  | 0.024 | 0.059 | 0.101 | 0.068 | 0.060 |
|  | rp |  |  |  |  |  |  |  |  | 0.022 | 0.054 | 0.076 | 0.061 | 0.057 |
| **BY** | rg |  |  |  |  |  |  |  |  |  | -0.144 | -0.099 | 0.038 | 0.883\*\* |
|  | rp |  |  |  |  |  |  |  |  |  | -0.172\* | -0.074 | 0.039 | 0.875\*\* |
| **HI** | rg |  |  |  |  |  |  |  |  |  |  | 0.102 | 0.278\* | 0.321\* |
|  | rp |  |  |  |  |  |  |  |  |  |  | 0.089 | 0.166\* | 0.304\*\* |
| **CH 1** | rg |  |  |  |  |  |  |  |  |  |  |  | 0.490 | -0.026 |
|  | rp |  |  |  |  |  |  |  |  |  |  |  | 0.307\*\* | -0.012 |
| **CH 2** | rg |  |  |  |  |  |  |  |  |  |  |  |  | 0.147 |
|  | rp |  |  |  |  |  |  |  |  |  |  |  |  | 0.114 |

**rg:** Genotypic correlation coefficients**; rp:** Phenotypic correlation coefficients**; DA**: Days to Anthesis; **PH**: Plant Height; **NOT**: Number of Effective Tillers per Plant; **SL**: Length of Main Spike; **DM**: Days to Maturity; **NOS**: Number of Spikelets per Main Spike; **GFP**: Grain Filling Period; **NOG**: Number of Grains per Main Spike; **100**-**GW**: 100-Grain Weight; **BY**: Biological Yield per Plant; **HI**: Harvest Index (%); **CH 1**: Chlorophyll Content at Anthesis; **CH 2**:Chlorophyll Content at 21 DAA; **GY**: Grain Yield per Plant

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| --- |
| **Table 2. Genotypic path showing direct and indirect effects of different characters on grain yield in bread wheat** |
|  | **DA** | **PH** | **NOT** | **SL** | **DM** | **NOS** | **GFP** | **NOG** | **100 GW** | **BY** | **HI** | **CH 1** | **CH 2** | **Genotypic correlation** **with GY** |
| **DA** | **-2.0358** | -0.0007 | 0.0119 | 0.0129 | 1.7642 | 0.0174 | 0.3129 | -0.0266 | -0.0212 | 0.1395 | -0.1010 | 0.0030 | 0.0015 | 0.078 |
| **PH** | -0.5650 | **-0.0027** | -0.0035 | 0.0275 | 0.4507 | 0.0128 | 0.1257 | -0.0200 | 0.0060 | 0.3912 | -0.0766 | -0.0010 | 0.0047 | 0.349\*\* |
| **NOT** | -0.3181 | 0.0001 | **0.0763** | -0.0174 | 0.2326 | 0.0023 | 0.0920 | 0.0142 | -0.0063 | 0.4301 | 0.0051 | 0.0007 | 0.0002 | 0.512\*\* |
| **SL** | -0.4784 | -0.0013 | -0.0242 | **0.0549** | 0.3490 | 0.0089 | 0.1391 | -0.0297 | -0.0047 | 0.0639 | -0.0959 | -0.0027 | 0.0024 | -0.019 |
| **DM** | -1.9255 | -0.0006 | 0.0095 | 0.0103 | **1.8653** | 0.0155 | 0.0993 | -0.0211 | -0.0217 | 0.1577 | -0.0671 | 0.0027 | 0.0010 | 0.125 |
| **NOS** | -1.1252 | -0.0011 | 0.0056 | 0.0154 | 0.9140 | **0.0316** | 0.2341 | -0.0478 | -0.0155 | 0.2515 | -0.0766 | -0.0023 | 0.0059 | 0.189 |
| **GFP** | 0.9346 | 0.0005 | -0.0103 | -0.0112 | -0.2718 | -0.0108 | **-0.6816** | 0.0234 | 0.0052 | 0.0064 | 0.1241 | -0.0017 | -0.0021 | 0.105 |
| **NOG** | -0.8712 | -0.0009 | -0.0174 | 0.0262 | 0.6323 | 0.0243 | 0.2565 | **-0.0622** | -0.0125 | 0.0994 | 0.0042 | -0.0019 | 0.0048 | 0.082 |
| **100 GW** | 1.0313 | -0.0004 | -0.0115 | -0.0062 | -0.9671 | -0.0117 | -0.0851 | 0.0186 | **0.0418** | 0.0221 | 0.0282 | 0.0023 | -0.0022 | 0.060 |
| **BY** | -0.3127 | -0.0012 | 0.0362 | 0.0039 | 0.3238 | 0.0087 | -0.0048 | -0.0068 | 0.0010 | **0.9081** | -0.0696 | -0.0023 | -0.0012 | 0.883\*\* |
| **HI** | 0.4280 | 0.0004 | 0.0008 | -0.0110 | -0.2606 | -0.0050 | -0.1761 | -0.0005 | 0.0025 | -0.1316 | **0.4804** | 0.0023 | -0.0091 | 0.321\* |
| **CH 1** | -0.2641 | 0.0001 | 0.0022 | -0.0065 | 0.2183 | -0.0031 | 0.0512 | 0.0051 | 0.0042 | -0.0896 | 0.0490 | **0.0230** | -0.0160 | -0.026 |
| **CH 2** | 0.0958 | 0.0004 | -0.0004 | -0.0041 | -0.0546 | -0.0057 | -0.0432 | 0.0092 | 0.0028 | 0.0341 | 0.1337 | 0.0113 | **-0.0326** | 0.147 |
| **Residual=** 0.0056; **Direct effect** (Diagonal Bold); **DA**: Days to Anthesis; **PH**: Plant Height; **NOT**: Number of Effective Tillers per Plant; **SL**: Length of Main Spike; **DM**: Days to Maturity; **NOS**: Number of Spikelets per Main Spike; **GFP**: Grain Filling Period; **NOG**: Number of Grains per Main Spike; **100**-**GW**: 100-Grain Weight; **BY**: Biological Yield per Plant; **HI**: Harvest Index (%); **CH 1**: Chlorophyll Content at Anthesis; **CH 2**:Chlorophyll Content at 21 DAA; **GY**: Grain Yield per Plant |

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**Figure 1: Genotypic path diagram depicting direct effects (in box) and genotypic correlations between various traits in bread wheat**