# Multivariate Correlation and Path Coefficient Analysis of Various Agro-Physiological Traits in CIMMYT Accessionsof Bread Wheat [*Triticum aestivum* (L.) em. Thell]

## Abstract

(Please mention the location year and season of research work conducted with statistical design and give the results of work done in short).Bread wheat (*Triticum aestivum* L. em. Thell) is one of the most vital staple crops globally, providing sustenance for billions of people. The continued increase in the global population, coupled with the ever-changing climate patterns and growing concerns about food security, has intensified the need for enhancing the productivity and adaptability of wheat varieties. In this context, the study of agro-physiological traits in bread wheat accessions assumes paramount significance. This research examines the association and interrelationships between thirteen different agro-physiological traits among fifty accessions of CIMMYT bread wheat. The results demonstrate significant positive correlations between grain yield and yield-related traits, including plant height, spike length, biological yield per plot, test weight, and harvest index at both genotypic and phenotypic levels. Further analysis using path coefficients shed light on the direct and indirect effects of these traits on grain yield. Among the studied traits, harvest index and biological yield per plot were found to have higher direct effects than others. These findings hold significant promise for informing and optimizing selection and breeding programs aimed at enhancing wheat varieties.

**Keywords:** Path analysis, Genotypic correlation, Residual effect, Phenotypic correlation

## 1. Introduction

Wheat (*Triticum aestivum* L. em. Thell) is a staple food crop of many countries across the globe, including India, which plays an important role in nutritional as well as food security (Pingali *et al.*, 2015). Wheat is an allohexaploid (2n = 6x = 42) self-pollinated annual plant which belongs to the Graminae (Poaceae) family, tribe Triticeae and of the genus *Triticum*. Cultivated wheat varieties were categorized based on their ploidy levels, include diploids (2n = 2x = 14, AA), tetraploids (2n = 4x = 28, BBAA), and hexaploids (2n = 6x = 42, BBAADD) (Tadesse *et al.*,2019). Notably, tetraploid and hexaploid wheats have chromosome sets that result from duplications of distinct genomes. Therefore, bread wheat and durum wheat are referred to as allopolyploids, specifically allotetraploids and allohexaploids, respectively. It is important to highlight that bread wheat dominates global wheat production, accessions for over 95% of the total output (Tadesse *et al.*,2019). It is the most widely cultivated crop in the world, cultivated on 217 million ha annually (Erenstein *et al.*, 2022). Wheat now supplies a fifth of food calories and protein to the world's population. China, India, and Russia are the three largest individual wheat producers in the world, accounting for about 41% of the world's total wheat production. As of 2019, wheat productivity averaged around 3.27 tons per hectare (FAO, 2021), showcasing its remarkable ability to provide substantial grain output even in challenging agricultural environments.

Traditionally, the cultivation of wheat has been prominent in Central and West Asia, North Africa (CWANA), Europe, America, and Australia. However, due to increasing urbanization and shifts in dietary preferences, the demand for wheat has been steadily rising in various regions, including Eastern and Southern Africa (5.8% increase), West and Central Africa (4.7% increase), and South Asia and the Pacific (4.3% increase). Central Asia (5.6%), Australia (2.2%), and North Africa (2.2%) have also seen an uptick in demand (Shiferaw *et al.*, 2013). By 2050, the demand for wheat is expected to expand by 50%, and it's important to note that there are no available options to increase the land area dedicated to wheat production (Naveen *et al.*, 2023). Currently, India is the world largest producer of wheat with a production of 74.25 Mt in an area of 27.2 Mha (FAO, 2022). Uttar Pradesh is the largest wheat producing state in India, followed by Punjab, Haryana and Madhya Pradesh (Balaganesh *et al.*, 2019).

The direct introduction and adoption of semi-dwarf, input-responsive wheat varieties, originating from CIMMYT, by national programs in countries such as Mexico, India, Pakistan, and Turkey played a pivotal role in ushering in the Green Revolution and played a crucial role in ensuring food security (Dixon *et al.,* 2009)The production of wheat faces a multitude of challenges, both abiotic (such as drought, cold, heat, and salinity) and biotic (including threats like yellow rust, leaf rust, stem rust, Septoria, root rots, Russian Wheat Aphid, Barley Yellow Dwarf Virus, Sun pest, and Hessian Fly) on a global, regional, and national scale. These challenges are further exacerbated by factors like a growing human population, land degradation, water scarcity, and the ever-escalating impacts of climate change. These collective pressures are placing substantial strains on wheat production at a broader level.

Yield is a complex and polygenic character resulting from the multiplicative interaction of its component traits and the cumulative effect of such traits determines the yield. Therefore, knowledge on the association of characters is of immense importance to estimate the nature and magnitude of relationship among yield and its components to improve the effectiveness of selection. The change in one character brings a series of changes in the other characters since they are interconnected. Therefore, the correlation studies are of considerable importance in any selection program as they provide the degree and direction of the relationship between two or more component traits. Path coefficient analysis was used by plant breeders to help identify traits that could be useful as a selection criterion for improving crop yield. The path coefficient divides correlation coefficients into direct and indirect effects within the correlation system of traits. Path coefficient analysis show a direct effect of the independent variable in the dependent variable, as well as an indirect effect of the independent variable in the dependent variable through another independent variable (Hadi *et al.,* 2018). Keeping these in view, the present study was carried out on CIMMYT bread wheat accessions to derive information on interrelationships of important agro-physiological traits through correlation and path coefficient analysis.

## 2. Material and methods

### 2.1. Experimental design and plant material:

In the Rabi season of 2019-20, a research study was conducted at the Agriculture Research Farm, Banaras Hindu University, Varanasi, focusing on the phenotypic evaluation of diverse bread wheat *gen*otypes. The experiment carried out using 49 distinct genotypes procured from CIMMYT, Mexico, alongside the local reference variety DBW 187. Employing a randomized block design (RBD) with 2 replications, the experimental plots were spaced at 50 cm intervals. Within each replication, genotypes were sown in rows of 5-meter length, maintaining a 20 cm inter-row spacing and 5 cm spacing between individual plants. Adherence to recommended agricultural practices ensured optimal crop growth, complemented by vigilant plant protection measures.

Meteorological conditions during the crop cycle were documented as illustrated in Supplementary Figure 1.

### 2.2. Phenotypic traits and measurements:

Thirteen distinct traits were evaluated during the study. These included 11 agro-morphological traits viz., germination percentage (GNP), days to 50 % flowering (DTFF), days to maturity (DTM), normalized difference vegetative index (NDVI), plant height (PTH) in cm, spike length (SKL) in cm, tillers per square metre (TPSM), test weight (TWT)in grams, biological yield per plot (BYPP) in kg, grain yield per plot (GYPP) in kg, harvest index (HI) in %, and 2 physiological traits such as chlorophyll content (CFC), canopy temperature (CNTP) in °C. With a Minolta SPAD-502 Chlorophyll metre, CFC was measured at the heading and anthesis phases, while CNTP was measured from the vegetative stage to dough stages using, a hand-held infrared thermometer. The observations were recorded on 5 plants for each genotype in accordance with established scientific protocols.

### 2.3. Statistical analysis

The recorded data of sampled plants were averaged to calculate mean values of its respective genotype. Phenotypic and genotypic correlations were worked out by using the formulae suggested by Falconer (1964).

$$r\ (\boldsymbol{xi}.\ \boldsymbol{xj}) = \boldsymbol{Cov}(\boldsymbol{xi}.\boldsymbol{xj})\ \surd \boldsymbol{V}(\boldsymbol{xi}).\boldsymbol{V}(\boldsymbol{xj})$$

The calculated value of correlation coefficients was tested for its significance by comparing the observed value of correlation coefficients with the table value of 'r' given by Fisher and Yates (1963) available in standard books at (n – 2) degrees of freedom as follows:

$$t = \boldsymbol{r}\ \surd \mathbf{1{-}r2} \times \surd \mathbf{n} - \mathbf{1}$$

Path coefficient was calculated to estimate the direct and indirect effects of studied traits to yield as proposed by Dewey and Lu (1959).

## 3. Results and discussion

### 3.1. Genotypic and phenotypic correlation coefficients

#### 3.1.1. Correlations between grain yield and yield-related traits(Mention the table no. in text for better understanding)

The genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients for all thirteen traits were presented in Table 1. Characters like PH, SKL, BYPP, TWT, HI showed positive significant correlation with GYPPat both genotypic and phenotypic level. Baye et al 2020 also reported that grain yield has significant positive correlation with PH, BYPP, TWT, HI which are in agreement with the present study. The findings of Dutamo et al. (2015) and Mecha et al. (2017) also showed that spike length, thousand seed weight, biomass, and harvest index had positive correlation with grain yield at both genotypic and phenotypic levels. The findings of Dutamo et al. (2015) and Mecha et al. (2017) also showed that SKL, BYPP and HI had positive correlation with grain yield at both genotypic and phenotypic levels. Whereas GNP, NDVI, DTM, CFC, TPSM exhibited positive nonsignificant correlation with GYPP at both genotypic and phenotypic level (Javed *et al.*, 2022). DTFF showed positive nonsignificant correlation with GYPP only at genotypic level. Similar results are also reported by Kumar et al. (2013). CNTP showed negative non-significant correlation with GYPP at both genotypic and phenotypic level. Similar relationship is also reported by Bennani et al. (2016). While days to 50 % flowering showed negative non-significant correlation with GYPP only at only at phenotypic level. Hassani et al. (2022) also reported that DTFF showed negative non-significant correlation with GYPP. Phenotypic and genotypic shaded correlation matrices, simplifying the intensity of correlations among 13 characters were also shown in Figure 1 and 2 respectively.

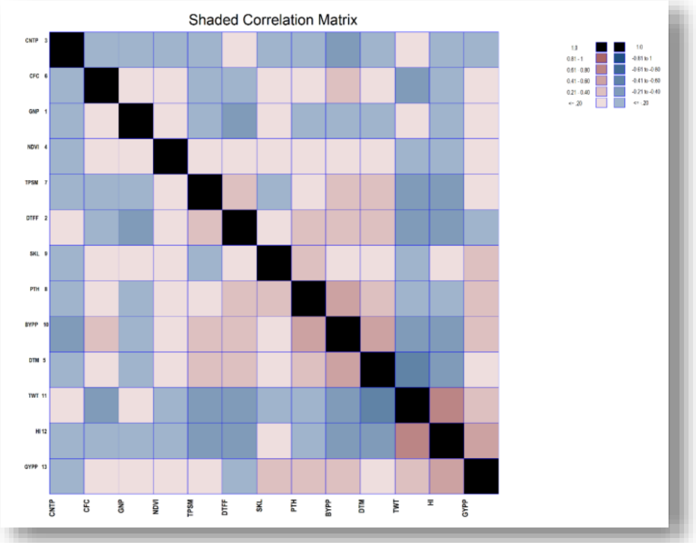
#### 3.1.2. Correlation among yield-related traits(Mention the table no. in text and value of GCC and PCC for better understanding)

GNP showed negative significant phenotypic correlation with only DTFF. DTFF showed positive significant correlation with DTM, TPSM, PTH, BYPP at both genotypic and phenotypic level. Maurya et al. (2020) also showed similar findings from their research. DTFF showed positive significant correlation with SKL only at phenotypic level. DTFF showed negative significant correlation with TWT, HI at both genotypic and phenotypic level. These results agree with the findings of Kumar et al. (2013). CNTP showed negative significant correlation with BYPP at both genotypic and phenotypic level. NDVI showed positive significant correlation with SKL only at genotypic level. DTM showed positive significant correlation with TPSM, PTH, BYPP at both genotypic and phenotypic level. DTM showed positive significant correlation with DTFF only at genotypic level. DTM showed negative significant correlation with TWT, HI at both genotypic and phenotypic level. CFC showed positive significant correlation with BYPP at both genotypic and phenotypic level. CFC showed negative significant correlation with TWT at both genotypic and phenotypic level. TPSM showed positive significant correlation with DTFF, DTM, BYPP at both genotypic and phenotypic level. TPSM showed negative significant correlation with TWT, HI at both genotypic and phenotypic level. PTH showed positive significant correlation with DTFF, DTM, SKL, BYPP at both genotypic and phenotypic level. SKL showed positive significant correlation with DTFF, PTH at phenotypic level.

SKL showed positive significant correlation with NDVI, PTH at genotypic level. BYPP showed positive significant correlation with DTFF, DTM, CFC, TPSM, PTH at both genotypic and phenotypic level. BYPP showed negative significant correlation with CNTP, TWT, HI at both genotypic and phenotypic level. TWT showed positive significant correlation with HI at both genotypic and phenotypic level. TWT showed negative significant correlation with DTFF, DTM, CFC, TPSM, BYPP at both genotypic and phenotypic level. HI showed positive significant correlation with TWT at both genotypic and phenotypic level.Azimi et al. (2017) also reported similar results from their research. HI showed negative significant correlation with DTFF, DTM, TPSM, BYPP, TWT.Singh et al. (2012) also reported similar correlations.

**Table 1: Genotypical (above diagonal) and phenotypical (below diagonal) correlation matrix of 13 traits at phenotypic level for bread wheat genotypes**

| | **GNP** | **DTFF** | **CNTP** | **NDVI** | **DTM** | **CFC** | **TPSM** | **PTH** | **SKL** | **BYPP** | **TWT** | **HI** | **GYPP** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **GNP** | **1.0000** | -0.1915 | -0.0517 | 0.0589 | -0.1063 | 0.0710 | -0.1395 | -0.0479 | 0.0827 | -0.1039 | 0.1540 | -0.0242 | 0.0299 |
| **DTFF** | -0.211* | **1.0000** | 0.1754 | 0.1790 | 0.384** | -0.1284 | 0.269* | 0.222* | 0.1069 | 0.227* | -0.313* | -0.239* | 0.0261 |



| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **CNTP** | -0.07 | | | | | | -0.1100 | -0.1116 | -0.1363 | -0.253* | -0.0402 | -0.0833 | -0.1639 |
| **NDVI** | 0.18 | | | | | | 0.0800 | 0.1097 | 0.199* | 0.0527 | 0.0175 | -0.0567 | 0.1092 |
| **DTM** | -0.01 | | | | | | 0.244* | 0.260* | 0.0802 | 0.461** | -0.468** | -0.373** | 0.0489 |
| **CFC** | 0.12 | | | | | | -0.1287 | 0.1084 | 0.0611 | 0.261* | -0.208* | -0.1442 | 0.1070 |
| **TPSM** | -0.02 | | | | | | **1.0000** | 0.0955 | -0.0158 | 0.251* | -0.273* | -0.215* | 0.0619 |
| **PTH** | -0.02 | | | | | | 0.1473 | 1.**0000** | 0.256* | 0.421** | -0.0915 | 0.0143 | 0.307* |
| **SKL** | 0.04 | | | | | | -0.0099 | 0.266* | **1.0000** | 0.1155 | 0.0552 | 0.1235 | 0.304* |
| **BYPP** | -0.05 | | | | | | 0.273* | 0.408** | 0.1319 | **1.0000** | -0.363** | -0.221* | 0.430** |
| **TWT** | 0.12 | | | | | | -0.297* | -0.1593 | -0.0327 | -0.378** | **1.0000** | 0.574** | 0.255* |
| **HI** | -0.03 | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | -0.201* | -0.0289 | 0.0208 | -0.248* | 0.609** | **1.0000** | 0.563** |
| **GYPP** | 0.0469 | -0.0040 | -0.1272 | 0.0918 | 0.0563 | 0.1121 | 0.1009 | 0.293* | 0.253* | 0.398** | 0.241* | 0.563** | **1.0000** |

* Significant at P = 0.05, ** Significant at P = 0.01

Where, GNP- Germination Percentage; DTM- Days to Maturity; DTFF- Days to 50 % Flowering; CNTP- Canopy Temperature; CFC- Chlorophyll Content; NDVI- Normalized Difference Vegetative Index; TPSM- Tillers Per Square Metre; PTH- Plant Height (cm); SKL- Spike Length(cm); TWT- Test Weight (g); HI- Harvest Index (%); BYPP- Biological Yield Per Plot (Kg); GYPP- Grain Yield Per Plot (Kg).

**Figure 1: Phen** **ad wheat**

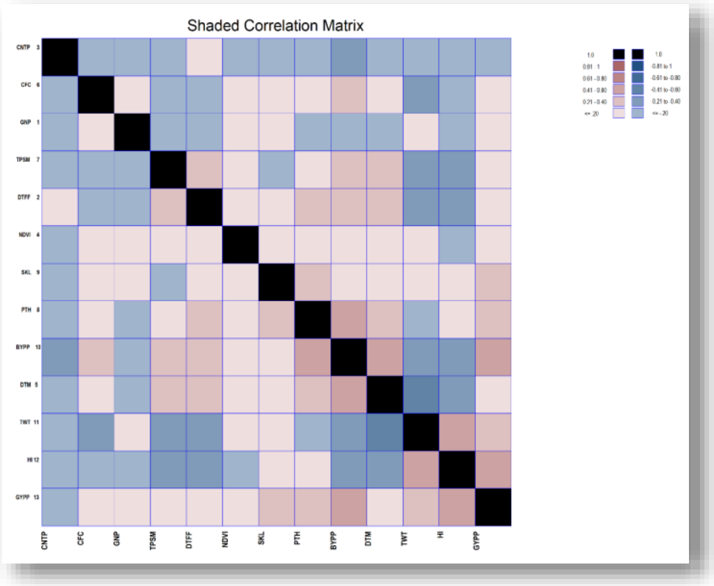


**Figure 2: Genotypic shaded correlation matrix of 13 characters of bread wheat**

## Path coefficient analysisraits(Mention the table no. in text for better understanding)

Association of character determined by correlation co-efficient may not provide an exact picture of the relative importance of direct and indirect influence of each of yield components of yield. In order to find out a clear picture of the inter-relationship between yield and other yield attributes, direct and indirect effects were worked out using path analysis both ant genotypic and phenotypic level which also measured relative importance of each component. Yield was considered as a resultant variable other character estimated as causal or independent variable.

The results of path coefficient analysis of the current study at genotypic (Table 3) and phenotypic levels (Table 2) were presented. HI, BYPP showed high positive direct effect on grain yield both at genotypic and phenotypic levels.Verma et al. (2019) also reported similar correlations. SKL, TWT, CFC, TPSM CHI, BYPP showed low positive direct effect on grain yield both at genotypic and phenotypic levels. Mohanty et al. (2016) also reported similar findings from their research. DTFF, CNTP, DTM, PTH showed negligible positive direct effect on grain yield both at genotypic and phenotypic levels. Lamara et al. (2022) also revealed similar results from their findings.

GNP showed positive indirect effects on grain yield via NDVI, CFC, SKL, TWT and negative indirect effects through remaining characters. DTFF showed negative indirect effects on grain yield via GNP, CFC, TWT, HI and positive indirect effects through remaining characters. CNTP showed positive indirect effects on grain yield via DTFF, TWT and negative indirect effects through remaining characters. NDVI showed negative indirect effects on grain yield via CNTP, TWT, HI and positive indirect effects through remaining characters. DTM showed negative indirect effects on grain yield via GNP, CNTP, TWT, HI and positive indirect effects through remaining characters. CFC showed negative indirect effects on grain yield via DTFF, CNTP, TPSM, TWT, HI and positive indirect effects through remaining characters. TPSM showed negative indirect effects on grain yield via GNP, CNTP, TWT, HI, CFC, SKL. PTH showed negative indirect effects on grain yield via GNP, CNTP, TWT, HI and positive indirect effects through remaining characters. SKL showed negative indirect effects on grain yield via CNTP, TPSM, TWT, HI and positive indirect effects through remaining characters. BYPP showed negative indirect effects on grain yield via GNP, CNTP, TWT, HI and positive indirect effects through remaining characters. TWT showed positive indirect effects on grain yield via GNP, CNTP, HI and negative indirect effects through remaining characters. The current results are in agreement with previous studies in wheat (Baye *et al.*,2020;Dutamo *et al.*,2015,Sabit *et al.*, 2017)

The residual effect at phenotypic level was 0.255 and at genotypic level was 0.195 indicating there were also some other characters which although not studied but influenced the seed yield. To simplify the results, path diagram was provided at both phenotypic(Figure 3) and genotypic(Figure 4) levels.

**Table 2: Estimates of direct effect (diagonal and bold face) and indirect effects (off diagonal) of 13 traits at phenotypic level for bread wheat genotypes**

| | **GNP** | **DTFF** | **CNTP** | **NDVI** | **DTM** | **CFC** | **TPSM** | **PTH** | **SKL** | **BYPP** | **TWT** | **HI** | **GYPP** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **GNP** | **0.0812** | -0.0171 | -0.0061 | 0.0151 | -0.0015 | 0.0102 | -0.0020 | -0.0020 | 0.0034 | -0.0047 | 0.0098 | -0.0026 | 0.0469 |
| **DTFF** | -0.0120 | **0.0569** | 0.0058 | 0.0072 | 0.0223 | -0.0068 | 0.0149 | 0.0140 | 0.0113 | 0.0138 | -0.0226 | -0.0171 | -0.0040 |
| **CNTP** | -0.0041 | 0.0055 | **0.0539** | -0.0031 | -0.0037 | -0.0029 | -0.0062 | -0.0078 | -0.0088 | -0.0132 | 0.0009 | -0.0006 | -0.1272 |
| **NDVI** | 0.0063 | 0.0043 | -0.0019 | **0.0339** | 0.0043 | 0.0049 | 0.0039 | 0.0033 | 0.0064 | 0.0030 | -0.0003 | -0.0034 | 0.0918 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **DTM** | -0.0011 | 0.0224 | -0.0040 | 0.0073 | **0.0573** | 0.0068 | 0.0153 | 0.0147 | 0.0057 | 0.0262 | -0.0269 | -0.0217 | 0.0563 |
| **CFC** | 0.0127 | -0.0120 | -0.0054 | 0.0145 | 0.0119 | **0.1009** | -0.0082 | 0.0108 | 0.0033 | 0.0258 | -0.0216 | -0.0149 | 0.1121 |
| **TPSM** | -0.0029 | 0.0306 | -0.0133 | 0.0134 | 0.0311 | -0.0094 | **0.1166** | 0.0172 | -0.0012 | 0.0318 | -0.0347 | -0.0234 | 0.1009 |
| **PTH** | -0.0010 | 0.0100 | -0.0059 | 0.0039 | 0.0104 | 0.0043 | 0.0060 | **0.0407** | 0.0108 | 0.0166 | -0.0065 | -0.0012 | 0.293* |
| **SKL** | 0.0061 | 0.0289 | -0.0238 | 0.0274 | 0.0144 | 0.0048 | -0.0014 | 0.0386 | **0.1453** | 0.0192 | -0.0048 | 0.0030 | 0.253* |
| **BYPP** | -0.0284 | 0.1198 | -0.1206 | 0.0437 | 0.2256 | 0.1262 | 0.1345 | 0.2012 | 0.0651 | **0.4935** | -0.1867 | -0.1222 | 0.398** |
| **TWT** | 0.0128 | -0.0422 | 0.0018 | -0.0010 | -0.0499 | -0.0228 | -0.0316 | -0.0169 | -0.0035 | -0.0402 | **0.1063** | 0.0647 | 0.241* |
| **HI** | -0.0227 | -0.2111 | -0.0078 | -0.0705 | -0.2659 | -0.1041 | -0.1411 | -0.0203 | 0.0146 | -0.1741 | 0.4275 | **0.7026** | 0.563** |
| **GYPP** | 0.0469 | -0.0040 | -0.1272 | 0.0918 | 0.0563 | 0.1121 | 0.1009 | 0.293* | 0.253* | 0.398** | 0.241* | 0.563** | **1.0000** |

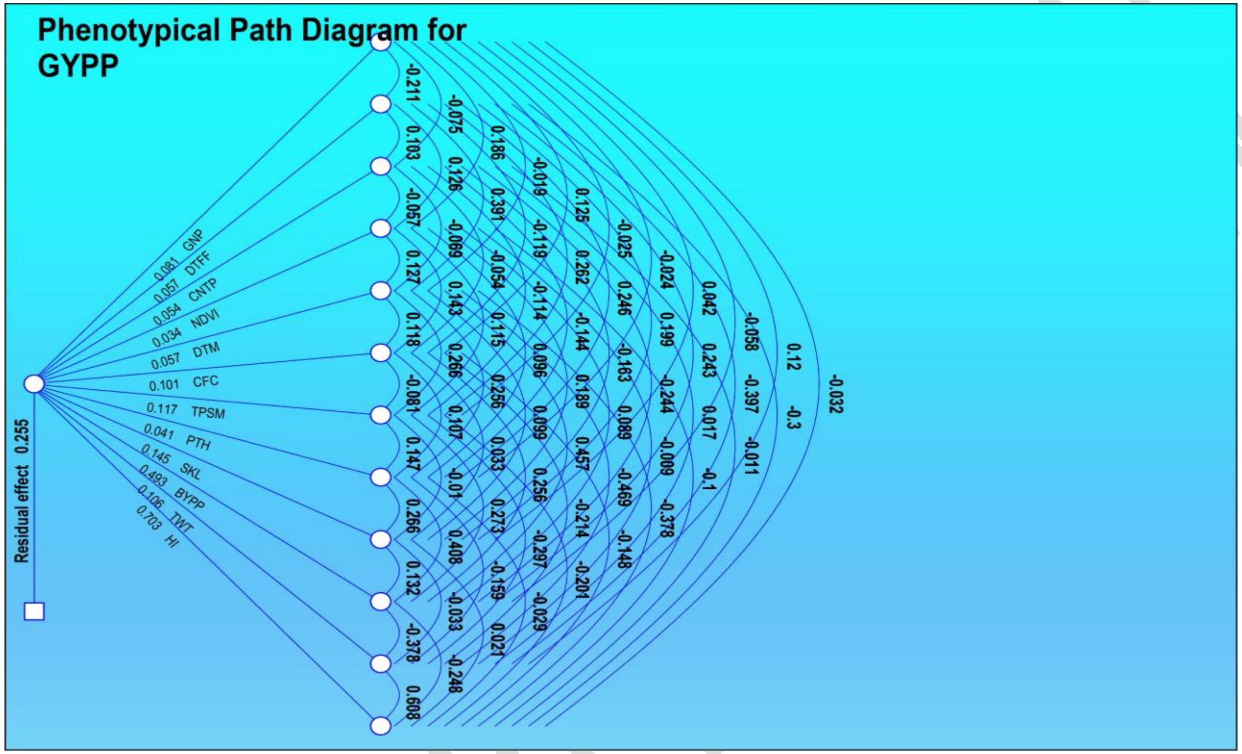


**Figure 3: Phenotypic path coefficient analysis of 13 characters of bread wheat**

**Table 3: Estimates of direct effect (diagonal and bold face) and indirect effects (off diagonal) of 13 traits at genotypic level for bread wheat genotypes**

| | GNP | DTFF | CNTP | NDVI | DTM | CFC | TPSM | PTH | SKL | BYPP | TWT | HI | GYPP |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **GNP** | **0.0957** | -0.0183 | -0.0049 | 0.0056 | -0.0102 | 0.0068 | -0.0133 | -0.0046 | 0.0079 | -0.0099 | 0.0147 | -0.0023 | 0.0299 |
| **DTFF** | -0.0085 | **0.0443** | 0.0078 | 0.0079 | 0.0170 | -0.0057 | 0.0119 | 0.0098 | 0.0047 | 0.0100 | -0.0139 | -0.0106 | 0.0261 |
| **CNTP** | -0.0039 | 0.0132 | **0.0752** | -0.0038 | -0.0047 | -0.0041 | -0.0083 | -0.0084 | -0.0103 | -0.0190 | -0.0030 | -0.0063 | -0.1639 |
| **NDVI** | 0.0035 | 0.0105 | -0.0029 | **0.0588** | 0.0040 | 0.0057 | 0.0047 | 0.0065 | 0.0117 | 0.0031 | 0.0010 | -0.0033 | 0.1092 |
| **DTM** | -0.0062 | 0.0222 | -0.0036 | 0.0039 | **0.0579** | 0.0050 | 0.0141 | 0.0151 | 0.0046 | 0.0267 | -0.0271 | -0.0216 | 0.0489 |
| **CFC** | 0.0062 | -0.0112 | -0.0047 | 0.0084 | 0.0075 | **0.0872** | -0.0112 | 0.0095 | 0.0053 | 0.0227 | -0.0182 | -0.0126 | 0.1070 |
| **TPSM** | -0.0152 | 0.0294 | -0.0120 | 0.0087 | 0.0267 | -0.0140 | **0.1092** | 0.0104 | -0.0017 | 0.0274 | -0.0298 | -0.0234 | 0.0619 |
| **PTH** | -0.0004 | 0.0019 | -0.0010 | 0.0010 | 0.0023 | 0.0009 | 0.0008 | **0.0087** | 0.0022 | 0.0037 | -0.0008 | 0.0001 | 0.307* |
| **SKL** | 0.0104 | 0.0134 | -0.0171 | 0.0250 | 0.0101 | 0.0077 | -0.0020 | 0.0321 | **0.1255** | 0.0145 | 0.0069 | 0.0155 | 0.304* |
| **BYPP** | -0.0571 | 0.1245 | -0.1391 | 0.0289 | 0.2534 | 0.1433 | 0.1378 | 0.2314 | 0.0635 | **0.5494** | -0.1995 | -0.1214 | 0.430** |
| **TWT** | 0.0217 | -0.0441 | -0.0057 | 0.0025 | -0.0659 | -0.0293 | -0.0385 | -0.0129 | 0.0078 | -0.0511 | **0.1408** | 0.0807 | 0.255* |
| **HI** | -0.0162 | -0.1598 | -0.0557 | -0.0379 | -0.2492 | -0.0964 | -0.1434 | 0.0096 | 0.0825 | -0.1477 | 0.3834 | **0.6685** | 0.563** |
| **GYPP** | 0.0299 | 0.0261 | -0.1639 | 0.1092 | 0.0489 | 0.1070 | 0.0619 | 0.307* | 0.304* | 0.430** | 0.255* | 0.563** | **1.0000** |

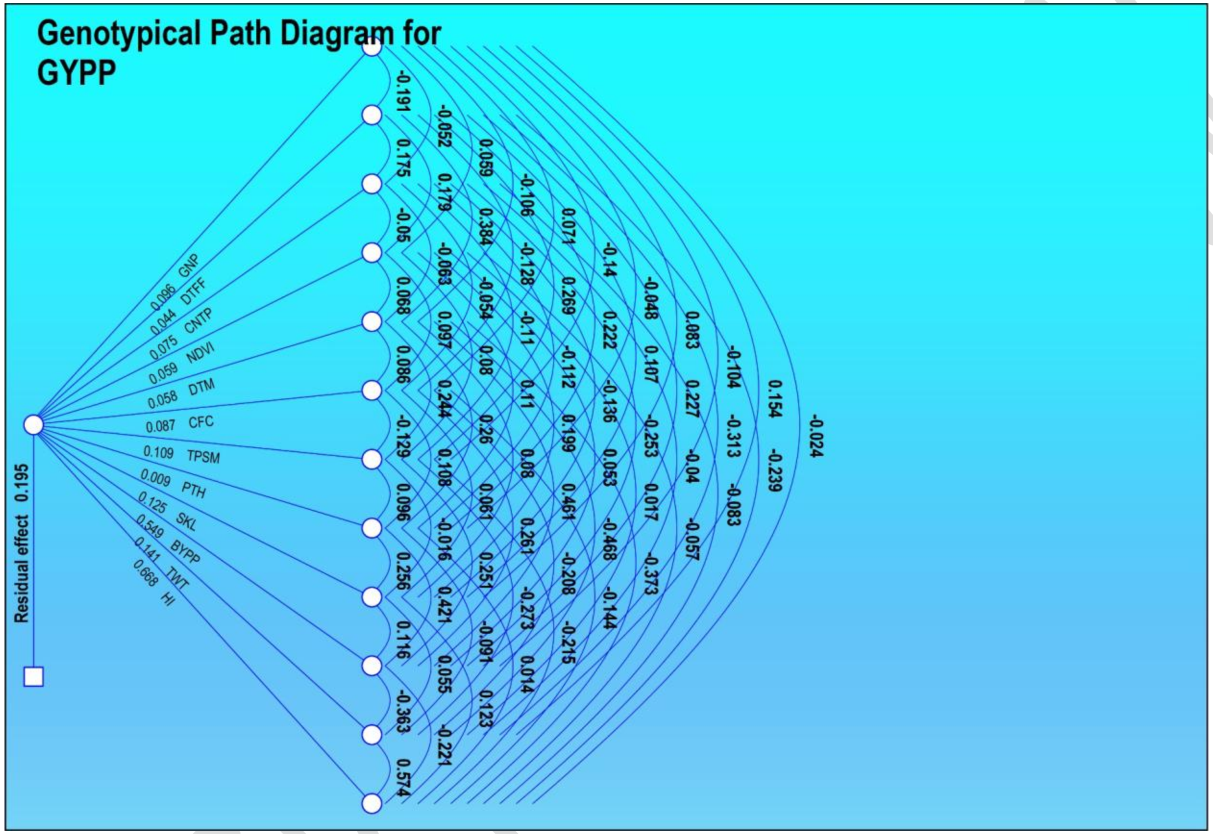


**Figure 4: Genotypic path coefficient analysis of 13 characters of bread wheat**

## Conclusion

Success in any breeding or selection programme requires careful selection criteria depending on nature of variability and associations between different traits for grain yield. Positive significant correlation of plant height, spike length, biological yield per plot, test weight (TWT), harvest index with grain yield per plot indicates the opportunity to improve grain yield through these characters.The correlation coefficient serves as a valuable tool for revealing relationships between pairs of individual traits. However, it's important to recognize that a dependent trait, such as grain yield, is not simply the result of a single characteristic but rather an intricate outcome influenced by the combined interactions of various interconnected component traits. Any alteration in one of these component traits can potentially disrupt the entire network of cause-and-effect relationships within the system.The utilization of path analysis in our study not only helped to unravel the intricacies of these associations but also provided a clearer understanding of how individual component traits influencing the grain yield. HI, BYPP showed high positive direct effect on grain yield both at genotypic and phenotypic levels indicates possibility of yield improvement through direct selection for these traits. PTH, SKL, TWT showed negligible to low positive direct effects but significant positive correlation indicates the importance of employing indirect selection for these traits to improve grain yield. The residual effect estimates through path analysis indicted the importance of considering few more component traits to improve grain yield.

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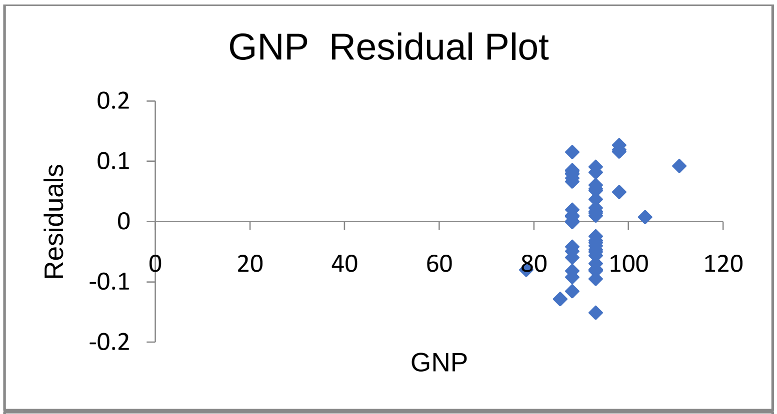
**Supplementary Table 1:** Genotypes procured from CIMMYT and their codes

| S.no | Genotype (GEN) | Name |
|---|---|---|
| 1 | *GEN*-1 | **DBW 187** |
| 2 | *GEN*-2 | **NADI #2** |
| 3 | *GEN*-3 | **QUAIU #1/SUP152** |
| 4 | *GEN*-4 | **WBLL1*2/BRAMBLING/4/BABAX/LR42//BABAX*2/3/SHAMA*2/5/PBW343*2/KUKUNA*2//FRTL/PIFED** |
| 5 | *GEN*-5 | **KACHU #1/KIRITATI//KACHU/3/BECARD/FRNCLN** |
| 6 | *GEN*-6 | **BABAX/LR42//BABAX*2/3/KUKUNA/4/BACEU #1/5/BECARD/6/KACHU/KINDE** |
| 7 | *GEN*-7 | **BABAX/LR42//BABAX/3/ER2000/4/KACHU #1/KIRITATI//KACHU** |
| 8 | *GEN*-8 | **KACHU*2/SUP152** |
| 9 | *GEN*-9 | **SAUAL/YANAC//SAUAL/3/2*KFA/2*KACHU** |
| 10 | *GEN*-10 | **KANCHAN*2/JUCHI//2*BORL14** |
| 11 | *GEN*-11 | **WBLL1*2/BRAMBLING//WBLL1*2/BRAMBLING/3/2*BORL14** |
| 12 | *GEN*-12 | **FRANCOLIN #1*2/HAWFINCH #1//2*MUCUY** |
| 13 | *GEN*-13 | **PBW65/2*PASTOR//TACUPETO F2001*2/BRAMBLING/3/TACUPETO F2001*2/BRAMBLING/6/2*SHORTENED SR26 TRANSLOCATION/4/ATTILA/3*BCN//BAV92/3/PASTOR/5/MUNAL** |
| 14 | *GEN*-14 | **MUU/KBIRD//2*KACHU/KIRITATI** |
| 15 | *GEN*-15 | **MUU/KBIRD//2*KACHU/KIRITATI** |
| 16 | *GEN*-16 | **WBLL1*2/BRAMBLING//VORB/FISCAL/3/BECARD/4/MUCUY/5/MUCUY** |
| 17 | *GEN*-17 | **SUP152/BLOUK #1//BECARD/FRNCLN** |
| 18 | *GEN*-18 | **ALTAR 84/AE.SQUARROSA (221)//3*BORL95/3/URES/JUN//KAUZ/4/WBLL1/5/MUTUS/6/SUP152/BAJ #1** |

| | | |
|---|---|---|
| 19 | *GEN*-19 | **BECARD/FRNCLN//BORL14** |
| 20 | *GEN*-20 | **SNTL/3/KACHU//WBLL1*2/BRAMBLING** |
| 21 | *GEN*-21 | **BORL14*2//BECARD/QUAIU #1** |
| 22 | *GEN*-22 | **BORL14*2//BECARD/QUAIU #1** |
| 23 | *GEN*-23 | **BORL14*2//BECARD/QUAIU #1** |
| 24 | *GEN*-24 | **WBLL1*2/BRAMBLING/4/BABAX/LR42//BABAX*2/3/SHAMA*2/5/BECARD/QUAIU #1** |
| 25 | *GEN*-25 | **NADI#1*2/3/MUTUS/AKURI #1//MUTUS** |
| 26 | *GEN*-26 | **SHAKTI/6/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/4/T.DICOCCON PI94625/AE.SQUARROSA (372)//SHA4/CHIL/5/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1** |
| 27 | *GEN*-27 | **CHIPAK/3/SWSR22T.B./2*BLOUK #1//WBLL1*2/KURUKU** |
| 28 | *GEN*-28 | **BORL14*2/MISR 1** |
| 29 | *GEN*-29 | **SAUAL/3/ACHTAR*3//KANZ/KS85-8-4/4/SAUAL/5/2*BAJ #1/3/KIRITATI//ATTILA*2/PASTOR** |
| 30 | *GEN*-30 | **SUP152/BLOUK #1//2*BECARD/FRNCLN** |
| 31 | *GEN*-31 | **MUTUS*2/MUU//2*MUCUY** |
| 32 | *GEN*-32 | **BECARD/FRNCLN*2//BORL14** |
| 33 | *GEN*-33 | **KACHU/BECARD//WBLL1*2/BRAMBLING*2/3/ONIX/KBIRD** |
| 34 | *GEN*-34 | **KACHU/BECARD//WBLL1*2/BRAMBLING*2/3/FRNCLN*2/TECUE #1** |
| 35 | *GEN*-35 | **KACHU/BECARD//WBLL1*2/BRAMBLING*2/3/KACHU/KINDE** |
| 36 | *GEN*-36 | **KACHU/BECARD//WBLL1*2/BRAMBLING*2/8/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213)//PGO/4/HUITES/5/T.DICOCCON PI94624/AE.SQUARROSA (409)//BCN/6/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213)//PGO/4/HUITES/7/MUTUS** |
| 37 | *GEN*-37 | **KACHU #1/3/T.DICOCCON PI94624/AE.SQUARROSA (409)//BCN/4/2*KACHU*2/5/KACHU/KINDE** |

|  |  |  |
|---|---|---|
| 38 | *GEN*-38 | **NADI#2*2/6/BECARD #1/5/KIRITATI/4/2*SERI.1B*2/3/KAUZ*2/BOW//KAUZ** |
| 39 | *GEN*-39 | **MEX94.27.1.20/3/SOKOLL//ATTILA/3*BCN/4/2*SUP152*2/TECUE #1** |
| 40 | *GEN*-40 | **MACE/5/TILILA/JUCHI/4/SERI.1B//KAUZ/HEVO/3/AMAD/6/KACHU/BECARD//WBLL1*2/BRAMBLING** |
| 41 | *GEN*-41 | **KACHU//KIRITATI/2*TRCH/3/KFA/2*KACHU** |
| 42 | *GEN*-42 | **KACHU//KIRITATI/2*TRCH/3/KFA/2*KACHU** |
| 43 | *GEN*-43 | **MUU/FRNCLN//FRANCOLIN #1/3/BORL14** |
| 44 | *GEN*-44 | **WBLL1*2/BRAMBLING*2//BAVIS/3/KACHU #1/KIRITATI//KACHU** |
| 45 | *GEN*-45 | **WBLL1*2/BRAMBLING*2//BAVIS/3/KFA/2*KACHU** |
| 46 | *GEN*-46 | **KENYA SUNBIRD/2*KACHU/3/WBLL1*2/BRAMBLING*2//BAVIS** |
| 47 | *GEN*-47 | **SUNCO.6/FRAME//PASTOR/3/NAVJ07/4/1447/PASTOR//KRICHAUFF/5/BORL14** |
| 48 | *GEN*-48 | **BABAX/LR42//BABAX*2/3/SHAMA/4/TACUPETO F2001*2/BRAMBLING/5/BORL14** |
| 49 | *GEN*-49 | **KACHU*2/3/ND643//2*PRL/2*PASTOR/4/KIDEA** |
| 50 | *GEN*-50 | **BORL14*2/FITIS** |

**Supplementary Figure 1.**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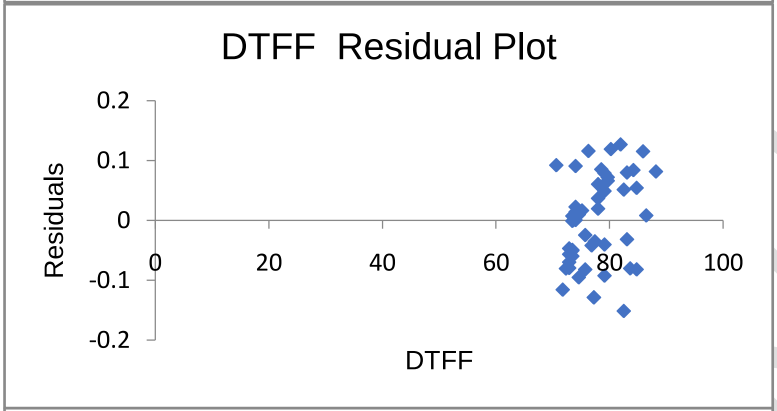
GNP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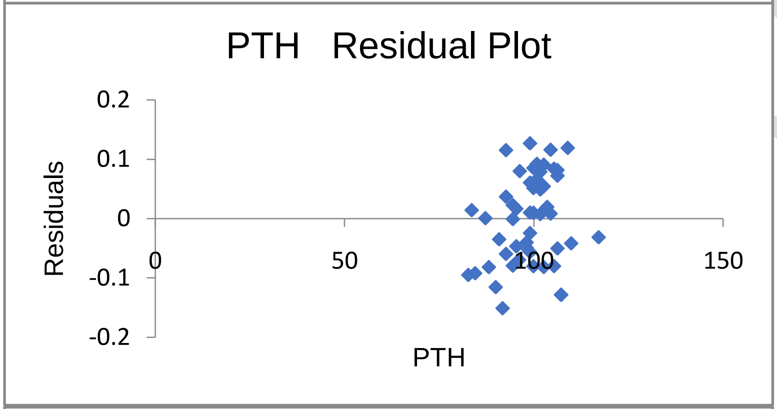
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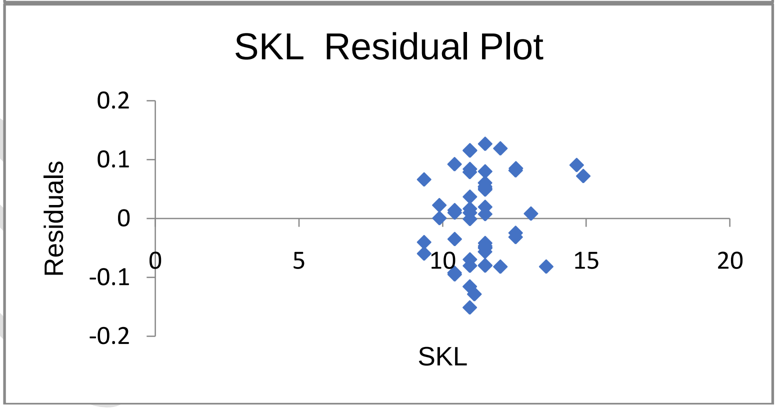
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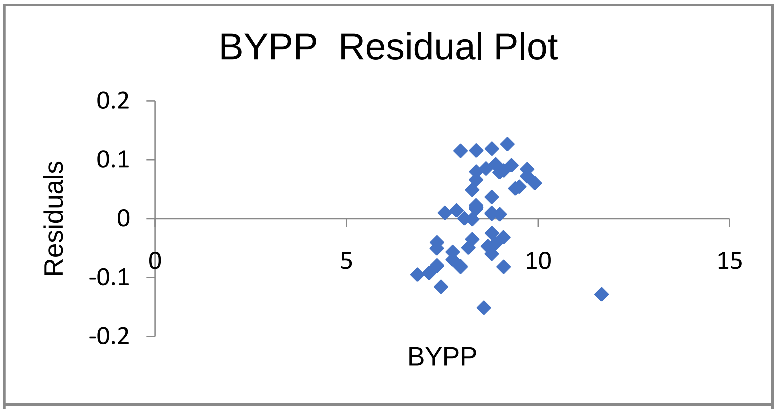
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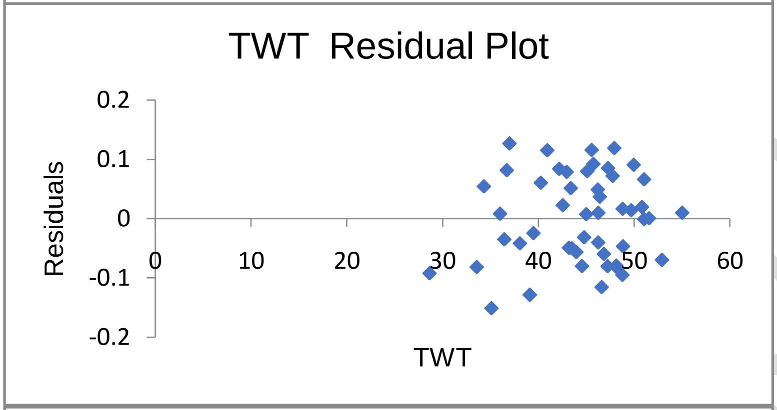
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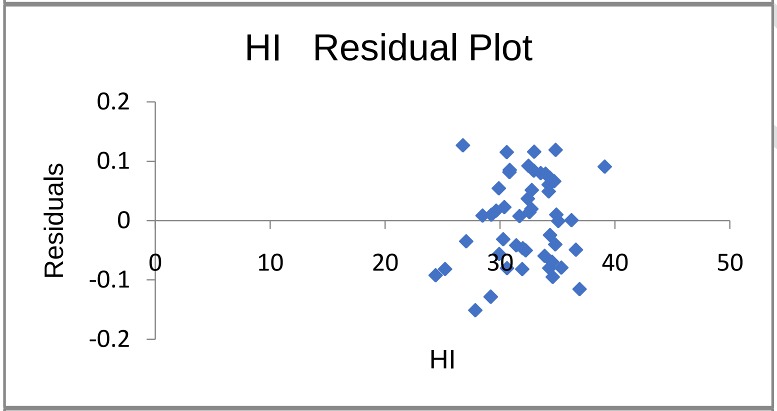
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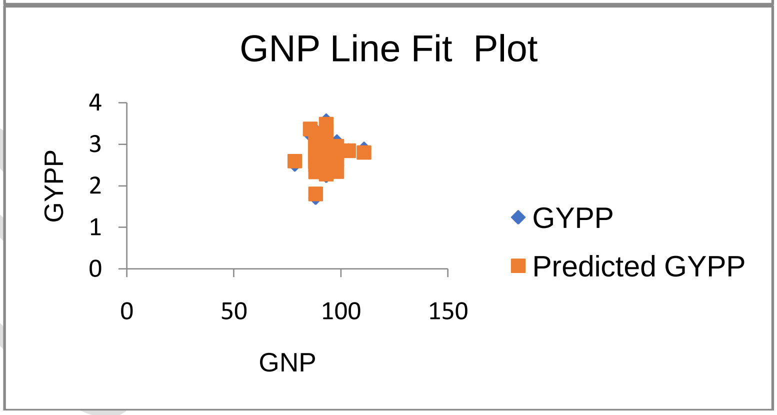
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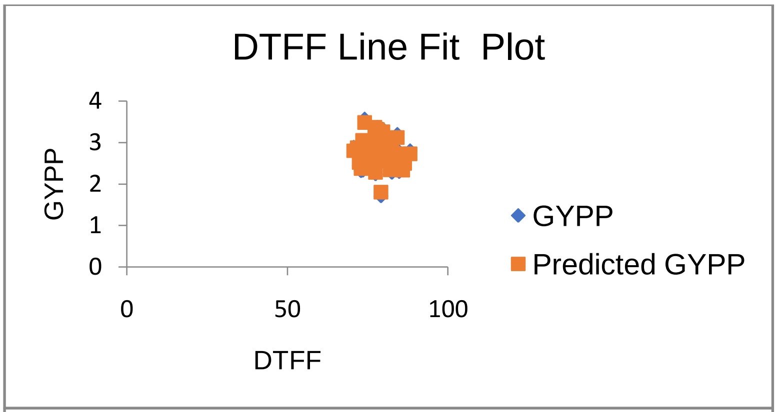
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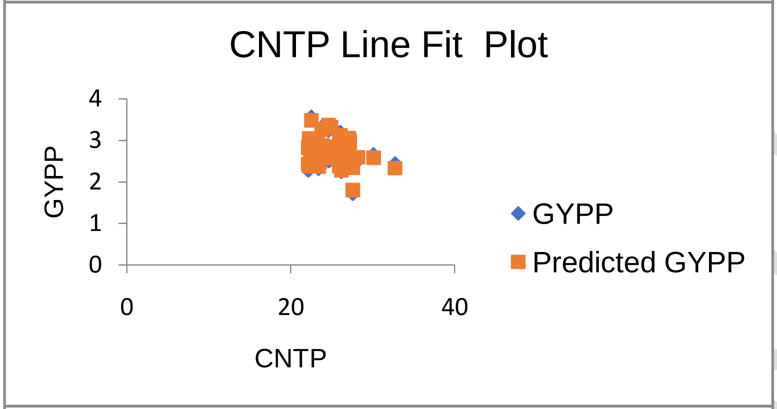
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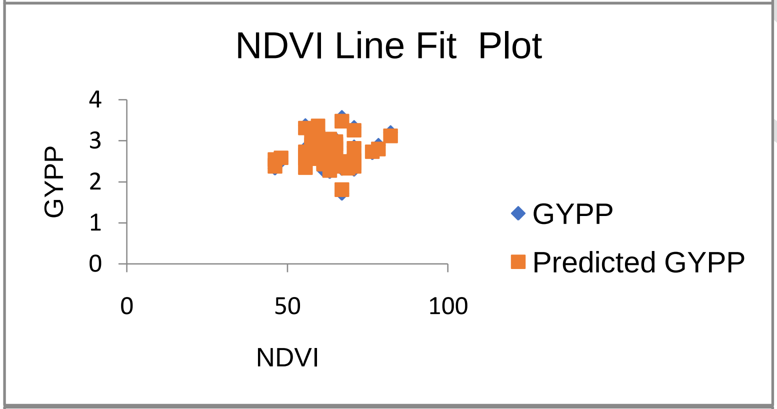
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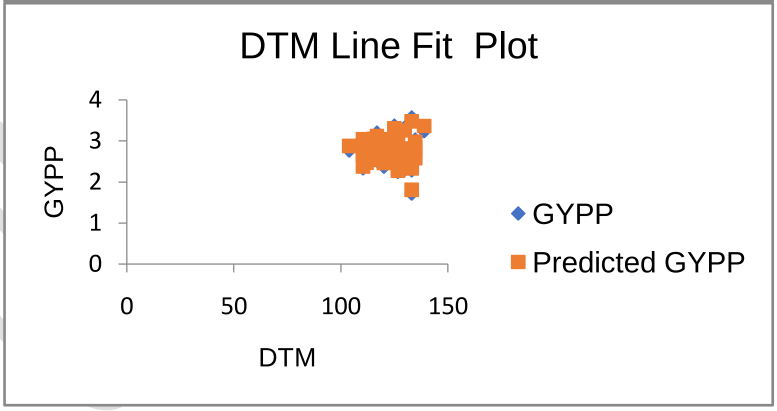
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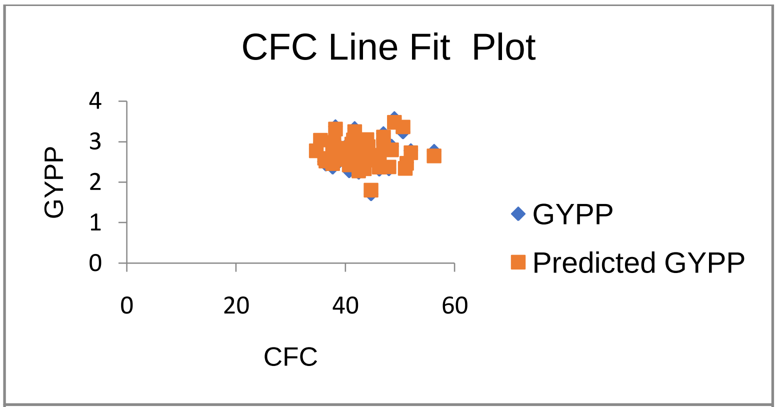
■ Predicted GYPP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GYPP
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CFC
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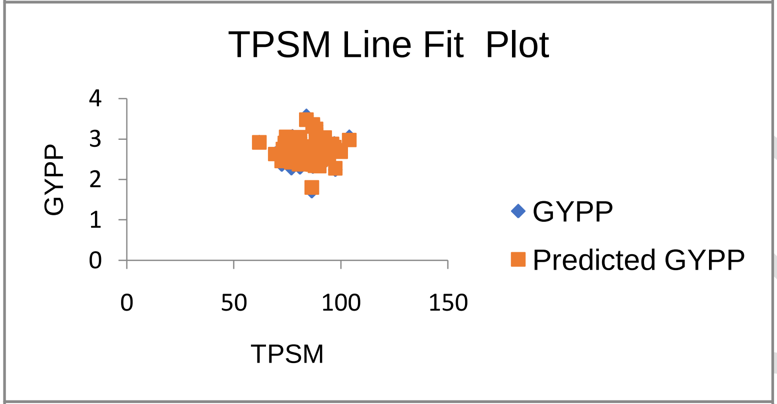
■ Predicted GYPP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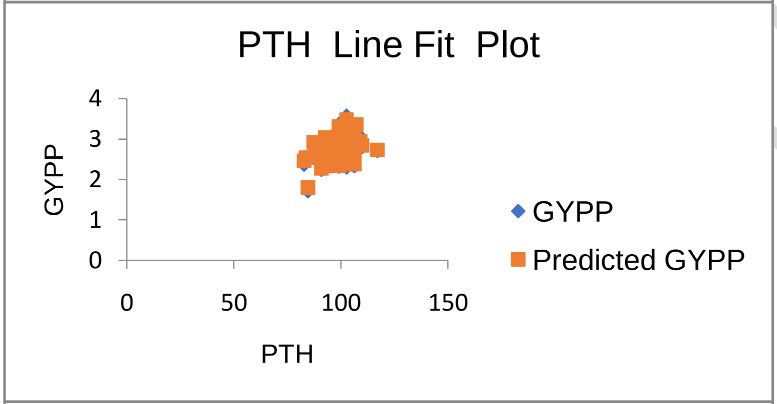
■ Predicted GYPP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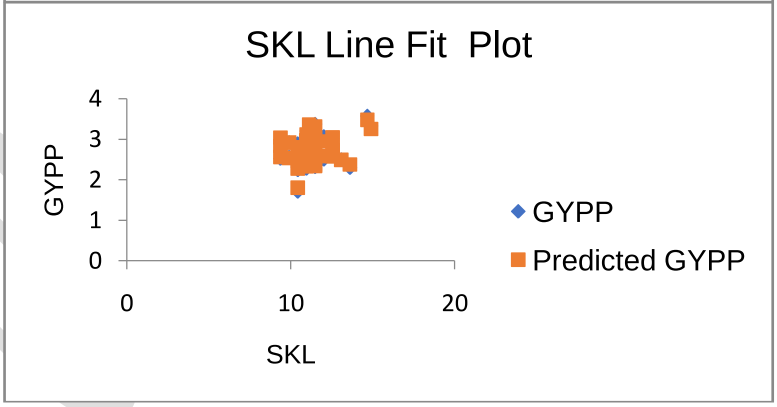
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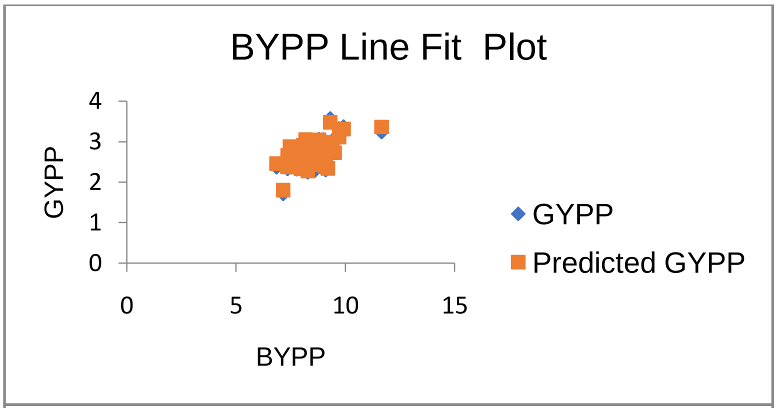
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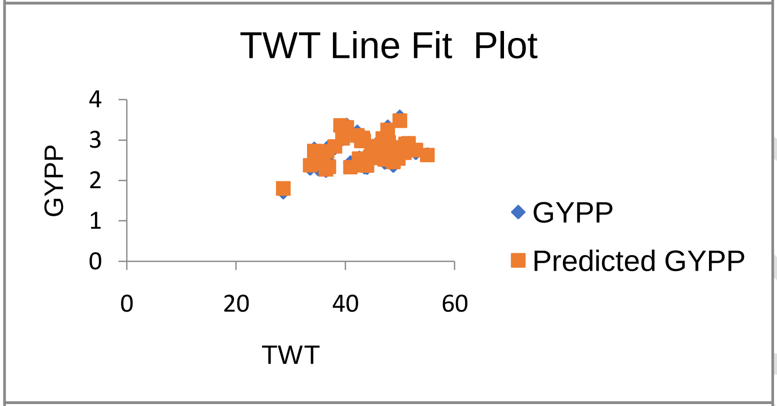
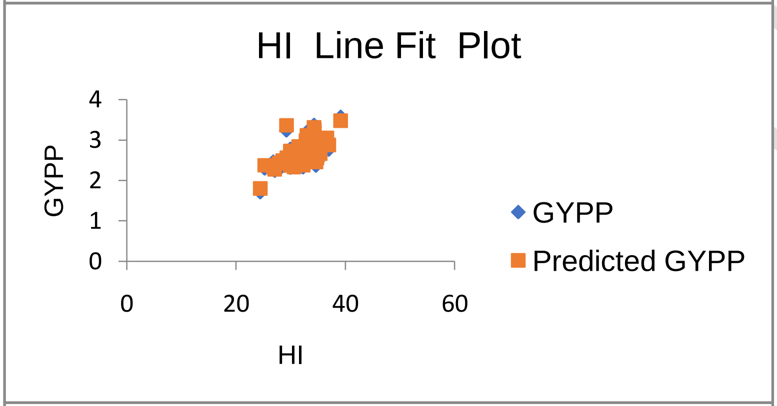
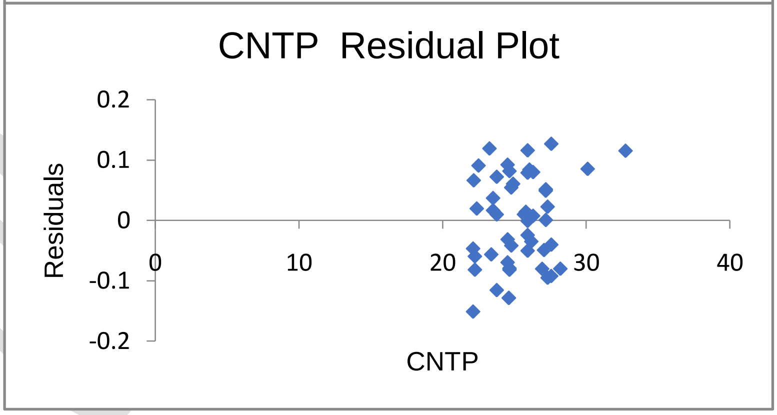
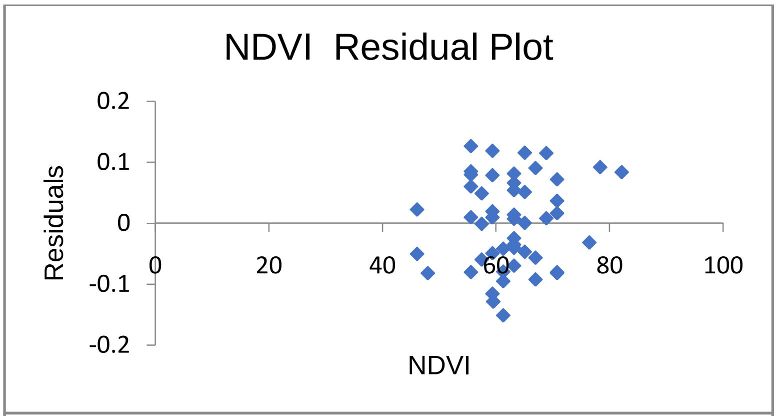
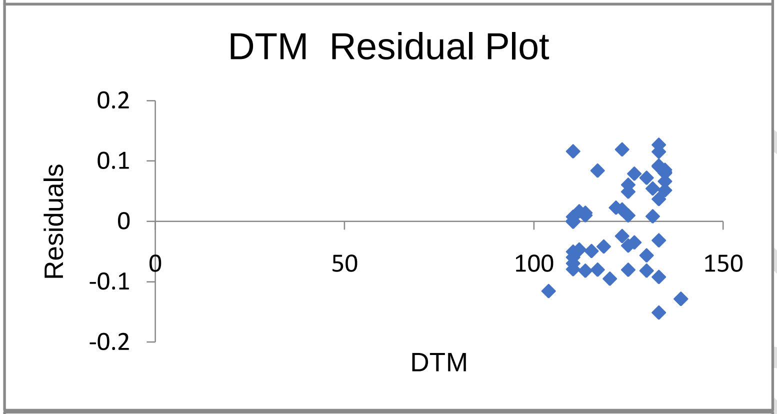
GYPP
Predicted GYPP

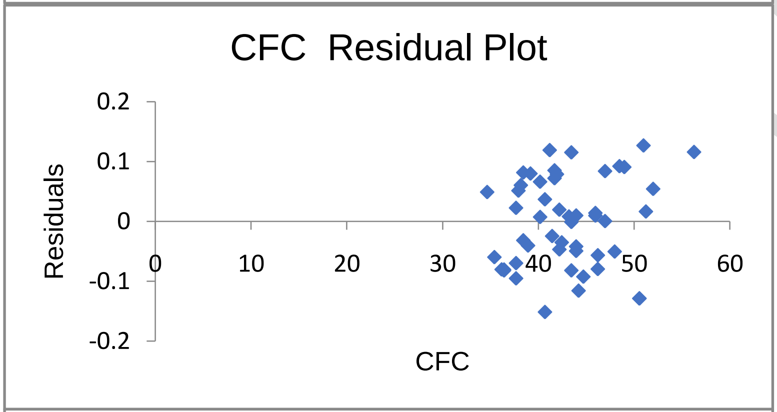

TWT Line Fit Plot
GYPP
4
3
2
1
0
0
20
40
60
TWT
GYPP
Predicted GYPP

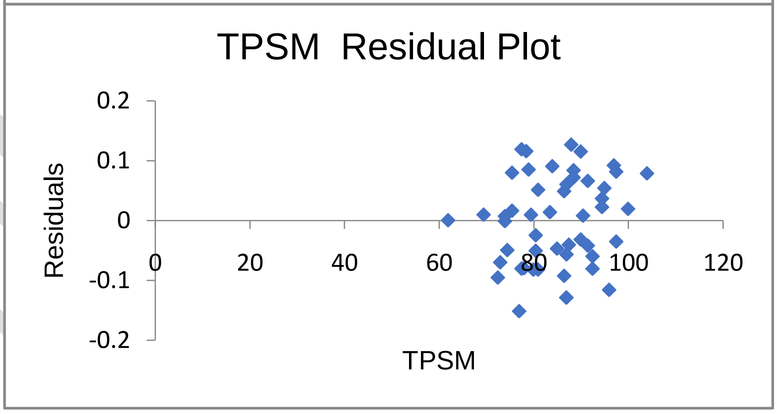

HI Line Fit Plot
GYPP
4
3
2
1
0
0
20
40
60
HI
GYPP
Predicted GYPP

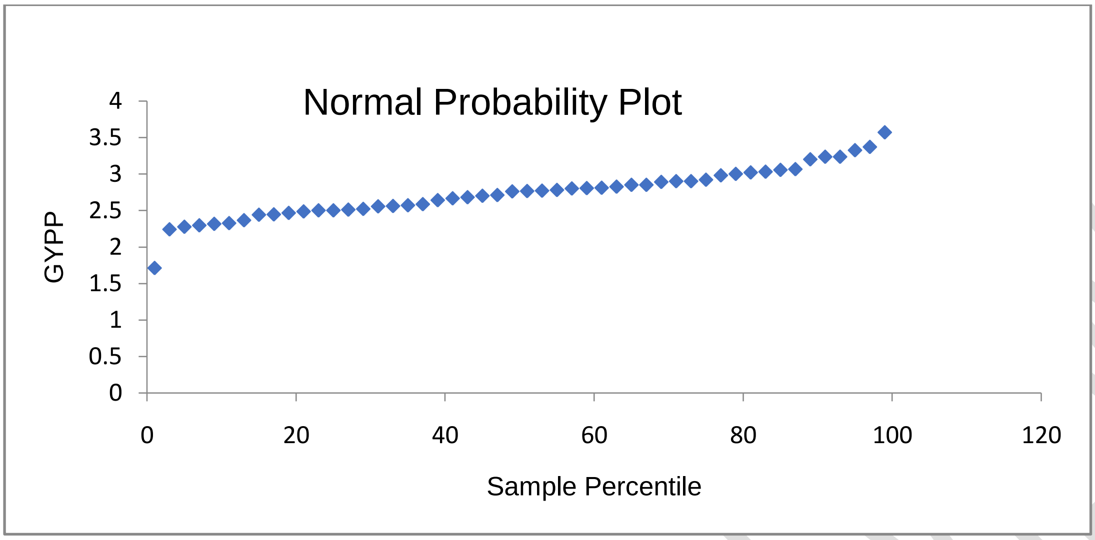

CNTP Residual Plot
Residuals
0.2
0.1
0
-0.1
-0.2
0
10
20
30
40
CNTP


NDVI Residual Plot
Residuals
0.2
0.1
0
-0.1
-0.2
0
20
40
60
80
100
NDVI


DTM Residual Plot
Residuals
0.2
0.1
0
-0.1
-0.2
0
50
100
150
DTM


CFC Residual Plot
Residuals
0.2
0.1
0
-0.1
-0.2
0
10
20
30
40
50
60
CFC


TPSM Residual Plot
Residuals
0.2
0.1
0
-0.1
-0.2
0
20
40
60
80
100
120
TPSM


Normal Probability Plot
GYPP
4
3.5
3
2.5
2
1.5
1
0.5
0
0
20
40
60
80
100
120
Sample Percentile