

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

Abstract

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, in the 2019-20 Rabi season, a research study was conducted at Banaras Hindu University's Agriculture Research Farm, Varanasi, in a randomized complete block design with two replications. 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. Days to 50 % flowering, days to maturity, plant height, canopy temperature showed negligible positive direct effect on grain yield. 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 [26]. 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 categorized based on their ploidy levels, include diploids ($2n = 2x = 14$, AA), tetraploids ($2n = 4x = 28$, BBAA), and hexaploids ($2n = 6x = 42$, BBAADD) [33]. 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 [33]. It is the most widely cultivated crop in the world, cultivated on 217 million ha annually [9]. 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 [10], 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 [31]. 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 [25]. Currently, India is the world largest producer of wheat with a production of 74.25 Mt in an area of 27.2 Mha [11]. Uttar Pradesh is the largest wheat producing state in India, followed by Punjab, Haryana and Madhya Pradesh [2].

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 [6]. 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. Therefore, it is crucial to prioritize the development of high-yielding wheat varieties that can withstand both biotic and abiotic stresses.

However, 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 [18]. 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 [27]. 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 [23]. The path coefficient divides correlation coefficients into direct and indirect effects within the correlation system of traits [16]. 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 [13]. 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:

As wheat is mainly a *Rabi* (winter) season crop in India, 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 *genotypes*. The experiment was carried out using 49 distinct *genotypes* procured from CIMMYT, Mexico, alongside the local reference variety DBW 187. Employing a randomized complete block design (RCBD) 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 also documented on weekly basis.

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. The observations were recorded on 5 plants for each genotype in accordance with established scientific protocols. The GNP was determined in the field by observing the seeds that had successfully sprouted out of the total number of seeds that were planted. DTM, PTH, SKL and TPSM were recorded at maturity in each plot. Three NDVI measurements were recorded from the vegetative stage to dough stages using GreenSeeker (NTech Industries, Inc.). 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. TWT was measured as weight in grams from 1000 wheat grains. At maturity, BYPP and GYPP were measured by harvesting total biomass and by threshing grains from spikes respectively from each experimental plot.

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).

$$r(x_i, x_j) = \frac{Cov(x_i, x_j)}{\sqrt{V(x_i) \cdot V(x_j)}}$$

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:

$$t = \frac{r}{\sqrt{1-r^2}} \times \sqrt{n-2}$$

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

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 GYPP at both genotypic and phenotypic level. Baye et al. [3] 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. [7] and Mecha et al. [21] 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 Bhushan et al. [5] and Mecha et al. [21] 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 [15]. DTFF showed positive nonsignificant correlation with GYPP only at genotypic level. Similar results are also reported by Salama et al. [29]. CNTP showed negative non-significant correlation with GYPP at both genotypic and phenotypic level. Similar relationship is also reported by Bennani et al. [4]. While days to 50 % flowering showed negative non-significant correlation with GYPP only at only at phenotypic level. Hassani et al. [14] 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 Figures 1 and 2 respectively.

3.1.2. Correlation among yield-related traits

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. [20] 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. [17], and El-Dayem et al. [8]. 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 [12]. 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. Nasri et al. [24] also showed similar findings from their research.

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. [1] also reported similar results from their research. HI showed negative significant correlation with DTFF, DTM, TPSM, BYPP, TWT. Singh et al. [32]) 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	-0.0755	0.1028	1.0000	-0.0501	-0.0629	-0.0543	-0.1100	-0.1116	-0.1363	-0.253*	-0.0402	-0.0833	-0.1639
NDVI	0.1859	0.1257	-0.0570	1.0000	0.0680	0.0966	0.0800	0.1097	0.199*	0.0527	0.0175	-0.0567	0.1092
DTM	-0.0189	0.391**	-0.0692	0.1270	1.0000	0.0863	0.244*	0.260*	0.0802	0.461**	-0.468**	-0.373**	0.0489
CFC	0.1254	-0.1188	-0.0536	0.1433	0.1185	1.0000	-0.1287	0.1084	0.0611	0.261*	-0.208*	-0.1442	0.1070
TPSM	-0.0245	0.262*	-0.1142	0.1146	0.266*	-0.0809	1.0000	0.0955	-0.0158	0.251*	-0.273*	-0.215*	0.0619
PTH	-0.0245	0.246*	-0.1441	0.0960	0.256*	0.1069	0.1473	1.0000	0.256*	0.421**	-0.0915	0.0143	0.307*
SKL	0.0420	0.199*	-0.1635	0.1889	0.0989	0.0330	-0.0099	0.266*	1.0000	0.1155	0.0552	0.1235	0.304*
BYPP	-0.0577	0.243*	-0.245*	0.0886	0.457**	0.256*	0.273*	0.408**	0.1319	1.0000	-0.363**	-0.221*	0.430**
TWT	0.1203	-0.397**	0.0169	-0.0091	-0.469**	-0.214*	-0.297*	-0.1593	-0.0327	-0.378**	1.0000	0.574**	0.255*
HI	-0.0323	-0.301*	-0.0111	-0.1003	-0.379**	-0.1482	-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).

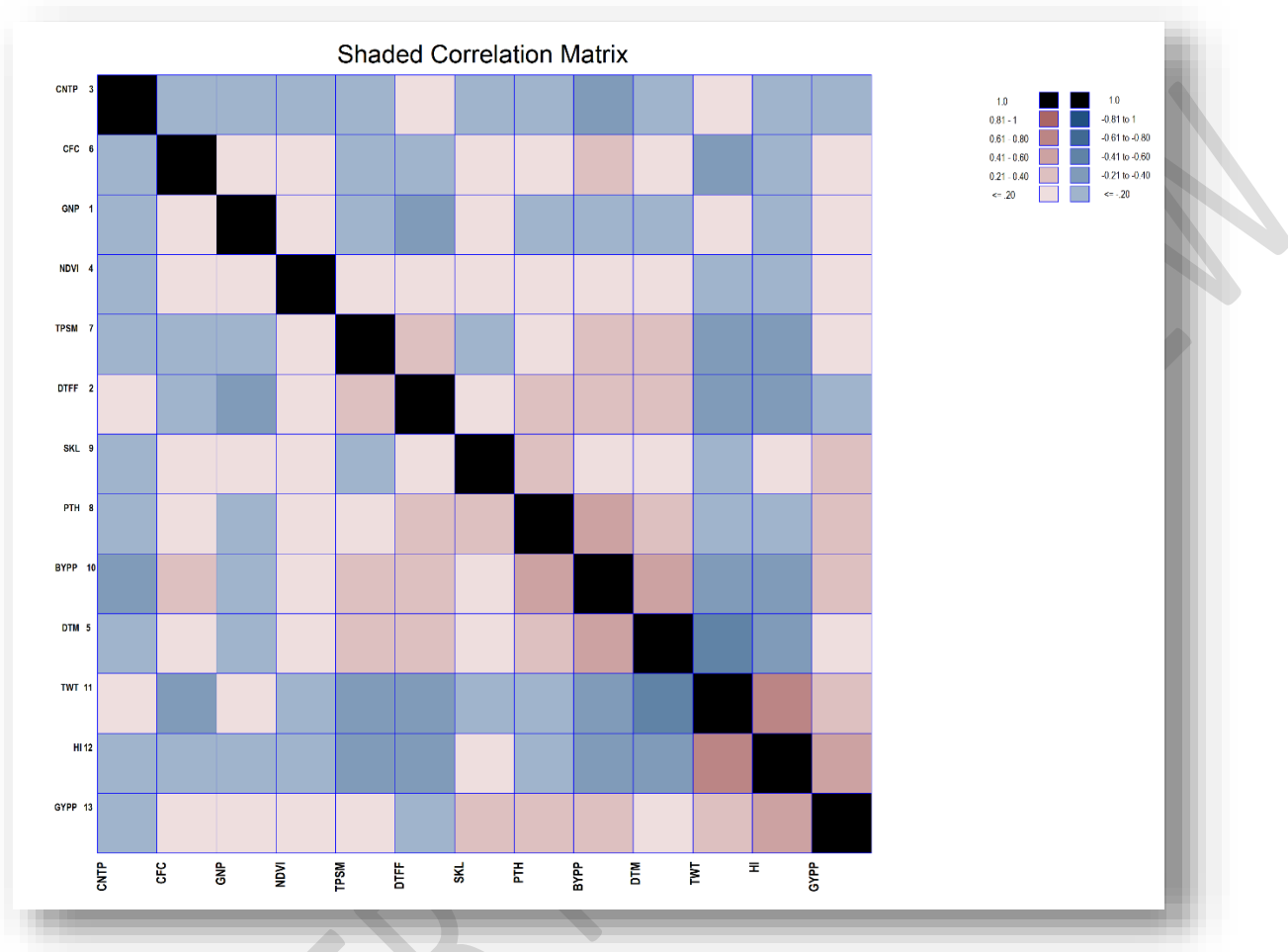


Figure 1: Phenotypic shaded correlation matrix of 13 characters of bread wheat

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

Path coefficient analysis

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 at 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. [34] 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. [22] 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. The results agree with earlier studies in bread wheat [19, 30]

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 [3, 7, 28]

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	DFFF	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
DFFF	-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

UNDER PEER REVIEW

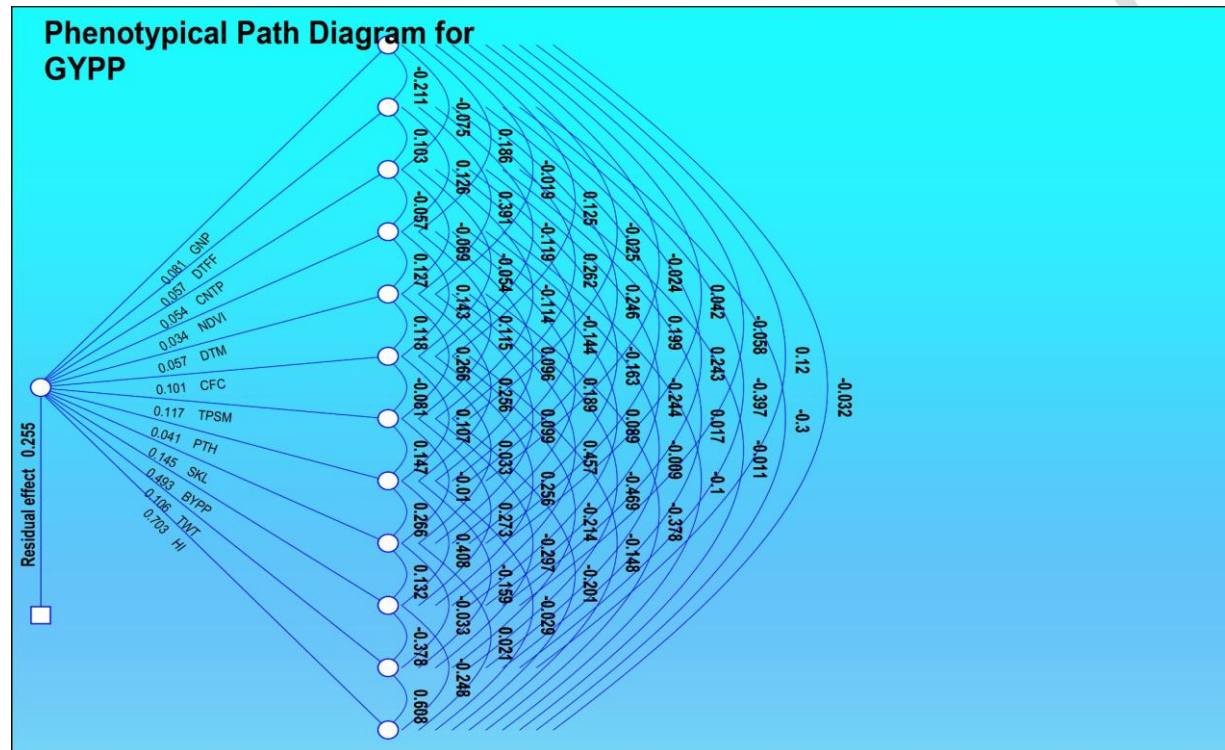


Figure 3: Phenotypic path coefficient analysis of 13 characters of bread wheat

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	DFFF	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
DFFF	-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

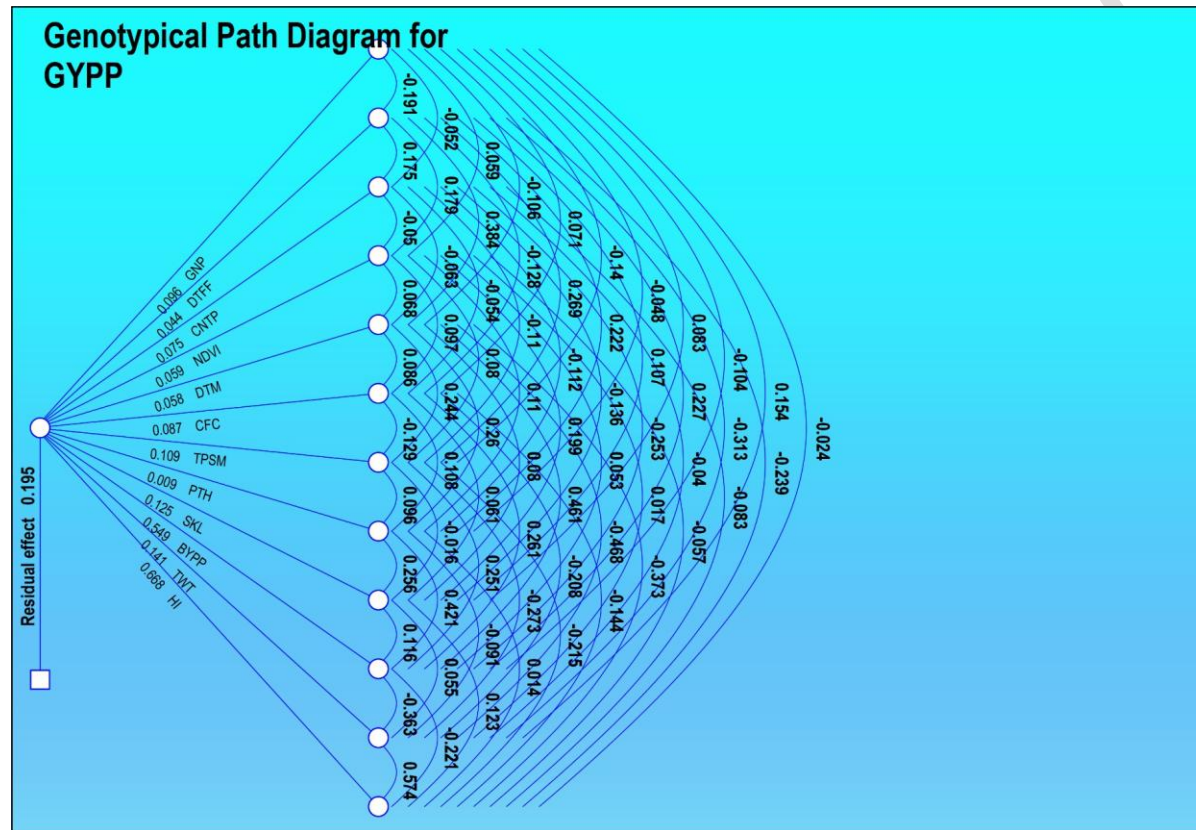


Figure 4: Genotypic path coefficient analysis of 13 characters of bread wheat

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 indicated the importance of considering few more component traits to improve grain yield.

References

- 1) Azimi, A. M., Marker, S., & Bhattacharjee, I. (2017). Genotypic and phenotypic variability and correlation analysis for yield and its components in late sown wheat (*Triticum aestivum* L.). *Journal of Pharmacognosy and Phytochemistry*, 6(4), 167-173.
- 2) Balaganesh, G., Makarabbi, G., and Sendhil, R. (2019). Tracking the performance of wheat production in Uttar Pradesh. *Indian Journal of Economics and Development*, 15(2): 216-224.
- 3) Baye, A., Berihun, B., Bantayehu, M., & Derebe, B. (2020). Genotypic and phenotypic correlation and path coefficient analysis for yield and yield-related traits in advanced bread wheat (*Triticum aestivum* L.) lines. *Cogent Food & Agriculture*, 6(1), 1752603.
- 4) Bennani, S., Nsarellah, N., Birouk, A., Ouabbou, H., & Tadesse, W. (2016). Effective selection criteria for screening drought tolerant and high yielding bread wheat genotypes. *Universal Journal of Agricultural Research*, 4(4), 134-142.
- 5) Bhushan, B., Bharti, S., Ojha, A., Pandey, M., Gourav, S. S., Tyagi, B. S., & Singh, G. (2013). Genetic variability, correlation coefficient and path analysis of some quantitative traits in bread wheat. *Journal of Wheat Research*, 5(1), 21-26.

- 6) Dixon, J., Braun, H. J., & Crouch, J. (2009). Overview: transitioning wheat research to serve the future needs of the developing world. *Wheat facts and futures*, 23(1).
- 7) Dutamo, D., Alamerew, S., Eticha, F., & Assefa, E. (2015). Path coefficient and correlation studies of yield and yield associated traits in bread wheat (*Triticum aestivum* L.) germplasm. *World Applied Sciences Journal*, 33(11), 1732-1739.
- 8) El-Dayem, A., EL-Gohary, Y. A., & Ibrahim, H. E. (2021). Path-coefficient analysis and correlation studies on grain yield and its components of some bread wheat genotypes under three irrigation treatments. *Journal of Plant Production*, 12(2), 115-123.
- 9) Erenstein, O., Jaleta, M., Mottaleb, K. A., Sonder, K., Donovan, J., & Braun, H. J. (2022). Global trends in wheat production, consumption and trade. In *Wheat improvement: food security in a changing climate* (pp. 47-66). Cham: Springer International Publishing.
- 10) FAO. (2021). FAOSTAT: Crops. Food and Agriculture Organization of the United Nations. Retrieved from <http://www.fao.org/faostat/en/#data/QC>
- 11) Food and Agriculture Organization of the United Nations. FAOSTAT Statistical Database; FAO: Rome, Italy, 2022; Available online: <https://www.fao.org/faostat/en/#home> (GENessed on 1 January 2022).
- 12) Gupta, V., Kumar, M., Singh, V., Chaudhary, L., Yashveer, S., Sheoran, R., ... & Nagpal, S. (2022). Genotype by environment interaction analysis for grain yield of wheat (*Triticum aestivum* (L.) em. Thell) genotypes. *Agriculture*, 12(7), 1002.
- 13) Hadi. B.H, AL-Maliky R.J.M, Zaid.M.A. and Hassan.W.A. (2018). Estimation of some genetic parameters in bread wheat *Triticum aestivum* L. for WASIT and DIWANIYYA locations. *Euphrates Journal of Agriculture Science*-10(1), 194-203
- 14) HASSANI, I., NIMBAL, S., SINGH, V., & NOORI, A. (2022). Genetic Variability Analysis and Correlation Studies of Bread Wheat (*Triticum aestivum* L.) Genotypes. *Ekin Journal of Crop Breeding and Genetics*, 8(2), 139-145.
- 15) Javed, A., Ahmad, N., Ahmed, J., Hameed, A., Ashraf, M. A., Zafar, S. A., ... & Ali, E. F. (2022). Grain yield, chlorophyll and protein contents of elite wheat genotypes under drought stress. *Journal of King Saud University-Science*, 34(7), 102279.
- 16) Khare, V. (2022). Multivariate analysis and role of direct–indirect effect for yield and its component traits in bread wheat (*Triticum aestivum* L.). *Electronic Journal of Plant Breeding*, 13(2), 447-454.
- 17) Kumar, B., Singh, C. M., & Jaiswal, K. K. (2013). Genetic variability, association and diversity studies in bread wheat (*Triticum aestivum* L.). *The*

Bioscan, 8(1), 143-147.

- 18) Kumar, D., Rana, V., Rana, A., & Guleria, P. (2023). Genetic variability, correlation and path analysis studies for grain yield and morpho-physiological traits under moisture-stress conditions in bread wheat (*Triticum aestivum* L.) under north-western Himalayan conditions. *Journal of Cereal Research* 15 (1): 92-102. <http://doi.org/10.25174/2582-2675/2023,124000>.
- 19) Lamara, A., Fellahi, Z. E. A., Hannachi, A., & Benniou, R. (2022). Assessing the phenotypic variation, heritability and genetic advance in bread wheat (*Triticum aestivum* L.) candidate lines grown under rainfed semi-arid region of Algeria. *Revista Facultad Nacional de Agronomía Medellín*, 75(3), 10107-10118.
- 20) Maurya, A. K., Yadav, R. K., Singh, A. K., Deep, A., & Yadav, V. (2020). Studies on correlation and path coefficients analysis in bread wheat (*Triticum aestivum* L.). *Journal of Pharmacognosy and Phytochemistry*, 9(4), 524-527.
- 21) Mecha, B., Alamerew, S., Assefa, A., Dutamo, D., & Assefa, E. (2017). Correlation and path coefficient studies of yield and yield associated traits in bread wheat (*Triticum aestivum* L.) genotypes. *Adv Plants Agric Res*, 6(5), 128-136.
- 22) Mohanty, S., Mukherjee, S., Mukhopadhyaya, S. K., & Dash, A. P. (2016). Genetic variability, correlation and path analysis of bread wheat (*Triticum aestivum* L.) genotypes under terminal heat stress. *International Journal of Bio-resource and Stress Management*, 7(6), 1232-1238.
- 23) Moosavi, S. S., Kian Ersi, F., & Abdollahi, M. R. (2013). Application of multivariate statistical methods in detection of effective traits on bread wheat (*Triticum aestivum* L.) yield under moisture stress condition. *Cereal Research*, 3(2), 119-130.
- 24) Nasri, R., Kashani, A., Paknejad, F., Vazan, S., & Barary, M. (2014). Correlation, path analysis and stepwise regression in yield and yield component in wheat (*Triticum aestivum* L.) under the temperate climate of Ilam province, Iran. *Indian Journal of Fundamental and Applied Life Sciences*, 4(4), 188-198.
- 25) Naveen, A., Mishra, V. K., Sinha, B., Harika, A. S., Supriya, P., & Reddy, M. B. (2023). Enumeration of Genetic Parameters and Genetic Diversity of Morpho-Physiological Traits in CIMMYT Bread Wheat GENessions [*Triticum aestivum* (L.) em. Thell]. *Int. J. Environ. Clim. Change*, 13(10), 629-637.
- 26) Pingali, P. (2015). Agricultural policy and nutrition outcomes—getting beyond the preoccupation with staple grains. *Food security*, 7, 583-591.

- 27) Rajput, R. S. (2018). Correlation, path analysis, heritability, and genetic advance for morpho-physiological character on bread wheat (*Triticum aestivum* L.). *Journal of Pharmacognosy and phytochemistry*, 7(2), 107-112.
- 28) Sabit, Z., Yadav, B., & Rai, P. K. (2017). Genetic variability, correlation and path analysis for yield and its components in f5 generation of bread wheat (*Triticum aestivum* L.). *Journal of Pharmacognosy and Phytochemistry*, 6(4), 680-687.
- 29) Salama, Y. E., & Saad, K. I. (2022). Evaluation of Genetic Variability of Bread Wheat Genotypes under Normal Irrigation and Water Stress Conditions Using Multivariate Analysis. *Journal of Plant Production*, 13(11), 833-838.
- 30) Shamuyarira, K. W., Shimelis, H., Figlan, S., & Chaplot, V. (2022). Path coefficient and principal component analyses for biomass allocation, drought tolerance and carbon sequestration potential in wheat. *Plants*, 11(11), 1407.
- 31) Shiferaw, B., Smale, M., Braun, H. J., Duveiller, E., Reynolds, M., & Muricho, G. (2013). Crops that feed the world 10. Past successes and future challenges to the role played by wheat in global food security. *Food Security*, 5, 291-317.
- 32) Singh, A. K., Singh, S. B., Singh, A. P., & Sharma, A. K. (2012). Genetic variability, character association and path analysis for seed yield and its component characters in wheat (*Triticum aestivum* L) under rainfed environment. *Indian Journal of Agricultural Research*, 46(1), 48-53.
- 33) Tadesse, W., Sanchez-Garcia, M., Assefa, S. G., Amri, A., Bishaw, Z., Ogonnaya, F. C., & Baum, M. (2019). Genetic gains in wheat breeding and its role in feeding the world. *Crop Breeding, Genetics and Genomics*, 1(1).
- 34) Verma, S. P., Pathak, V. N., & Verma, O. P. (2019). Interrelationship between yield and its contributing traits in wheat (*Triticum aestivum* L.). *International Journal of Current Microbiology and Applied Sciences*, 8(2), 3209-3215.

Supplementary Table 1: Genotypes procured from CIMMYT and their codes

S.no	Genotype (GEN)	Name
1	<i>GEN-1</i>	DBW 187
2	<i>GEN-2</i>	NADI #2
3	<i>GEN-3</i>	QUAIU #1/SUP152

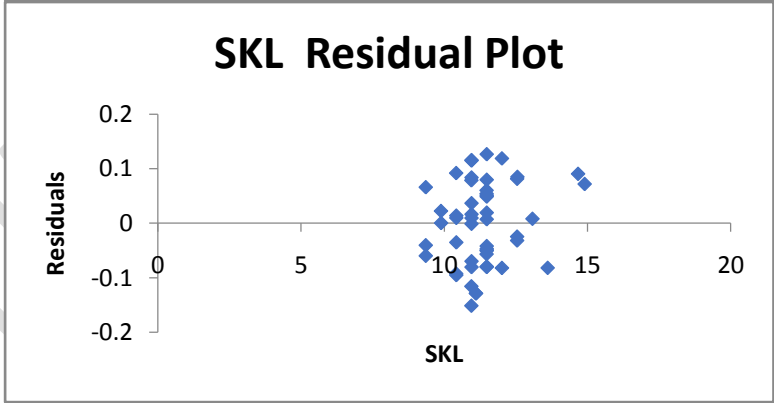
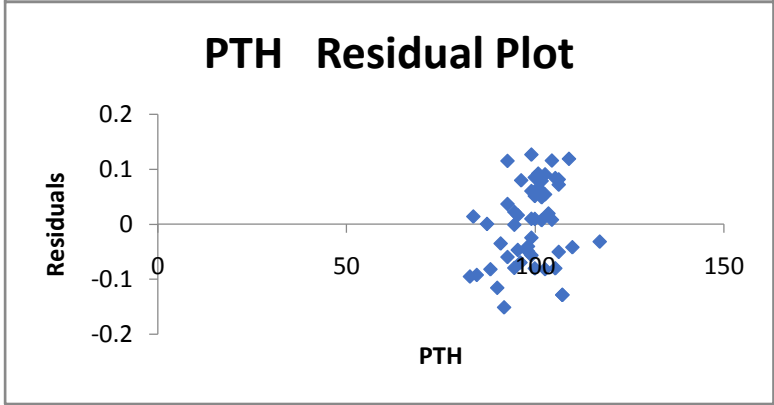
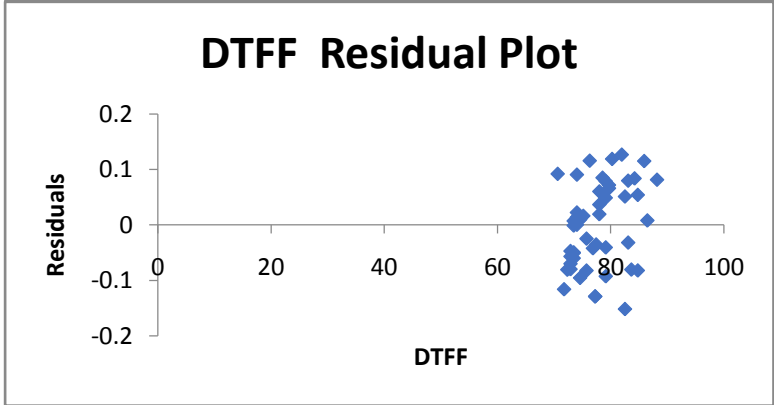
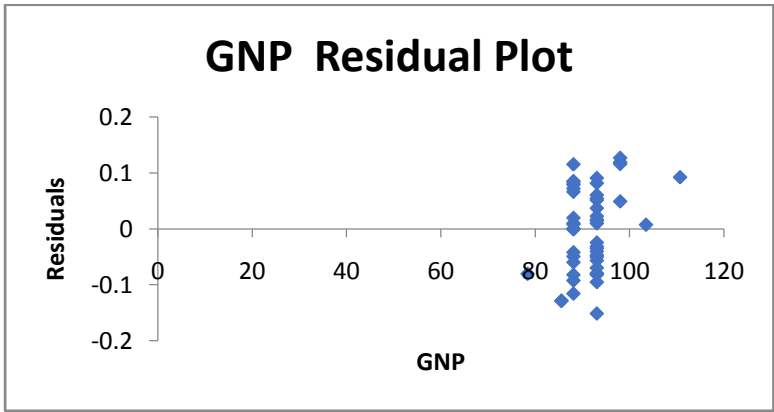
4	GEN-4	WBLL1*2/BRAMBLING/4/BABAX/LR42//BABAX*2/3/SHAMA*2/5/PBW343*2/KUKUNA*2//FRTL/PIFED
5	GEN-5	KACHU #1/KIRITATI//KACHU/3/BECARD/FRNCLN
6	GEN-6	BABAX/LR42//BABAX*2/3/KUKUNA/4/BACEU #1/5/BECARD/6/KACHU/KINDE
7	GEN-7	BABAX/LR42//BABAX/3/ER2000/4/KACHU #1/KIRITATI//KACHU
8	GEN-8	KACHU*2/SUP152
9	GEN-9	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/ATTLA/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//ATILIA*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//ATILIA/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

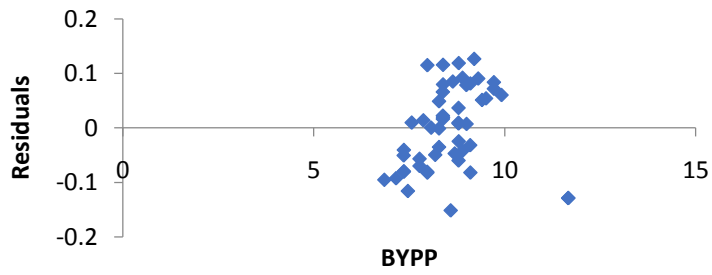
43	GEN-43	MUU/FRNCLN//FRANCOLIN #1/3/BORL14
44	GEN-44	WBLL1*2/BRAMBLING*2//BAVIS/3/KACHU #1/KIRITATI//KACHU
45	GEN-45	WBLL1*2/BRAMBLING*2//BAVIS/3/KFA/2*KACHU
46	GEN-46	KENYA SUNBIRD/2*KACHU/3/WBLL1*2/BRAMBLING*2//BAVIS
47	GEN-47	SUNCO.6/FRAME//PASTOR/3/NAVJ07/4/1447/PASTOR//KRICHAUFF/5/BORL14
48	GEN-48	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.

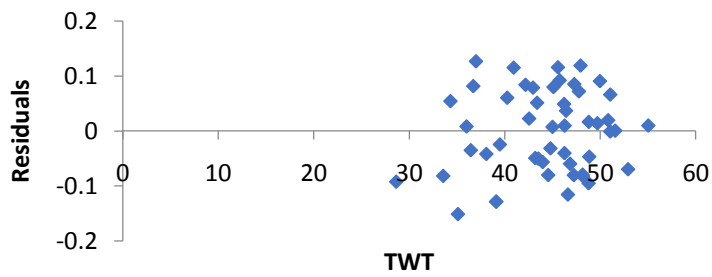
UNDER PEER REVIEW



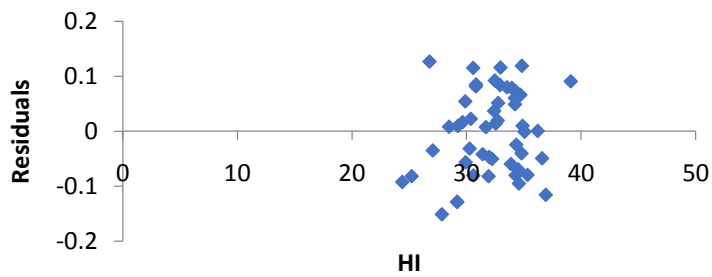
BYPP Residual Plot



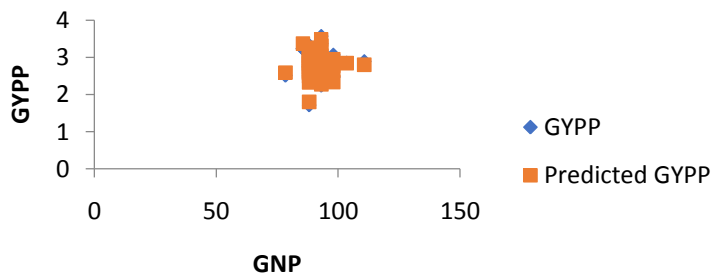
TWT Residual Plot

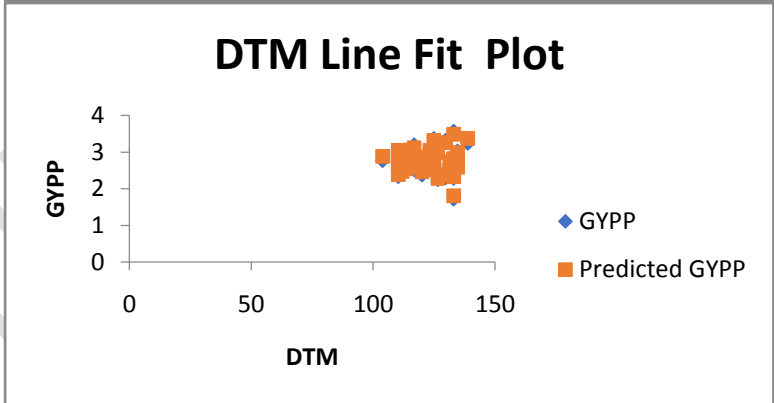
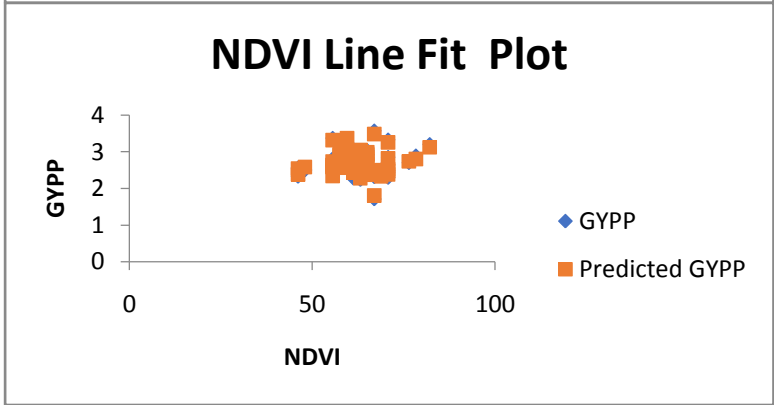
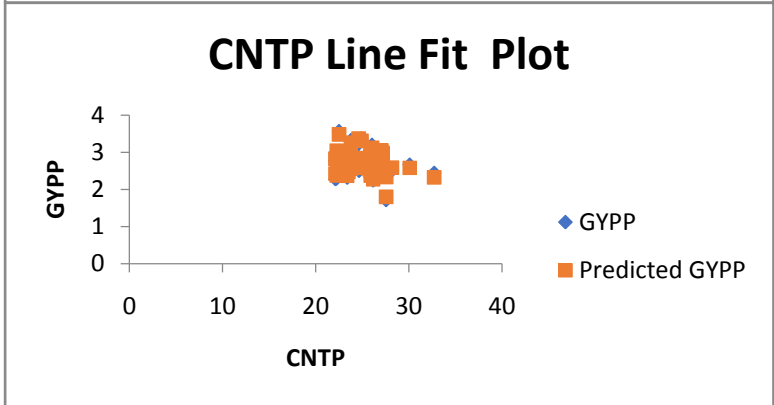
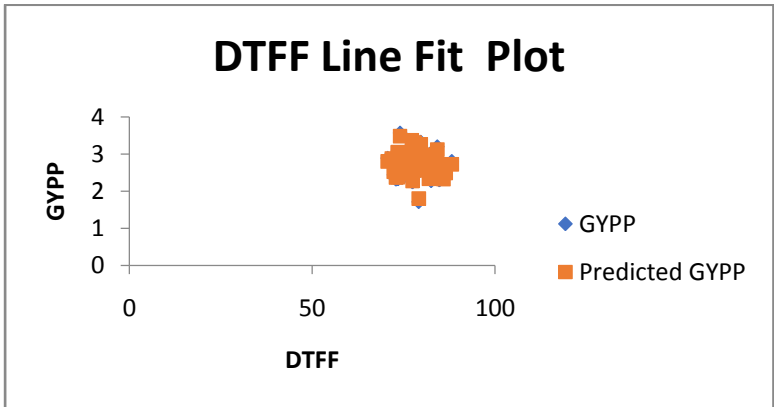


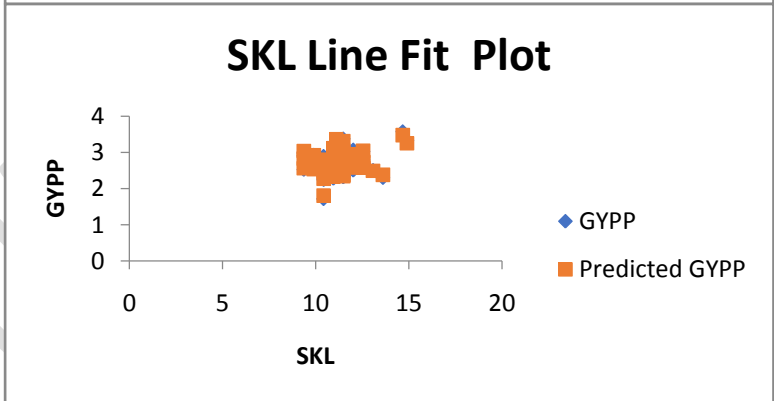
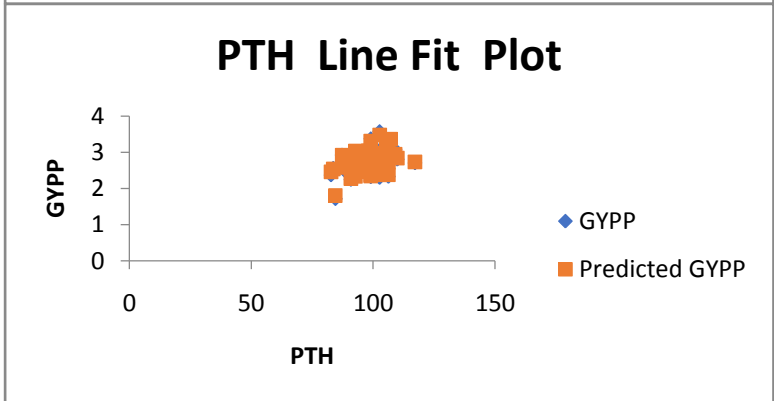
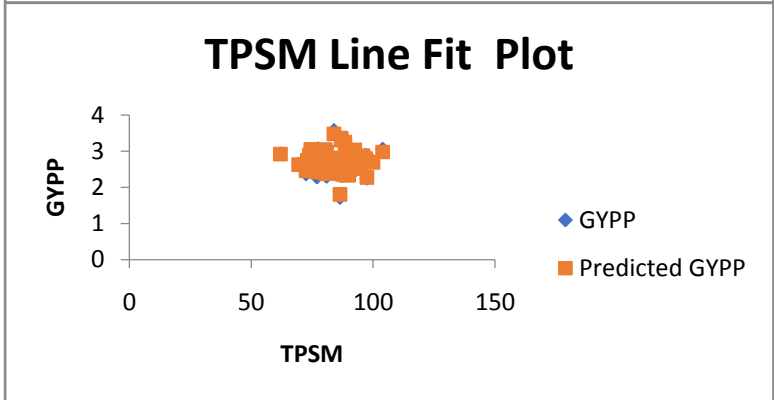
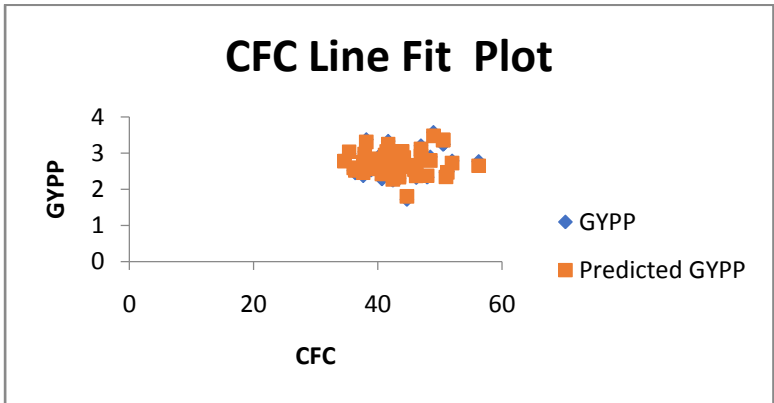
HI Residual Plot

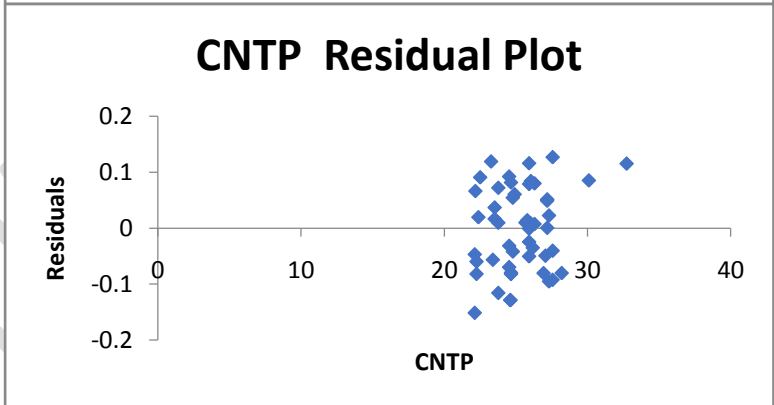
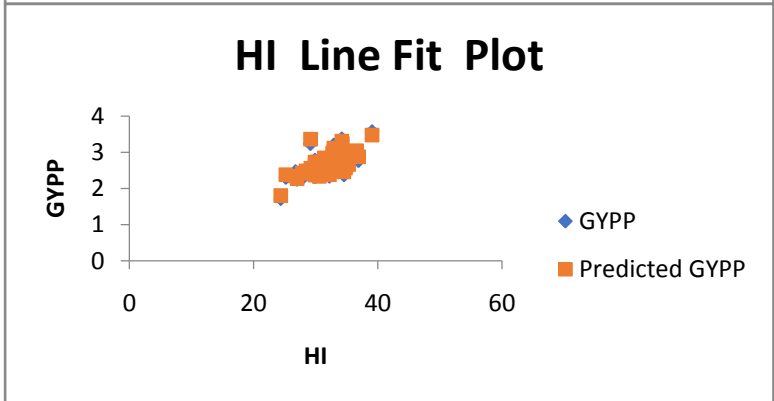
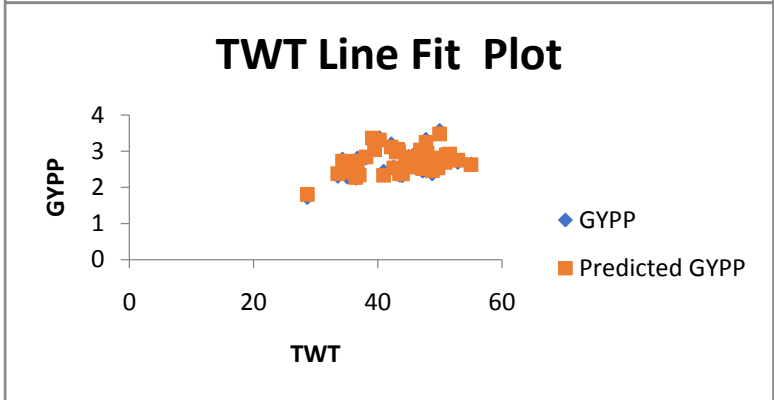
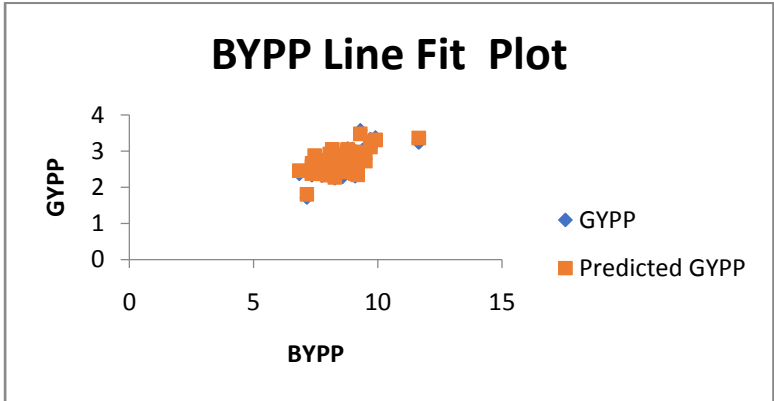


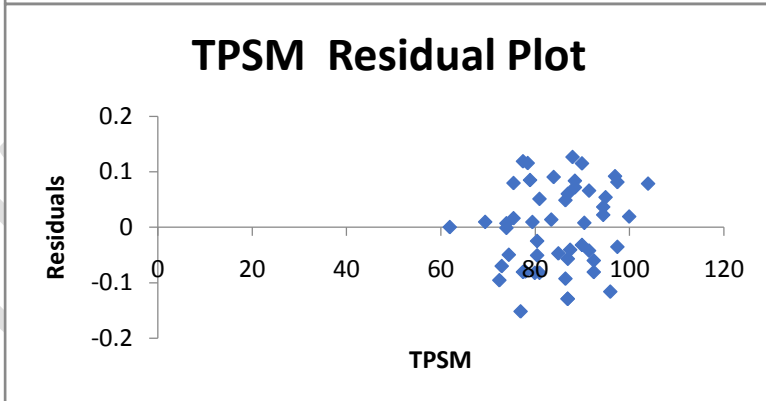
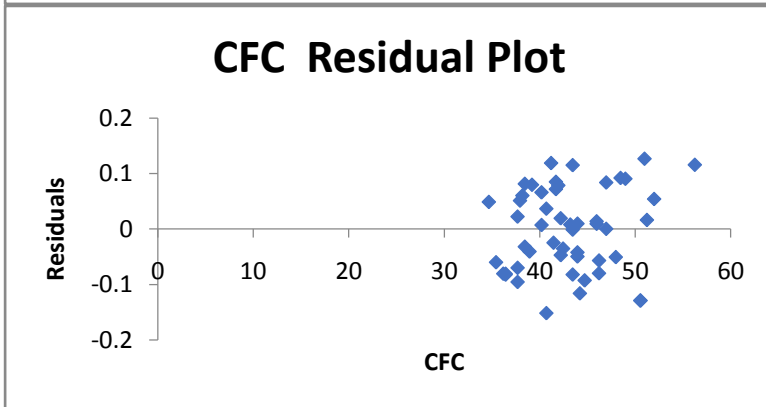
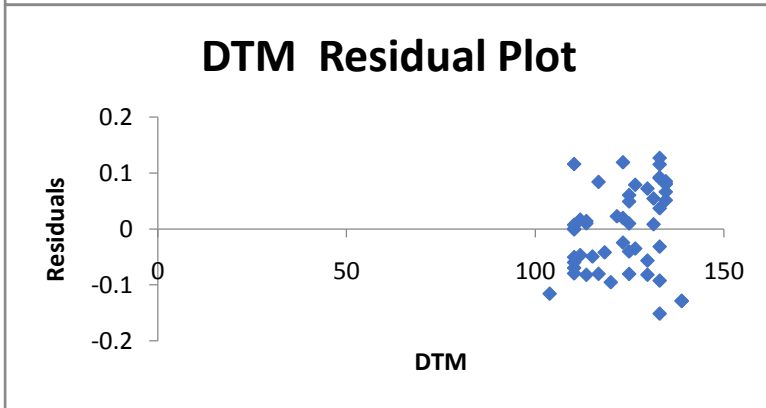
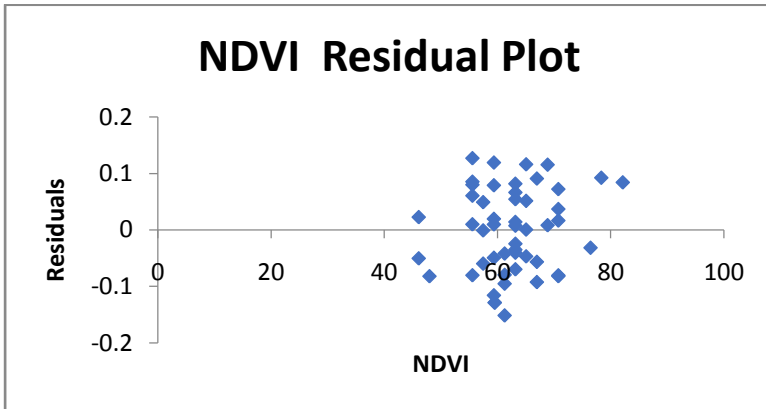
GNP Line Fit Plot



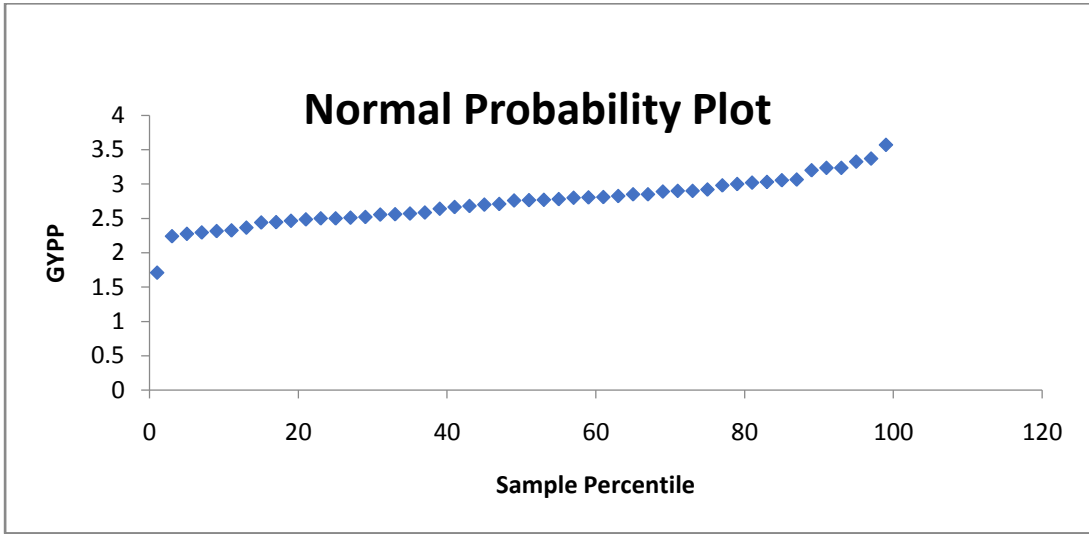








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