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Correlation and Path Coefficient Analysis of Yield, Morpho-Physiological and Quality Traits in Wheat (Triticum aestivum L.) Genotypes

Gaddam Tarun[1],Dr Krishan Pal[1*], Dr R P Saharan[2]
[1]Ph.D. Scholar, Department of Genetics and Plant Breeding, Guru Kashi University, Talwandi Sabo, Punjab, India
[1*]Head & Associate Professor, Department ofGenetics and Plant Breeding, Guru Kashi University, Talwandi Sabo, Punjab, India
[2]Dean, Faculty of Agriculture, Guru Kashi University, Talwandi Sabo, Punjab, India

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Abstract:

Problem: Understanding the intricate interactions between yield, morphophysiological, and quality variables is critical for developing effective selection techniques in wheat (Triticum aestivum L.) breeding. **Approach**: This two-year study (2023-2025) investigated these connections by evaluating 43 different wheat genotypes in ideal (Talwandi Sabo, 2023-24) and late-sown heat stress (Ongole, 2024-25) field conditions, with quality attributes assessed through laboratory analysis. Correlation coefficient analysis and path analysis were used to assess the nature and magnitude of relationships, as well as the direct and indirect contributions to grain yield and quality. **Findings**: All of the investigated traits showed significant genotypic variance. Under ideal conditions, grain yield per plot had a high positive genotypic correlation with biological yield per plot (rg =0.833**) and test weight (rg =0.213**), with biological yield per plot having a very substantial positive direct effect (1.3183) on grain yield. In contrast, days to maturity exhibited a high negative genotypic connection with yield (rg = -0.523**). Under heat stress, grain yield per plot was strongly and positively correlated with the number of grains per spike (rg =0.802**), grain weight per spike (rg =0.803**), and grain yield per plant (rg =0.733**); path analysis revealed that grain weight per spike had the largest positive direct effect (2.5916) on yield under these conditions. Protein content had a limited direct link with grain yield but was impacted by other morpho-physiological variables. Seedling dry weight, a measure of early vigor, had a substantial positive relationship with eventual plant biomass. **Conclusion**: These findings demonstrate that qualities such as biological yield and test weight are important for selection under ideal conditions, but spike components (grains per spike, grain weight per spike) and effective heat escape mechanisms (e.g., improved phenology) are vital under heat stress. Path analysis successfully identified features having the greatest direct influence on production.

Keywords: Wheat, Correlation, Path Coefficient Analysis, Grain Yield, Morpho-physiological Traits, Quality Traits, Heat Stress, Selection Criteria.

1. Introduction:

Wheat (Triticum aestivum L.) is the world's most important cereal crop, providing the dietary foundation for a large section of the worldwide population and accounting for over 20% of total dietary calories and proteins. Wheat output in India is consistently among the greatest in the world, highlighting its importance in national food security and the agricultural economy. The fundamental goal of wheat breeding efforts around the world is to increase grain production and improve quality features in order to meet the needs of a growing population and a wide range of end uses. Grain yield in wheat, like in other cereals, is a quantitatively inherited complex trait that is heavily impacted by various interconnected morpho-physiological and yield component factors, as well as environmental changes (Liu et al., 2025). Direct selection for yield can be difficult because to these complicated relationships and the comparatively low heredity of yield itself under certain situations. Understanding the nature and size of relationships between grain yield and other easily measured morpho-physiological and quality variables is critical for developing effective breeding strategies (Pervin et al., 2025).

Correlation coefficient analysis is a useful statistical tool for determining the level of correlation between two or more variables. It enables breeders to understand how selection for one characteristic may affect another, leading the selection of acceptable selection criteria. However, correlation does not reveal the underlying cause of these connections. Wright (1921) created path coefficient analysis to address this by categorizing correlation coefficients as direct effects (one variable's direct influence on another) or indirect effects (influence exerted through other intermediary qualities). This powerful analytical technique provides a more precise understanding of how various morpho-physiological and quality attributes contribute to grain yield, allowing breeders to identify key traits with the greatest direct influence and thus more reliable as selection indices.

The development of these features and their interrelationships can be considerably influenced by environmental factors, such as optimal vs stress situations (e.g., terminal heat stress). Terminal heat stress, which occurs during the sensitive grain-filling period, is a significant abiotic constraint on wheat productivity in several areas, including parts of India. It has the potential to significantly disrupt plant phenology, diminish the efficiency of critical morpho-physiological processes, and eventually impact production and quality (Mustafa et al., 2023). As a result, investigating trait connections and their direct/indirect impacts in different contexts is critical for finding qualities that contribute to yield stability and stress adaption.

While extensive research has focused on genetic variability and heritability, detailed comparative correlation and path coefficient analyses delineating the influence of a broad range of morpho-physiological traits (including those related to canopy architecture such as flag leaf dimensions, plant stature, and phenology) and quality attributes (like protein content and seedling vigor indicators) on wheat grain yield under both optimal and late-sown heat stress conditions are Such analyses can reveal changes in the relative relevance of various features in response to changing environmental stressors. For example, characteristics that are important for yield under ideal conditions may differ from those that impart resilience and productivity under heat stress.

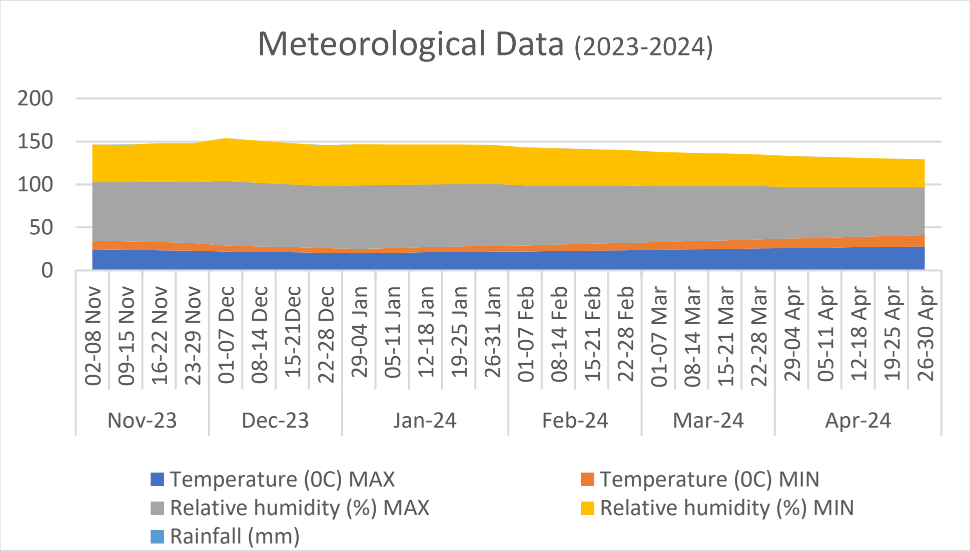
2. Materials and Methods:

The study used a diverse set of 43 wheat (Triticum aestivum L.) genotypes were G1. WH1124 – V, G2. WH1100, G3. WH1136, G4. WH1140, G5. WH1126, G6. WH1202, G7. WH1160, G8. WH715, G9. WH542 – V, G10. WH522, G11. WH1132, G12. WH1063, G13. WH1185, G14. WH1270 - V (Check), G15. WH1105 – V, G16. WH1182, G17. WH283 – V, G18. WH1127, G19. WH1164, G20. WH1134, G21. WH1152, G22. WH1135, G23. WH1184 – V, G24. HD2307, G25. HD2687 – V, G26. HD3043, G27. HD3386 - V (Check), G28. HD3219, G29. HD3182, G30. PBW761, G31. PBW163, G32. PBW706, G33. PBW769, G34. PBW826, G35. PBW677, G36. PBW681, G37. PBW644, G38. PBW750, G39. PBW165, G40. PBW475, G41. DBW222 - V (Check), G42. DBW303, G43. DBW187 – V. These genetic resources were obtained from Chaudhary Charan Singh Haryana Agricultural University (CCS HAU) in Hisar and the Regional Research Station (RRS) of Punjab Agricultural University (PAU) in Bathinda. To offer a performance baseline, three standard check varieties—WH 1270, HD 3386, and DBW 222—were evaluated in the field under both experimental conditions.

2.1 Experimental Sites and Sowing Conditions

The study was carried out across two Rabi seasons, 2023-2024 and 2024-2025, in two separate agro-climatic zones of India, to evaluate genotype performance under optimal and terminal heat stress conditions. The trial depicting optimal growing circumstances was set up at the Field Research Farm, Department of Genetics and Plant Breeding, Guru Kashi University, Talwandi Sabo, Bathinda, Punjab (29°57'37.5" N, 75°07'16.6" E, 37 m elevation). Sowing was completed on time, on December 7, 2023. The soil was Sandy Loam with a pH of 9.8, EC of 0.38 dS/m, and organic carbon content of 0.75%. Talwandi Sabo's normal chilly, dry winter climate made for ideal wheat growing conditions. Plate 1 includes detailed meteorological data for the season.

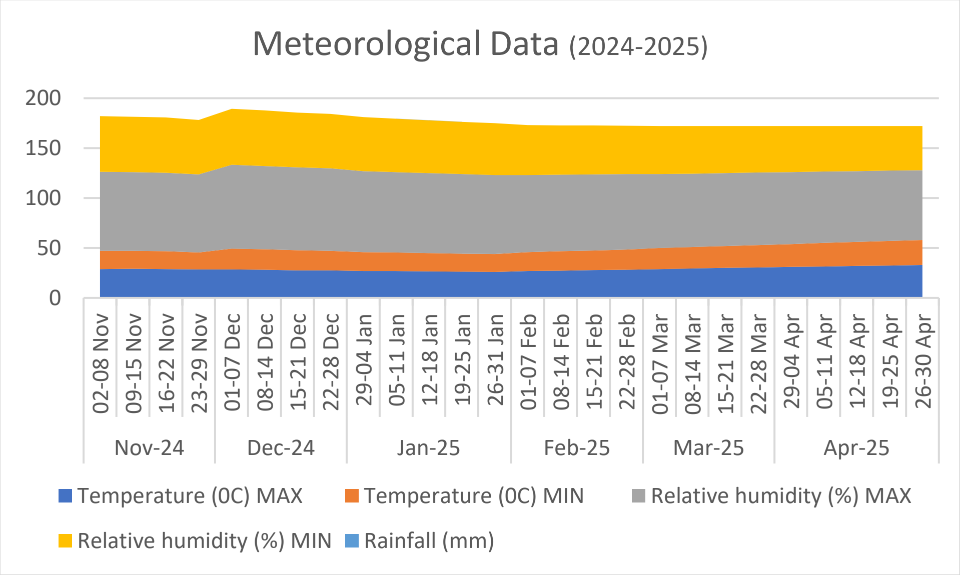
Plate 1. Meteorological Data 2023-2024



*Comparison of Metrological Data Between the 2024-25 Season.

To simulate terminal heat stress, a second trial was held in a private farm in Ongole, Prakasam District, Andhra Pradesh (15.5105929" N, 80.0557416" E, 10 m altitude). Sowing was purposefully postponed until December 24, 2024, to ensure that the reproductive and grain-filling periods corresponded with the higher ambient temperatures typical of this tropical area. Genotypes were grown in grow bags to ensure uniform moisture management. The soil was Red Sandy Loam with a pH of 7.5, EC of 2.1 dS/m, and organic carbon content of 0.42%. The weather data for Ongole for the experimental period are shown in Plate 2. This set-up was intended to subject the plants to substantial heat stress at critical developmental stages.

Plate 2. Meteorological Data 2024-2025



*Comparison of Metrological Data Between the 2023-24 Season.

2.2 Experimental Design and Agronomic Practices

Field experiments at both sites were carried out utilizing a Randomized Block Design (RBD) with three replications. Each genotype was planted in two rows, with a 25 cm inter-row spacing and 10 cm intra-row spacing. A prescribed fertilizer dosage of 80:40:40 kg/ha N:P:K was used. Standard agronomic and plant protection measures were implemented, and laboratory trials for seed quality and vigor assessments were carried out using a Completely Randomized Design (CRD).

2.2.1 Data Collection on Yield, Morpho-Physiological, and Quality Traits

Data were rigorously documented for sixteen field variables and ten laboratory traits. The main dependent variable for correlation and path coefficient analysis was grain yield per plot, with the following critical independent morpho-physiological and quality traits:

- Phenological Traits: Days to 50% flowering, Days to maturity.
- Plant Architectural and Canopy Traits: Plant height (cm), Peduncle length (cm), Number of tillers per plant, Flag leaf length (cm), Flag leaf width (cm), Flag leaf area (cm^2).
- Spike and Grain Characteristics (Yield Components): Spike length (cm), Number of grains per spike, Grain weight per spike (g), Test weight (1000-grain weight, g).
- Biomass and Overall Yield Traits: Biological yield per plant (g), Grains yield per plant (g), and the primary dependent variable for path analysis, Grain yield per plot (g).
- Seedling Morpho-Physiological and qualityTraits (as indicators of initial vigor potentially influencing adult plant traits): Seedling dry weight (g) and Seed Vigor Index-II (SVI-II), calculated as Germination (%) × Seedling dry weight (mg) and Protein Content (%).

2.2.2 Statistical Analysis

The gathered data for all traits were initially subjected to Analysis of Variance (ANOVA) to detect significant differences between genotypes, which is suited for RBD and CRD designs. This step was required to demonstrate the presence of genetic diversity before moving further with correlation and route studies.

2.2.2.1 Correlation Coefficient Analysis

Phenotypic (rp) and genotypic (rg) correlation coefficients were determined for all feasible pairs of yield, morphophysiological, and quality parameters under both optimum and heat stress circumstances. The methodology used variance and covariance components produced from the ANOVA. The correlation coefficients' significance was assessed with (n-2) degrees of freedom.

2.2.2.2 Path Coefficient Analysis

To investigate the direct and indirect effects of the chosen morpho-physiological and quality attributes (independent factors) on grain yield per plot (dependent variable). The route coefficients were estimated using both phenotypic and genotypic correlation matrices. Simultaneous equations were solved to determine the direct effects (Piy) and indirect effects (rij x Pjy) of each causative component on the outcome variable, grain yield per plot. The residual effect (x), which represents unexplained variation, was estimated as $(1\text{-}R^2)^{0.5}$, where $R^2 = \sum P_{iy}r_{iy}$. The magnitude of path coefficients was graded using the scale given by Lenka and Mishra (1973).

Results and Discussion:

The data on the interrelationships between yield, morpho-physiological parameters, and important quality features in 43 different wheat genotypes. The assessments were carried out under ideal (2023-24, Talwandi Sabo) and late-sown heat stress (2024-25, Ongole) field conditions, with pertinent quality features measured in the laboratory. The primary goal is to elucidate the nature and extent of these interactions using correlation and path coefficient studies to guide wheat breeding techniques.

Analysis of variance (ANOVA) revealed significant genetic differences ($P<0.01$ or $P<0.05$) among 43 wheat genotypes for 16 field traits (e.g., grain yield per plot, days to 50% flowering, plant height, flag leaf area, number of grains per spike, test weight, etc.) and ten laboratory traits (e.g., protein content and seedling dry weight) under both operations. This underlying genetic variability is critical for meaningful correlation and path coefficient investigations because it provides the range required to express relationships and distinguish direct/indirect effects (Pervin et al., 2025).

3.1 Correlation Coefficient Analysis: Unveiling Trait Interrelationships

Understanding the relationship between grain yield, key morphophysiological parameters, and quality traits is critical for focused wheat development.

3.1.1 Associations under Optimal Conditions (2023-24, Talwandi Sabo)

Table 1 shows that under optimal growing conditions, grain production per plot had significant relationships with numerous morpho-physiological and component trait variables. At the genotypic level, which captures heritable relationships, grain yield per plot had a very strong and extremely significant positive correlation with biological yield per plot (rg = 0.833**). This suggests that genotypes with higher overall biomass output had better grain yields, which is a typical finding (Roy et al., 2021). Grain yield per plot showed significant positive genotypic associations with plant height (rg =0.332**), peduncle length (rg =0.259**), number of tillers per plant (rg =0.183*), and test weight (rg

=0.213*). These data indicate that, under optimal conditions, taller plants with more tillers and heavier grains contributed to higher plot yields. Baye et al. (2020) found similar favorable relationships between yield, biomass, and tillering.

In contrast, there were large and significant negative genotypic associations between grain yield per plot and phenological parameters such days to maturity (rg =-0.523**) and days to 50% flowering (rg =-0.253**). This suggests that early mature genotypes had higher yields under these specific ideal conditions, either due to better alignment with natural resources or avoidance of unintentionally imposed late-season pressures (Ayyub & Salmanpour et al., 2024). Negative correlations were also found with spike length (rg =-0.227**) and number of grains per spike (rg =-0.222**) at the genotypic level, which may appear contradictory but emphasize the intricacy of component compensation and the need of route analysis in dissecting such interactions.

In terms of quality attributes, direct correlations between protein content and grain yield per plot were not consistently robust or significant under ideal conditions. Seedling vigor parameters, such as seedling dry weight, are fundamental; their relationships with eventual yield components are usually indirect, mediated by total plant establishment and biomass buildup (Addad et al., 2025).

3.1.2 Associations under Heat Stress Conditions (2024-25, Ongole)

The application of late-sown heat stress considerably changed the landscape of trait relationships depicted in Table 2. Under these settings, grain yield per plot shown highly substantial positive genotypic correlations with numerous critical yield components as well as some morpho-physiological features that aid in stress adaptation. Strong positive genotypic relationships were found with the quantity of grains per spike (rg =0.802**), grain weight per spike (rg =0.803**), and hence grain yield per plant (rg =0.733**). This underlines that under heat stress, the ability to efficiently lay and fill grains becomes critical for increasing yields. Poudel et al. (2021) also found considerable associations between yield and spike characteristics under stress.

Positive genotypic associations with grain yield per plot were also found for plant height (rg = 0.367**), peduncle length (rg = 0.347**), number of tillers per plant (rg = 0.312**), and test weight (rg = 0.261). Interestingly, flag leaf width had a substantial positive genotypic connection with yield under stress (rg =0.242**), implying that preserving canopy structure and photosynthetic capability through this trait could be advantageous. A major morpho-physiological adaptation, days to 50% flowering, showed a robust and significant negative genotypic connection with grain yield per plot (rg = -0.390**). This significantly supports the idea of heat escape, in which earlier flowering allows genotypes to complete sensitive reproductive phases before the peak of heat stress, which is an important strategy for yield preservation (Abdurezake et al., 2024).

The number of genotypic correlations was often greater than phenotypic correlations in both contexts, demonstrating that, while environmental influences influence trait expression, the underlying genetic relationships are strong.

Table 1; Correlation Matrix

Genotypic Correlation Matrix																
	DFF	**DTM**	**PH**	**PL**	**NTP**	**FLL**	**FLW**	**FLA**	**SL**	**NGS**	**GWS**	**BYPP**	**GYPP**	**BYP**	**TW**	**G YP**
DFF	1	0.882**	0.775**	0.311**	0.1699	0.428**	0.500**	0.629**	0.394**	0.495**	0.577**	0.480**	0.342**	0.002	-0.377**	-0.253**
DTM		1	0.401**	-0.0085	0.321**	0.673**	0.292**	0.612**	0.400**	0.409**	0.625**	0.348**	0.0071	-0.0273	-0.591**	-0.523**
PH			1	0.778**	0.262**	0.377**	0.610**	0.701**	0.353**	0.259**	0.406**	0.670**	0.523**	0.526**	-0.0256	0.332**
PL				1	0.1521	0.1295	0.390**	0.373**	0.271**	0.0459	0.1352	0.413**	0.404**	0.440**	-0.0245	0.259**
NTP					1	0.488**	0.072	0.356**	0.1255	-0.0427	0.1568	0.376**	0.306**	0.240**	0.207*	0.183*
FLL						1	0.220*	0.721**	0.0759	0.1722	0.539**	0.388**	0.1112	0.206*	0.1304	-0.0165
FLW							1	0.819**	0.459**	0.215*	0.376**	0.444**	0.402**	0.1483	-0.0824	-0.0766
FLA								1	0.395**	0.276**	0.573**	0.627**	0.424**	0.228**	0.0556	-0.0825
SL									1	0.1321	0.279**	0.339**	0.524**	-0.204*	-0.283**	-0.227**
NGS										1	0.742**	0.437**	0.335**	-0.0506	-0.223*	-0.222*
GWS											1	0.496**	0.376**	0.0285	0.0261	-0.075
BYPP												1	0.811**	0.1501	0.0938	-0.0765
GYPP													1	0.0049	0.0299	-0.0725
BYP														1	0.1167	0.833**
TW															1	0.213*
G YP																1

Table 2; Correlation matrix (2024-25)

Genotypic Correlation Matrix																
	DFF	**DTM**	**PH**	**PL**	**NTP**	**FLL**	**FLW**	**FLA**	**SL**	**NGS**	**GWS**	**BYPP**	**GYPP**	**BYP**	**TW**	**G YP**
DFF	1	0.373**	0.0302	-0.0881	-0.0448	0.333**	-0.006	0.270**	0.0785	-0.349**	-0.367**	-0.0216	-0.268**	-0.0733	-0.0456	-0.390**
DTM		1	0.651**	0.277**	-0.0628	-0.199*	0.296**	0.0151	0.559**	-0.0949	0.1122	-0.0446	0.076	0.309**	0.279**	0.0227
PH			1	0.551**	0.261**	-0.251**	0.494**	0.0578	0.811**	0.310**	0.427**	0.407**	0.404**	0.594**	0.345**	0.367**
PL				1	0.204*	-0.192*	0.205*	-0.044	0.313**	0.291**	0.365**	0.363**	0.327**	0.318**	0.304**	0.347**
NTP					1	-0.240**	0.0072	-0.184*	0.346**	0.347**	0.376**	0.800**	0.648**	0.413**	0.15	0.312**
FLL						1	0.253**	0.921**	0.196*	-0.0646	-0.1664	-0.1576	-0.225*	-0.1709	-0.276**	-0.0452
FLW							1	0.723**	0.619**	0.238**	0.314**	0.184*	0.217*	0.389**	0.470**	0.242**
FLA								1	0.404**	0.0599	0.0313	-0.0236	-0.0532	0.0645	0.0285	0.0784
SL									1	0.441**	0.479**	0.514**	0.492**	0.670**	0.1665	0.472**
NGS										1	0.926**	0.419**	0.866**	0.434**	0.0434	0.802**
GWS											1	0.403**	0.930**	0.500**	0.338**	0.803**
BYPP												1	0.608**	0.594**	0.231**	0.435**
GYPP													1	0.561**	0.310**	0.733**
BYP														1	0.346**	0.526**
TW															1	0.261**
G YP																1

3.2 Path Coefficient Analysis: Dissecting Trait Contributions to Yield

Path coefficient analysis was used to separate the observed correlation coefficients into direct and indirect impacts via other features, with grain yield per plot serving as the outcome variable. This improves our understanding of which morpho-physiological and quality factors are the key determinants of yield.

3.2.1 Trait Pathways under Optimal Conditions (2023-24)

At the genotypic level, biological yield per plot had a significantly positive direct effect (1.3183) on grain yield per plot. This finding, which is consistent with Table 3, emphasizes that overall biomass buildup is a key driver of grain yield under optimal conditions. Test weight also had a fairly high positive direct effect (0.9915) at the genotypic level, demonstrating its value not only as a yield component but also as a direct contributor to plot yield, most likely due to improved grain packing and density.

Morphophysiological variables such as flag leaf length (direct impact = 4.7563) and flag leaf width (direct effect = 5.6165) had extremely large positive direct effects at the genotypic level, but flag leaf area had a very large negative direct effect (-9.3031). Number of grains per spike (-1.627) had a significant negative direct genotypic effect. Such exceptionally large route coefficients frequently reflect multicollinearity among predictor variables, implying that their substantial correlations with yield are mediated by complicated interactions and indirect pathways, notably biological yield (Lau et al., 2025). As a result, while flag leaf traits are biologically essential, selecting them based only on their precise route coefficients warrants prudence. The negative direct effects of some yield components, such as number of grains per spike, which are frequently positively correlated with yield, emphasize compensating effects in which their influence is routed through other variables such as overall biomass or individual grain weight (Koshraj et al., 2020).

3.2.2 Trait Pathways under Heat Stress Conditions (2024-25)

Under heat stress, the importance of direct influences on grain yield per plot changed. At the genotypic level, grain weight per spike had a very strong positive direct effect (2.5916), as did spike length (1.846), as seen in Table 4. This clearly shows that at high temperatures, the capacity to preserve individual grain weight and create longer spikes (which might accommodate more or heavier grains) becomes a major predictor of eventual yield. This is consistent with Redhu et al., (2021), who stressed the importance of spike characteristics during stress.

The number of grains per spike had a significant negative direct genotypic effect (-1.627) on yield under stress, indicating that while the correlation was positive, its contribution was heavily mediated by other factors, possibly reflecting source limitations affecting grain filling when many grains are set.

Similarly, grain production per plant had a negative direct genotypic influence (-0.4382). However, phenotypically, the number of grains per spike had the most positive direct effect (0.821) under stress, followed by test weight (0.2530) and biological yield per plot (0.1675). Days to 50% flowering had a negative direct effect (-0.1794 phenotype) on yield under stress, confirming its function in heat escape (Combs-Giroir et al., 2024).

In general, quality parameters such as protein content have little or no direct effect on grain yield. Seedling vigor features, such as high seedling dry weight, are projected to indirectly contribute to ultimate output by improving plant establishment and early biomass accumulation, resulting in a more robust plant framework (morpho-physiology) capable of higher productivity (Narendra et al., 2021).

Table 3; Path Matrix (2023-24)

Genotypic Path Matrix																
	DFF	**DTM**	**PH**	**PL**	**NTP**	**FLL**	**FLW**	**FLA**	**SL**	**NGS**	**GWS**	**BYPP**	**GYPP**	**BYP**	**TW**	**G YP**
DFF	0.9692	0.8543	0.7508	0.3016	0.1646	0.4147	0.4848	0.6095	0.3821	0.4794	0.5591	0.4649	0.3314	0.0019	-0.3653	-0.253**
DTM	0.0467	0.053	0.0212	-0.0005	0.017	0.0357	0.0155	0.0325	0.0212	0.0217	0.0331	0.0184	0.0004	-0.0014	-0.0313	-0.523**
PH	-0.2077	-0.1074	-0.2681	-0.2086	-0.0702	-0.1012	-0.1636	-0.1879	-0.0947	-0.0695	-0.1089	-0.1798	-0.1401	-0.141	0.0069	0.332**
PL	-0.0679	0.0019	-0.1698	-0.2183	-0.0332	-0.0283	-0.085	-0.0813	-0.0591	-0.01	-0.0295	-0.0901	-0.0883	-0.096	0.0053	0.259**
NTP	-0.0309	-0.0583	-0.0476	-0.0276	-0.1818	-0.0887	-0.0131	-0.0647	-0.0228	0.0078	-0.0285	-0.0683	-0.0556	-0.0436	-0.0376	0.183*
FLL	2.0351	3.1998	1.7945	0.6159	2.3209	4.7563	1.0484	3.4311	0.3609	0.8188	2.5642	1.8433	0.5288	0.9814	0.6201	-0.0165
FLW	2.8094	1.6416	3.4279	2.1878	0.4043	1.2381	5.6165	4.5975	2.5801	1.2072	2.1141	2.4948	2.2602	0.8329	-0.4629	-0.0766
FLA	-5.8507	-5.6967	-6.5207	-3.4665	-3.3085	-6.7111	-7.6151	-9.3031	-3.6705	-2.5717	-5.3267	-5.8366	-3.9399	-2.1246	-0.5172	-0.0825
SL	0.2519	0.2554	0.2256	0.173	0.0802	0.0485	0.2935	0.2521	0.639	0.0844	0.1784	0.2167	0.3347	-0.1305	-0.1809	-0.227**
NGS	0.1035	0.0855	0.0543	0.0096	-0.0089	0.036	0.045	0.0579	0.0276	0.2093	0.1553	0.0915	0.0701	-0.0106	-0.0467	-0.222*
GWS	-0.4465	-0.4836	-0.3145	-0.1047	-0.1213	-0.4173	-0.2913	-0.4432	-0.2161	-0.5743	-0.774	-0.3839	-0.2909	-0.022	-0.0202	-0.075
BYPP	0.4863	0.3524	0.6798	0.4184	0.3811	0.393	0.4504	0.6361	0.3439	0.4434	0.503	1.014	0.8218	0.1522	0.0951	-0.0765
GYPP	0.0202	0.0004	0.0308	0.0238	0.018	0.0066	0.0237	0.025	0.0309	0.0197	0.0221	0.0478	0.0589	0.0003	0.0018	-0.0725
BYP	0.0026	-0.036	0.6932	0.5797	0.3162	0.272	0.1955	0.3011	-0.2692	-0.0667	0.0375	0.1979	0.0064	1.3183	0.1538	0.833**
TW	-0.3737	-0.5856	-0.0254	-0.0243	0.205	0.1293	-0.0817	0.0551	-0.2807	-0.2212	0.0259	0.093	0.0296	0.1157	0.9915	0.213*
G YP	-0.253**	-0.523**	0.332**	0.259**	0.183*	-0.0165	-0.0766	-0.0825	-0.227**	-0.222*	-0.075	-0.0765	-0.0725	0.833**	0.213*	

Table 4; Path matrix (2024-25)

Genotypic Path Matrix															
	DFF	**DTM**	**PH**	**PL**	**NTP**	**FLL**	**FLW**	**FLA**	**SL**	**NGS**	**GWS**	**BYPP**	**GYPP**	**BYP**	**TW**	**G YP**
DFF	0.5401	0.2012	0.0163	-0.0476	-0.0242	0.1799	-0.0032	0.1457	0.0424	-0.1887	-0.198	-0.0117	-0.145	-0.0396	-0.0246	-0.390**
DTM	-0.46	-1.2345	-0.8037	-0.3417	0.0776	0.246	-0.3653	-0.0186	-0.6902	0.1171	-0.1385	0.055	-0.0938	-0.381	-0.3447	0.0227
PH	-0.0277	-0.5972	-0.9172	-0.5057	-0.239	0.2305	-0.4526	-0.053	-0.7439	-0.2843	-0.3918	-0.3732	-0.3703	-0.545	-0.3161	0.367**
PL	-0.0353	0.1109	0.2209	0.4007	0.0819	-0.0769	0.0822	-0.0176	0.1252	0.1166	0.1463	0.1453	0.1312	0.1273	0.1219	0.347**
NTP	0.0174	0.0243	-0.101	-0.0792	-0.3874	0.0928	-0.0028	0.0712	-0.1342	-0.1345	-0.1457	-0.3097	-0.251	-0.1598	-0.0581	0.312**
FLL	0.0145	-0.0087	-0.011	-0.0084	-0.0105	0.0437	0.011	0.0402	0.0086	-0.0028	-0.0073	-0.0069	-0.0098	-0.0075	-0.012	-0.0452
FLW	-0.0032	0.1569	0.2616	0.1087	0.0038	0.1341	0.53	0.3829	0.328	0.126	0.1665	0.0977	0.1149	0.206	0.2492	0.242**
FLA	-0.3303	-0.0185	-0.0707	0.0539	0.2251	-1.1278	-0.8846	-1.2244	-0.4949	-0.0734	-0.0383	0.0289	0.0651	-0.079	-0.0349	0.0784
SL	0.1449	1.0321	1.4972	0.5769	0.6394	0.3625	1.1425	0.7462	1.846	0.8134	0.8837	0.9489	0.9083	1.2361	0.3074	0.472**
NGS	0.5685	0.1543	-0.5043	-0.4733	-0.565	0.1051	-0.3866	-0.0975	-0.7168	-1.627	-1.5059	-0.6811	-1.4081	-0.7059	-0.0706	0.802**
GWS	-0.9502	0.2908	1.107	0.946	0.9749	-0.4312	0.8139	0.0811	1.2406	2.3987	2.5916	1.0432	2.4112	1.2966	0.8749	0.803**
BYPP	0.0041	0.0085	-0.0779	-0.0694	-0.1531	0.0302	-0.0353	0.0045	-0.0984	-0.0802	-0.0771	-0.1915	-0.1164	-0.1138	-0.0443	0.435**
GYPP	0.1176	-0.0333	-0.1769	-0.1434	-0.2839	0.0986	-0.095	0.0233	-0.2156	-0.3793	-0.4077	-0.2663	-0.4382	-0.2458	-0.1357	0.733**
BYP	-0.0021	0.0087	0.0167	0.009	0.0116	-0.0048	0.011	0.0018	0.0189	0.0122	0.0141	0.0168	0.0158	0.0282	0.0098	0.526**
TW	0.0119	-0.073	-0.0902	-0.0796	-0.0392	0.0722	-0.123	-0.0075	-0.0436	-0.0113	-0.0883	-0.0605	-0.081	-0.0906	-0.2616	0.261**
G YP	-0.390**	0.0227	0.367**	0.347**	0.312**	-0.0452	0.242**	0.0784	0.472**	0.802**	0.803**	0.435**	0.733**	0.526**	0.261**	

3.3 Implications for Selection Strategies

The correlation and route coefficient analyses provide important insights for developing effective wheat selection techniques. Under ideal conditions, selection algorithms should prioritize qualities such as biological yield per plot and test weight, which have a strong positive direct effect on grain production. Morpho-physiological variables associated with increased biomass, such as optimal plant height and tillering, should also be evaluated. Under heat stress conditions, the emphasis should shift to qualities that directly improve grain development and stress resistance. Grain weight per spike, spike length (genotypically), and number of grains per spike (phenotypically) were identified as important direct contributors. Important tactics include selecting for early flowering (a critical morpho-physiological adaptation) to avoid peak stress, as well as preserving test weight and total biological productivity (Combs-Giroir et al., 2024).

The study found that indirect selection can be more effective than direct selection for yield alone. For example, while the number of grains per spike may have a negative direct genotypic effect under certain conditions, its strong positive correlation with yield suggests its overall importance, which is most likely channeled through positive indirect effects via other traits that path analysis can reveal (Sebsibe et al., 2023). The intricate interplay shows that persistent genetic improvement in wheat requires a balanced selection method that takes into account different morpho-physiological features, yield components, and quality indicators, as well as unique environmental conditions (optimal vs. stress-prone)..

4. Conclusion:

This study on the correlation and path coefficient analysis of yield, morpho-physiological, and quality variables in 43 different wheat genotypes under optimal and heat stress conditions provided vital insights for strategic wheat development. The study was successful in delineating the intricate web of interrelationships between these qualities and identifying important characters that have a direct influence on grain output.

Under optimal growth conditions, biological yield per plot (rg=0.833**) and test weight (rg=0.213**) showed substantial positive genotypic correlations and had the most significant positive direct effects on grain yield per plot (direct genotypic effects of 1.3183 and 0.9915, respectively). This highlights the necessity of selecting for overall biomass accumulation and efficient grain filling under favorable conditions. In contrast, phenological variables such as days to maturity exhibited a substantial negative genotypic correlation (rg = -0.523**) with yield in ideal conditions, indicating that early genotypes may have an advantage.

The kinetics of trait contributions changed dramatically with late-sown heat stress. Here, the number of grains per spike (rg =0.802**) and grain weight per spike (rg =0.803**) had the largest positive genotypic relationships with grain yield per plot. Path analysis found that grain weight per spike had a very large positive direct genotypic effect (2.5916) on yield under stress, as did spike length (1.846). This demonstrates that under high-temperature stress, the ability to set and, more importantly, fill individual grains properly, as well as the development of appropriate spike architecture, are critical for preserving production. The substantial negative genotypic correlation of days to 50% flowering (rg =-0.390**) with yield under stress, combined with its negative direct effect, clearly supports selecting for early blooming as a primary heat escape mechanism (Roy et al., 2021).

While direct relationships between quality parameters such as protein content and grain production were not consistently strong, their expression is frequently mediated by the plant's general morpho-physiological health and source-sink balance, as seen in the correlation patterns (Miao et al., 2025). Seedling vigor parameters, such as seedling dry weight, play an important role in robust plant establishment, which indirectly determines the mature plant's ability to support yield and quality attribute development.

This study underlines that wheat selection procedures should be customized to the target environment. For best results, focus on increasing biological yield and test weight through direct and indirect selection of supporting morpho-physiological features. Prioritizing features such as grain weight per spike, number of grains per spike, spike length, and early flowering for heat escape is crucial in heat-stressed situations (Lau et al., 2025). The route coefficient analysis successfully revealed the most influential qualities for direct selection, providing a more precise approach than simply relying on correlation. These findings provide a useful framework for breeders to make informed decisions when selecting parental lines and designing crossing programs aimed at developing high-yielding, high-quality wheat cultivars with improved adaptation to both favorable and increasingly challenging production conditions.

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