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Trait Association Analysis of Morphological and Yield Components in Rice (Oryza sativa L.)

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Abstract

Rice (Oryza sativa L.) is a major staple and economic crop, and improving grain yield while maintaining grain quality remains a primary objective of rice breeding programs. This study evaluated the genetic variability and trait associations among 25 rice genotypes, comprising 22 advanced breeding lines and three commercial check varieties, under field conditions using a randomized complete block design with three replications. Fourteen agronomic, yield, and grain quality traits were recorded and analyzed using descriptive statistics, analysis of variance (ANOVA), correlation, and covariance analyses. ANOVA revealed highly significant ($P \leq 0.01$) differences among genotypes for all traits except tillers per plant, which was significant at $P \leq 0.05$, indicating substantial genetic variability within the germplasm. Grain yield exhibited wide variation (2524.80–4250.57 kg ha^{-1}), highlighting the presence of superior-performing genotypes. Correlation analysis showed a highly significant positive association between days to 50% flowering and days to maturity ($r = 0.9992$), whereas panicle length was negatively associated with grain yield ($r = –0.4521$). Grain length-to-breadth ratio was strongly and positively correlated with average grain length ($r = 0.7798$) but negatively correlated with grain breadth ($r = –0.6161$), confirming the slender grain characteristics of the evaluated germplasm. Covariance analysis further demonstrated considerable variability among agronomic and grain quality traits and revealed both positive and negative relationships among yield-contributing characters. The observed genetic variability and trait associations indicate that the evaluated rice genotypes constitute valuable breeding material for the development of high-yielding cultivars with desirable grain quality characteristics.

KEYWORDS: Rice, Morphological traits, Correlation, Covariance, Association, Grain yield, Grain quality.

Introduction

In Pakistan, rice (Oryza sativa L.) dominates the export-oriented cereal crop market, serving as the second most important staple food crop following wheat. Over 50% of the global population depends on it as their primary food source, and it is grown on over 150 Mha worldwide, producing approximately 537 million metric tons of rice annually (Abeysekara & Rathnayake, 2024). 90% of the global rice production is from Asian countries. Among these, Pakistan holds the 9th position as a major rice producer (Shahzadi et al., 2018). Rice holds the position of a critical cash crop, contributing substantially to rural livelihoods and Pakistan's economy (Ministry of Finance, 2024). Pakistan ranked 4th largest rice exporter with an export worth of 3.4 billion US dollars (Ministry of Commerce, 2024). In Pakistan, approximately 3.6 t/ha of rice is produced on average per hectare, yielding 9.4 million tons of milled rice and contributing 1.9% to the value added in agriculture sector and 0.4% to the country's GDP (Ministry of

Finance, 2024). It is primarily cultivated across two major provincial ecosystems—Punjab and Sindh—which account for roughly 61% and 31% of the country's total rice area, heavily relying on the irrigated Indus Basin network (Nizamania et al., 2019) (Pakistan Bureau of Statistics, 2023). Despite its economic and nutritional importance, rice productivity in Pakistan remains lower than its potential because of various biotic and abiotic constraints. Furthermore, the increasing population and growing demand for food necessitate the development of high-yielding rice varieties with improved agronomic performance (Bin Rahman & Zhang, 2023).

Development of high-yielding crop varieties requires a comprehensive understanding of the genetic diversity and divergence within germplasm, the relationships among agro-morphological traits, and the influence of environmental factors on the expression of these characteristics (Sar et al., 2024). The success of trait improvement largely depends on the level of genetic divergence among the parental lines used in breeding programs (Xie et al., 2015) . Greater genetic variability enhances resilience, facilitates adaptation to diverse environmental conditions, improves resistance to pests and diseases, and contributes to higher yield and better quality (Singh & Solanki, 2026). Therefore, the existence of substantial morpho-genetic variation in agronomic traits is essential for the effective selection and improvement of desirable characteristics in rice (Debsharma et al., 2022).

Grain yield is a complex quantitative trait governed by several morphological and yield-contributing characters (Cuthbert et al., 2008). Furthermore, a thorough understanding of the genetic variability of yield-contributing traits, their interrelationships, and their association with grain yield is essential for the successful implementation of any crop breeding program (Ali et al., 2026). Correlation analysis provides valuable insights into the relationships among different traits, enabling plant breeders to make more accurate and efficient selection decisions (Vieira et al., 2025).

Correlation analysis is a valuable statistical tool that measures the degree and direction of association among different plant traits. It helps breeders identify important characters that are positively associated with grain yield and can be utilized as selection criteria in breeding programs (Gogtay & Thatte, 2017). However, correlation coefficients alone do not reveal whether the observed associations are due to direct effects or indirect influences through other traits. Therefore, the combined use of correlation and path coefficient analyses is crucial for elucidating the relationships among morphological and yield-related traits and for formulating effective selection strategies aimed at improving rice productivity in Punjab, Pakistan.

MATERIALS AND METHODS

The experimental material, comprising 25 rice genotypes, comprising twenty-two (22) candidate advanced breeding lines and three (3) commercial check varieties, were obtained from the National Coordinator, NARC, ISD, and evaluated at the Rice Research Institute (RRI), Kala Shah Kaku (KSK) Punjab, Pakistan. Prior to sowing, the experimental field was thoroughly prepared, and a sandy clay loam soil was selected for raising the nursery. Seeds of each genotype were sown separately on nursery beds, and healthy seedlings were raised under standard management practices. Seedlings were transplanted to the main field 30 days after sowing.

The field experiment was established following a randomized complete block design (RCBD) with three replications. Each experimental plot consisted of seven rows, with 25 plants per row for each genotype. A spacing of 9 inches (approximately 22.5 cm) was maintained between rows as well as between plants to ensure uniform crop establishment. Standard agronomic practices were followed throughout the growing season. Weeds were managed using recommended herbicides, while appropriate agrochemicals were applied to protect the crop from insect pests and diseases.

Data were recorded from five randomly selected competitive plants in each genotype from every replication for the following traits: days to 50% flowering (DF), plant height (PH, cm), number of tillers per plant (TPP), panicle length (PL, cm), number of grains per panicle (GPP), thousand-grain weight (TGW, g), and grain yield (GY). The mean values of the five sampled plants were used for statistical analyses. Ten milled rice kernels were randomly selected from each genotype after harvesting. The average grain length (AGL) and grain breadth were measured in millimeters (mm) using a digital Vernier caliper with an accuracy of 0.01 mm. The mean values were calculated and used for statistical analysis.The length-to-breadth ratio was calculated by dividing the average kernel length by the average kernel breadth using the following formula:

L/B Ratio= Average Grain Length (mm) / Average Grain Breadth (mm)

This ratio was used to classify grain shape.

To determine elongation ratio, ten milled rice kernels from each genotype were soaked in distilled water for 30 minutes and then cooked in boiling water until fully gelatinized. The cooked kernels were allowed to cool to room temperature, and their average length was measured. The elongation ratio was calculated as:

Elongation Ratio = Average Length of Cooked Kernel / Average Length of Uncooked Kernel

After cooking, the number of burst or split kernels was counted. Bursting percentage was calculated using the following equation:

Bursting (%) = (Number of Burst Kernels / Total Number of Cooked Kernels) ×100

Lower bursting percentage indicates better cooking quality.

Head rice recovery was determined after milling by separating whole kernels from broken kernels. The weight of whole kernels was recorded and expressed as a percentage of the total weight of milled rice using the following formula:

Head Rice Recovery (%) = (Weight of Whole Kernels / Total Weight of Milled Rice) ×100

These measurements were recorded for each genotype in all three replications, and the average values were subjected to statistical analysis. Data were analyzed by two-way analysis of variance (ANOVA). Each data analysis was conducted by using SAS (Statistical Analysis System) version 9.2 (SAS Institute, 2008).

Results and Discussion

The experimental material evaluated in this study comprised 25 distinct rice (Oryza sativa L.) genotypes, consisting of 22 elite candidate advanced breeding lines and three commercially cultivated varieties utilized as checks (PK1121 Aromatic, Basmati 515, and Super Basmati). The complete nomenclature and designation codes (G1 to G25) for the advanced lines are explicitly detailed in Table 1.

Table 1: List of Rice Genotypes tested at Rice Research Institute Kala Shah Kaku (RRI, KSK)

Genotypes	Decoded Name	Genotypes	Decoded Name
G1	P-47	G13	NB- 1395
G2	PK 9966	G14	BASMATI 515 (Check)
G3	PK1121 Aromatic (Check)	G15	PK 10324
G4	RRI 3	G16	NB-13122
G5	PKBB- 15-116	G17	BBF-BB- EM-25-7- 4
G6	NS-5	G18	P-35

G7	PK 8892	G19	BR-51
G8	NB-1519	G20	BBF-AP- EM-117- 23-23
G9	BBF-BB- EM-25-7- 2	G21	P-48
G10	PK 10683	G22	SRI-25
G11	PK 9444	G23	PK PB8
G12	SRI-23	G24	BR-1
		G25	Super Basmati (check)

The developmental traits showed distinct variations among the genotypes. Days to 50% Flowering (DF) ranged from 86.67 to 120.67 days with a mean of 109.88 days, while Days to Maturity (DM) varied from 118.67 to 152.67 days (mean = 141.83 days). The low standard deviations for both DF (8.70) and DM (8.66) suggest a relatively uniform distribution around the maturity window, though the wide range implies the presence of both early and late-maturing genotypes within the source. Plant Height (PH) exhibited a mean of 112.70 cm, spanning from 91.73 cm to 130.47 cm, indicating a mix of semi-dwarf and tall traditional statures (Table 2)

Substantial variation was observed for primary yield components. Tillers per Plant (TPP) ranged from 13.73 to 20.87 (mean = 17.25), while Panicle Length (PL) maintained a mean of 25.81 cm. A high degree of phenotypic variance was prominent in Grains Per Panicle (GPP), which extended from 68.40 to 132.50 grains, paired with a high standard deviation (18.23). This reflects a broad genetic base for sink capacity. Thousand Grain Weight (TGW) averaged 25.20 g (range: 19.01–32.44 g), which is highly characteristic of premium long-grain and aromatic rice germplasm. Consequently, Paddy Yield (PY) displayed a vast range from 2524.80 kg/ha to 4250.57 kg/ha, with a substantial mean yield of 3511.96 kg/ha, highlighting certain elite genotypes that outperform the standard check varieties.

Physical grain dimensions and quality coefficients showed notable diversity. Average Grain Length (AGL) ranged from 6.85 mm to 9.25 mm with a mean of 7.86 mm, while grain breadth (Breath) remained narrow, averaging 1.75 mm (range: 1.59–2.00 mm). This resulted in a high Length-to-Breadth Ratio (LB Ratio) averaging 4.50 (range: 3.42–5.40), confirming the slender, premium classification of the tested genotypes.

The Elongation Ratio (ER) showed a mean value of 1.95, indicating excellent linear expansion upon cooking, highly prized cooking quality in Basmati lineages. Hulling/Milling recovery properties, indicated by the Head Rice Recovery/Milling trait (HRR), exhibited stable performance across genotypes, ranging tightly between 53.00% and 61.00% (mean = 56.32%, SD = 2.16). Conversely, the Bursting percentage during cooking displayed the highest relative volatility, spanning from 6.00% to 22.00% (mean = 12.68%, SD = 4.71), suggesting that while some genotypes maintain excellent structural integrity during cooking, others are prone to severe splitting (Table 2).

Table 2: Descriptive Statistics of 14 morphological parameters of rice under field condition

Variable	Min	Max	Mean	Std. Dev.
DF	86.67	120.67	109.88	8.70
DM	118.67	152.67	141.83	8.66
PH	91.73	130.47	112.70	8.91
TPP	13.73	20.87	17.25	1.88
PL	22.20	31.30	25.81	2.01

GPP	68.40	132.50	97.60	18.23
TGW	19.01	32.44	25.20	3.53
GY	2524.80	4250.57	3511.96	460.33
AGL	6.85	9.25	7.86	0.64
Breadth	1.59	2.00	1.75	0.12
LB Ratio	3.42	5.40	4.50	0.44
ER	0.32	2.32	1.95	0.37
Bursting	6.00	22.00	12.68	4.71
HRR	53.00	61.00	56.32	2.16

*days to 50% flowering (DF, days), days to maturity (DM, days), plant height (PH, cm), tillers per plant (TPP), panicle length (PL, cm), grains per panicle (GPP), thousand-grain weight (TGW, g), and grain yield (GY, kg/ha), average grain length (AGL, mm) and breadth (mm), grain length/breadth (LB Ratio), elongation ratio (ER), bursting (%), and head rice recovery (HRR, %)

The analysis of variance (ANOVA) revealed significant differences among the rice genotypes for all the traits studied (Table 1). Highly significant ($P \leq 0.01$) differences were observed for days to flowering (DF), days to maturity (DM), plant height (PH), panicle length (PL), thousand grain weight (TGW), grains per panicle (GPP), , grain yield (GY), average grain length (AGL), grain breadth, bursting percentage, head rice recovery (HRR), length-to-breadth ratio (LB ratio), and elongation ratio (ER), while tillers per plant (TPP) showed significant differences at the 5% level ($P \leq 0.05$). These significant differences indicate the presence of considerable genetic variability among the rice genotypes, suggesting good potential for selection and crop improvement. Grain yield, grains per panicle, plant height, days to flowering, and days to maturity exhibited comparatively higher mean square values, indicating greater variation among the genotypes. Such results are reported by (Amare et al., 2015). The non-significant replication effects and low error mean squares further confirmed the reliability and precision of the experiment (Table 3).

To understand the direction and magnitude of the relationships among various phenological, morphological, yield-contributing, and grain-quality traits, a Pearson correlation matrix was computed (Table 4). The analysis revealed several critical and statistically significant character associations that reflect physiological trade-offs and genetic linkages within the evaluated rice germplasm. A strong, positive, and highly significant correlation was observed between Days to 50% Flowering (DF) and Days to Maturity (DM) (0.9992). This confirms that the vegetative duration is the primary determinant of total crop maturity within this population. Interestingly, Panicle Length (PL) exhibited a significant negative correlation with both DF (r = -0.5029) and DM (r = -0.5052). This indicates that earlier-maturing genotypes in this germplasm pool possess longer panicles, representing an advantageous selection direction for developing short-duration varieties without sacrificing panicle framework architecture. Furthermore, Plant Height (PH) showed a significant negative correlation with Tillers per Plant (TPP) (r = -0.4370). This negative association suggests a classic morpho-physiological trade-off where taller genotypes, likely due to increased vegetative sink demands or mutual shading, produce fewer productive tillers and panicles per plant compared to semi-dwarf counterparts (Table 4). The correlation matrix highlighted prominent trade-offs among primary yield-contributing characters, aligning with the concept of component compensation in cereal crops. Tillers per Plant (TPP) was significantly and negatively correlated with Grains per Panicle (GPP) (r = -0.4846), Similarly, GPP maintained a significant negative relationship with Thousand Grain Weight (TGW) (r = -0.4557). These findings indicate strong internal competition for maternal resources and carbohydrate partitioning during the sink-development and grain-filling stages.

Genotypes that maximize the number of panicles or grains per panicle encounter source limitations, which ultimately reduces final grain size and weight (TGW) (Wang et al., 2007).

Table 3: Mean square values of 14 morphological parameters of rice under field condition

Source of Variation	df	DF	DM	PH	TPP	PL	GPP	TGW	YIELD	AGL	Breadth	LB Ratio	ER	BURSTING	HRR
Genotypes	24	227.02**	224.84**	244.12**	10.39*	16.06**	997.54**	37.47**	635725.00**	1.219**	0.0407**	0.6007**	0.4070**	66.68**	14.77**
Replication	2	13.72	20.25	12.91	50.33	42.16	26.63	1.28	19397.00	0.293	0.3025	2.5263	0.1225	25.00	58.33
Error	48	2.873	3.212	7.85	5.26	0.222	16.06	1.509	25893.00	2.48×10^{-31}	7.94×10^{-33}	0.00182	1.56×10^{-32}	5.26×10^{-31}	2.45×10^{-30}

* At $P \leq 0.05$, significant; ** = significant at $P < 0.01$

days to 50% flowering (DF, days), Days to maturity (DM, days), Plant height (PH, cm), tillers per plant (TPP), panicle length (PL, cm), grains per panicle (GPP), thousand-grain weight (TGW, g), and grain yield (GY, kg/ha); average grain length (AGL, mm) and breadth (mm); grain length/breadth (LB Ratio); elongation ratio (ER); bursting (%); and head rice recovery (HRR, %).

Table 4: Correlation matrix among 14 morphological traits of rice under field condition

Trait	DF	DM	PH	TPP	PL	GPP	TGW	PY	AGL	Breadth	LB Ratio	ER	Bursting	HRR
DF	1.0000													
DM	0.9992**	1.0000												
PH	-0.1136	-0.1090	1.0000											
TPP	0.2012	0.1927	-0.4370*	1.0000										
PL	-0.5029*	-0.5052*	0.0824	-0.1894	1.0000									

GPP	-0.1259	-0.1133	0.1698	-0.4846*	0.3638	1.0000								
TGW	0.0888	0.0932	0.3418	0.0148	-0.3904	-0.4557*	1.0000							
PY	0.2284	0.2281	-0.2459	0.2329	-0.4521*	-0.2445	0.0167	1.0000						
AGL	-0.2468	-0.2666	0.0577	0.0043	0.3636	-0.1466	-0.0431	-0.1941	1.0000					
Breadth	-0.0998	-0.1028	-0.1113	-0.0613	-0.1108	-0.0213	0.2262	0.1274	0.0093	1.0000				
LB Ratio	-0.1407	-0.1540	0.1234	0.0293	0.3663	-0.0790	-0.1884	-0.2276	0.7798**	-0.6161**	1.0000			
ER	0.0358	0.0356	0.0420	-0.1386	0.2463	-0.1645	-0.0769	-0.1338	0.1280	-0.4119*	0.1451	1.0000		
Bursting	-0.3826	-0.3760	0.3509	-0.4282*	0.0929	0.2259	0.0190	-0.2266	-0.1431	-0.0410	-0.0940	0.2477	1.0000	
HRR	-0.1000	-0.0977	0.0022	0.0529	-0.1655	-0.0005	-0.0017	0.1243	-0.1398	-0.1348	-0.0250	0.0300	-0.0258	1.0000

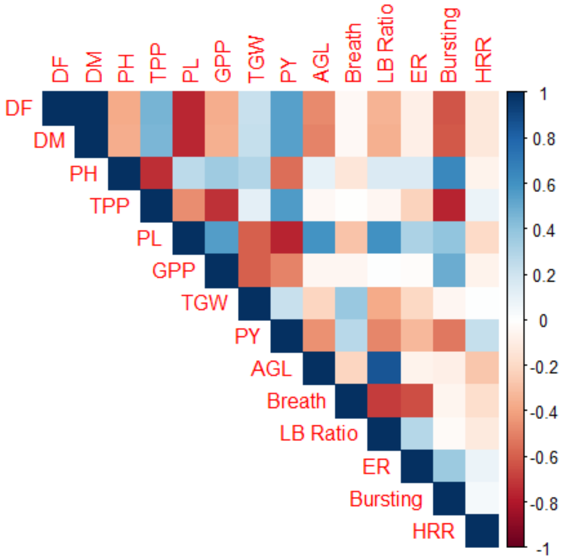
*Days to 50% flowering (DF, days), Days to maturity (DM, days), Plant height (PH, cm), Tillers per plant (TPP), panicle length (PL, cm), Grains per panicle (GPP), thousand-grain weight (TGW, g), and grain yield (GY, kg/ha), average grain length (AGL, mm) and grain breadth (mm), grain length/ breadth (LB Ratio) Elongation ratio (ER), Bursting (%), Head rice recovery (HRR, %)

Paddy Yield (PY) displayed a significant negative correlation exclusively with Panicle Length (r = -0.4521), while maintaining non-significant positive trends with DF, DM, and TPP. This negative association implies that larger panicle length alone does not guarantee elevated grain yield in this population; instead, long panicles might be poorly filled or lack the grain density (compactness) required to drive higher grain yields. Refining grain quality metrics is essential for premium aromatic and Basmati rice breeding programs. The Length-to-Breadth Ratio (LB Ratio)—the primary standard for slender grain classification—showed a highly significant positive correlation with Average Grain Length (AGL) (r = 0.7798) and an expected, highly significant negative correlation with Grain Breadth (r = -0.6161). This confirms that the desired slender phenotype in this germplasm is predominantly driven by longitudinal grain elongation combined with narrow grain width. Regarding cooking and physical traits, Elongation Ratio (ER) exhibited a significant negative correlation with Grain Breadth (r = -0.4119). This relationship is of substantial breeding value, as it proves that genotypes with narrower initial grains undergo superior linear elongation during cooking, a hallmark quality standard of premium Basmati lineages.

Additionally, Bursting percentage during cooking displayed a significant negative correlation with TPP (r = -0.4282). Head Rice Recovery (HRR) showed weak, non-significant correlations with all evaluated agronomic and physical dimensions, suggesting that milling recovery is relatively independent of these traits and can be selected for separately in advanced generations (Table 4).

The color bar on the right dictates the strength and direction of the relationships, ranging from -1 (perfect negative correlation, dark red) to +1 (perfect positive correlation, dark blue). Values near 0 (light grey/white) indicate no linear relationship. Diagonal Values: The deep blue diagonal line represents the perfect positive correlation (r=1) of each variable with itself. DF There is a strong, dark-blue positive correlation between DF (Days to Flowering) and DM (Days to Maturity) traits. This indicates that genotypes taking longer to flower also take longer to reach physiological maturity. A prominent dark blue square indicates a highly positive relationship between these AGL and LB Ratio parameters. Paddy yield shows moderate to strong positive correlations with variables like DF, DM, and TPP, suggesting these traits may directly contribute to higher overall yields. Panicle length exhibits a distinct negative (red) correlation with Paddy yield, indicating an inverse relationship where an increase in length metrics correspond to lower grain yields in this specific population. A strong negative correlation is visible here, marked by a deep red block at their intersection (Figure 1).

Fig 1: Correlation matrix among 14 morphological traits of 25 rice genotypes under field condition



*Days to 50% flowering (DF, days), Days to maturity (DM, days), Plant height (PH, cm), Tillers per plant (TPP), panicle length (PL, cm), Grains per panicle (GPP), thousand-grain weight (TGW, g), and grain yield (GY, kg/ha), average grain length (AGL, mm) and grain breadth (mm), grain length/ breadth (LB Ratio) Elongation ratio (ER), Bursting (%), Head rice recovery (HRR, %)

The covariance matrix (Table 5) revealed the extent and direction of variation among the morphological, yield, and grain quality traits of rice. Positive covariance values indicate that two traits tend to increase together, whereas negative covariance values indicate an inverse relationship between the traits. Paddy yield (PY) showed strong positive covariance with days to 50% flowering (DF; 914.587), days to maturity (DM; 908.952), tillers per plant (TPP; 201.223), thousand-grain weight (TGW; 27.191), and head rice recovery (HRR; 126.935). In contrast, grain yield exhibited negative covariance with plant height (PH; −1008.107), panicle length (PL; −418.828), average grain length (AGL; −56.949), length-to-breadth ratio (LB ratio; −46.360), elongation ratio (ER; −22.687), and bursting percentage (−491.722).

Among the remaining traits, days to 50% flowering and days to maturity exhibited high positive covariance (75.262), indicating that later flowering genotypes generally matured later. Plant height showed positive covariance with grains per panicle (27.586), thousand-grain weight (10.760), and bursting percentage (14.733), while grains per panicle showed a strong positive covariance with panicle length (13.351) but negative covariance with thousand-grain weight (−29.367). Overall, the covariance matrix demonstrated substantial variability and diverse relationships among the studied traits, suggesting that these traits may respond differently during selection and could be effectively utilized in rice improvement programs (Faysal et al., 2022).

Table 5: Covariance matrix of 14 morphological, yield and grain quality traits of 25 rice genotypes

Trait	**DF**	**DM**	**PH**	**TPP**	**PL**	**GPP**	**TGW**	**PY**	**AGL**	**Breadth**	**LB Ratio**	**ER**	**Bursting**	**HRR**
DF	75.684	75.262	-8.805	3.285	-8.805	-19.976	2.729	914.587	-1.369	-0.101	-0.542	0.115	-15.692	-1.930
DM	75.262	74.958	-8.407	3.131	-8.802	-17.881	2.852	908.952	-1.471	-0.104	-0.590	0.113	-15.348	-1.878
PH	-8.805	-8.407	79.338	-7.305	1.477	27.586	10.760	-1008.107	0.328	-0.116	0.486	0.138	14.733	0.043
TPP	3.285	3.131	-7.305	3.522	-0.715	-16.585	0.098	201.223	0.005	-0.013	0.024	-0.096	-3.789	0.220
PL	-8.805	-8.802	1.477	-0.715	13.351	-29.367	-2.777	-418.828	0.467	-0.026	0.326	0.183	0.881	-0.739
GPP	-19.976	-17.881	27.586	-16.585	13.351	332.501	-29.367	-2052.072	-1.705	-0.045	-0.638	-1.105	19.420	-0.019
TGW	2.729	2.852	10.760	0.098	-2.777	-29.367	12.491	27.191	0.097	0.093	-0.295	-0.100	0.316	-0.014
PY	914.587	908.952	-1008.107	201.223	-418.828	-2052.072	27.191	211900.290	-56.949	6.832	-46.360	-22.687	-491.722	126.935
AGL	-1.369	-1.471	0.328	0.005	0.467	-1.705	0.097	-56.949	0.406	0.001	0.220	-0.030	-0.430	-0.198
Breadth	-0.101	-0.104	-0.116	-0.013	-0.026	-0.045	0.093	6.832	0.001	0.014	-0.032	-0.018	-0.023	-0.035
LB Ratio	-0.542	-0.590	0.486	0.024	0.326	-0.638	-0.295	-46.360	0.220	-0.032	0.196	0.024	-0.196	-0.025
ER	0.115	0.113	0.138	-0.096	0.183	-1.105	-0.100	-22.687	-0.030	-0.018	0.024	0.136	0.430	0.025
Bursting	-15.692	-15.348	14.733	-3.789	0.881	19.420	0.316	-491.722	-0.430	-0.023	-0.196	0.430	22.227	-0.270
HRR	-1.930	-1.878	0.043	0.220	-0.739	-0.019	-0.014	126.935	-0.198	-0.035	-0.025	0.025	-0.270	4.923

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