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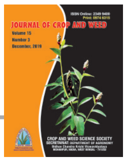

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Variability assessment of rice genotypes by yield traits in diverse environments of Himachal Pradesh

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ABSTRACT

Thirty rice germplasms were grown in randomized block design at five research centers in the NW Himalayas during kharif 2017 to examine the variability and correlations among yield and quality traits. ANOVA revealed significant variation among genotypes for studied traits in each as well as pooled environments. In pooled environment, heritability varied from 37.46 % to 98.70 % while, genetic advance as per cent of mean ranged from 2.62% to 29.94%. In individual and pooled environments, genotypic correlation was higher than their corresponding phenotypic correlation for all concerned traits. Grain yield per plant had significant positive phenotypic correlations and direct effect with days to 75 % maturity, fertility percentage and harvest index while genotypic correlations with days to maturity, fertility percentage and milling percentage. Consequently, days to maturity, fertility percentage, harvest index and milling percentage can be used as selection criteria for grain yield.

***Keywords*:** Direct effects**,** inter-relationship, multi-location testing, rice, variability

Rice (*Oryza sativa* L.) is the staple food for a large proportion of the world's population (Zhang, 2007). Rice is grown worldwide over an area of 164.19 mha with total production of 756.74 mt and 4.61 t ha^{-1} productivity (FAOSTAT, 2020). In our country rice is produced on 45 mha area with a production of 178.30 mt and productivity 3.96 t ha^{-1} (FAOSTAT 2020). India is blessed with a huge diversity of rice grown across different agro-climatic zones. Basmati rice is scented rice having high kernel length breadth ratio before cooking and high volume expansion after cooking. Six states Punjab, Haryana, Uttar Pradesh, Uttarakhand, Delhi and Himachal Pradesh and one UT (Jammu and Kashmir) has specific environment which is responsible to develop its quality traits and has got Geographical Indication (Singh *et al*., 2018). India is the leading exporter of the basmati rice and contributes much in the gross domestic product of the country. Haryana is a leading state in basmati cultivation followed by Punjab and Himachal Pradesh (APEDA, 2019).The basmati cultivation in Himachal Pradesh is only restricted to lower altitude area as Kangra and Mandi but higher altitude region incurs low temperature leading to stronger accumulation of aroma. Grain yield is the economic trait in any crop plants and being a complex quantitative trait is highly influenced by the environment (Dwivedi *et al*., 2020). The inter-relationship of the grain yield with other agro-morphological traits could be studied with the help of correlation and path coefficient which hence saves time and efforts by breeders while selecting for the trait. Thus, this study aimed to characterize yield traits in a collection of 30 rice genotypes used in Himachal Pradesh.

MATERIALS AND METHODS

Plant material and field experiments

The materials comprised of thirty rice genotypes including basmati (Pusa Basmati-1121, Hasansarai, Vasumati, Lakhamandal, Basmati-370, Pusa Basmati-1509, T-23 and Kasturi) and non-basmati advanced breeding lines (ABLs) of rice procured from Rice and Wheat Research centre (RWRC), CSK HPKV, Malan (Table 1). Field trials were conducted over five different locations namely, Dhaulakuan (E1), Una (E2), Palampur (E3), Malan (E4) and Sundernagar (E5) during *kharif* 2017. Previously a research has been conducted to determine diversity and stability factors of genotypes in the five different locations as Dhaulakuan (30°50'N latitude and 77°48'E longitude), Una (31°45'N latitude and 76°27'E longitude), Palampur (32°10'N latitude and 76°56'E longitude), Malan (32°12' N latitude76°42'E longitude) and Sundernagar (31°54' N and 76°90' E longitude) using principal component analysis and AMMI biplot for grain yield in rice genotypes, respectively and researchers confirmed that these locations are highly diverse and identified as mega environments for the evaluation of rice germplasm (Dwivedi *et al*., 2020). The experiment was laid out in randomized complete block design (RCBD) with three replications in each location. Seeds were sown in nursery beds, and transplanted after 25 days old seedlings into the field. Each genotype was grown in 15 cm x 20 cm plant to plant and row to row distance, respectively with 6 m^2 plot size. Observations were recorded on five randomly selected plants in each plot for concerned traits

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namely days to 75 % maturity (DM), plant height (PH), harvest index (HI),number of tillers per plant (NOT), fertility percentage (F%), grain yield per plant (GYP) and test weight (TW), quality parameters namely milling percentage (M%) and length breadth ratio (LBR).

Statistical analysis

The data were subjected to analysis of variance (ANOVA) for each trait and genetic variability parameters, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as per cent of mean (GA as % mean) were also estimated. Correlation and path coefficients were calculated using the OPSTAT software developed by CCS HAU, Hisar, India (Sheoran *et al*., 1998).

RESULTS AND DISCUSSION

Analysis of variance

Analysis of variance for agro-quality traits in five different locations is presented in Table 1. ANOVA in individual environment revealed that mean squares due to genotypes were significant for all the studied characters. Later the data were tested for homogeneity of error variance using Bartlett's test. Results showed the error mean square for grain yield per plant and test weight, the studied traits were not homogenous in all the locations and hence, data of aforesaid traits were transformed using square root transformation method before further analysis. After the data transformation, a pooled ANOVA was used to test for significant differences of the mean between the genotypes and the interaction between genotypes and environment at a significance level of 0.05 and 0.01. The pooled analysis of variance over the environments for different traits is presented in Table 2. The combined ANOVA revealed significant differences for the five locations and genotypes for all characters in the thirty genotypes. The GE interaction was also significant in all the genotypes.

Basmati and non-basmati genotypes were grown in five different agro-climatic conditions of NW Himalayan region of Himachal Pradesh. ANOVA in individual environment revealed significance for all the studied characters indicating sufficient variability among studied genotypes at all the locations for the studied traits. The combined ANOVA revealed significant differences for the five locations and genotypes for all characters in the thirty genotypes indicating the existence of genetic variation and possibility of selection for quality and yield improvement. The genotypes × location interaction was also significant in all the genotypes; therefore the effect of environment persisted for the differential and similar trait expression. The result was in agreement with Saleh *et al*. (2021) who also found significant interaction in all the characters.

Table 1: List of rice germplasm used for present investigation

S. No.	Variety	S. No.	Variety
1.	Pusa Basmati-1121	16.	HPR 2761
2.	Hasansarai	17.	HPR 2763
3.	Vasumati	18.	HPR 2852
4.	Lakhamandal	19.	HPR 2855
5.	Basmati-370	20.	HPR 2858
6.	Pusa Basmati-1509	21.	HPR 2667
7.	T-23	22.	HPR 2861
8.	Kasturi	23.	HPR 2862
9.	HPR 2612	24.	HPR 2863
10.	HPR 2323	25.	HPR 2864
11.	HPR 2692	26.	Sharbati
12.	HPR 2693	27.	PR-121
13.	HPR2746	28.	HPR 2880
14.	HPR 2747	29.	HPR 2795
15.	HPR 2749	30.	HPR 2720

Genetic variability parameters

The results of estimation of genotypic (GCV) and phenotypic coefficient of variation (PCV), heritability, genetic advance (GA) and genetic advance as % of mean (GA as % of mean) for the nine traits are showed in Table 4. Pooled PCV and GCVwere ranged from 3.40%, 2.08% (M %) to 19.93%, 17.02% (NOT), respectively. Moderate estimates of PCV and GCV (10-20%) were observed in all the concerned traits except M % (3.40 %, 2.08 %), F% (7.11 %, 6.28 %) and DM (4.49 %, 4.42 %).

All the characters namely DM (97.12 %), PH (96.25 %), NOT (72.93 %), F% (78.19 %), HI (76.76 %), TW (98.70 %), LBR (97.07 %) and GYP (71.11 %) showed high heritability except M% (37.46 %). In the present study, the high estimates of heritability in broad sense were obtained for all the traits indicating that these traits were least affected by the environment. However, the selection for improvement of these traits may not be useful simply because broad sense heritability is based on the total genetic variance which includes both the fixable (additive) and non-fixable (dominance and epistatic) variances. High GA as % of meanwas observed PH (26.22 %), NOT (29.94 %), TW (20.57 %), LBR (22.49 %) and GYP (21.64 %). Moderate GA as % of mean was observed for F% (11.45 %) and HI (18.38 %) whereas DM (8.98 %) and M% (2.62 %) observed low GA as % of mean.

Selection based of any crop improvement programme mainly depends upon the variability (existing or novel) within the population. From the results it was observed that sufficient genetic variability existed in the experimental genotypes for most of these traits and hence, the genotypes can be a useful source for improvement in rice for these traits. The variability at

Table 2: Mean square from the analysis of variance of rice genotypes evaluated for yield and quality traits at five different locations of Himachal Pradesh

Environment	df	DM	PH	NOT	F%	GYP	HI	TW	M%	LBR
Sundernagar	2	0.37	20.48	11.16**	182.22	9.04	10.36	13.00**	39.04**	0.01
	29	96.59**	744.61**	12.25**	315.08**	56.09**	430.26**	18.92**	12.23**	0.83**
	58	0.49	14.31	2.45	59.02	13.42	68.64	1.32	5.37	0.009
Dhaulakuan	2	8.71**	50.96	23.55**	5.13	1.55	1.19	0.19**	41.45	0.01
	29	148.76**	839.50**	8.41**	97.28%**	18.18**	121.24**	16.00**	80.28**	0.85**
	58	0.78	50.53	2.03	25.29	1.09	8.72	0.05	38.75	0.02
Una	2	2.43	28.36	6.32	1.72	47.53	338.22	0.79**	55.67	0.08
	29	174.94**	983.67**	15.89**	139.49**	80.00**	362.54**	23.70**	45.01**	0.78**
	58	1.1	23.35	3.23	19.97	10.12	42.34	0.15	18.17	0.04
Palampur	2	822.14	15.5	3.86	28.71	3.72	11.14	0.18	70.85**	0.002
	29	88.00**	855.18**	13.94**	323.71**	60.78**	118.21**	20.81**	49.10**	0.67**
	58	16.81	24.05	2.99	16.58	5.86	11.96	0.13	8.06	0.01
Malan	2	0.88	42.78	4.56	3.24	1.7	1.4	0.09	11.09	0.02
	29	38.89**	579.36**	2.92**	162.13**	22.05**	151.74**	17.41**	42.58**	1.01**
	58	0.86	30.99	1.06	21.5	5.24	17.97	0.13	16.18	0.03

*p< 0.05; ** p< 0.01

Table 3: Combined ANOVA for different traits over the environments among rice genotypes

Source of Variation	df	Mean Squares								
		DM	PH	NOT	HI	TW	M%	F%	LBR	GYP
Environ. (A)	4	240,581.8**	2,804.5**	11.2**	1,954.2**	63,358.5**	5,004.2**	979.1**	7,014.2**	3,800.5**
Genotype (B)	29	366.8**	146.4**	15.6**	13.0**	476.4**	3.7**	18.3**	144.5**	12.3**
A X B	116	57.6**	4.7**	1.5**	8.5**	69.6**	3.0**	6.2**	16.6**	7.8**
Pooled Error	290	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0

Table 4: Estimates of variability parameters in basmati and non-basmati rice germplasm across the locations

Variability parameters	PCV	GCV	Heritability	GA % of mean
DM	4.49	4.42	97.12	8.98
PH	13.23	12.98	96.25	26.22
NOT	19.93	17.02	72.93	29.94
F%	7.11	6.28	78.19	11.45
HI	11.63	10.19	76.76	18.38
TW	10.12	10.05	98.70	20.57
M%	3.40	2.08	37.46	2.62
LBR	11.24	11.08	97.07	22.49
GYP	14.77	12.46	71.11	21.64

phenotypic level arises due to genotypic and environmental influences that contribute towards the development of phenotype. The results on phenotypic (PCV) and genotypic (GCV) coefficients of variation revealed that PCV was higher than the corresponding GCV for all the studied traits indicating the influence of environment on these characters. In individual environment, grain yield per plant showed comparable results as pooled analysis indicating all environments can be considered as mega environment.

Low estimates of GA as % of mean (<10%) indicated that these traits are mainly governed by non-additive genes and the direct selection would be ineffective to improve these traits. High heritability with high GA as % of mean was registered for characters like PH, NOT, TW, LBR and GYP indicating additive gene action and direct selection may be effective. Similar results for the estimates of heritability and genetic advance as per cent mean were also reported earlier in rice germplasm by Yumnam *et al.* (2011), Dhanwani *et al.* (2013) and Srujana *et al.* (2017).

Correlation analysis

In five distinct environmental conditions DM was found significant and positively associated with GYP at Dhaulakuan, Una and Malan for phenotypic as well as genotypic level. Plant height pertained significant and positive correlation only at Sundernagar for both levels, likewise at the phenotypic level, there was a significant negative association with the NOT at Una, while at the genotypic level, there was a significant negative association at Sundernagar, Una, and Malan. At Palampur and Malan, F % was positive as well as significantly kindred with GYP for both levels. HI was found significantly and positively correlated with GYP in Sundernagar, Palampur and Malan at phenotypic as well as genotypic level, while significantly negative at Dhaulakuan for genotypic level. M % was observed to be significantly associated with GYP only at one location (Dhaulakuan) for genotypic level, whereas at genotypic level it came out to be significantly and positively correlated in Dhaulakuan, Una as well as Malan. On phenotypic level LBR exhibited significant positive and negative association at Palampur and Malan respectively, while at genotypic level it persisted significant positive association in Dhaulakuan and Palampur, likewise significantly negative in Sundernagar as well as in Malan (Table 5). Phenotypic correlation coefficient revealed that grain yield per plant had significant positive association with DM (0.316), F % (0.245) and HI (0.236). At genotypic level grain yield per plant manifested significant and positive association with DM (0.378), F % (0.326) and M % (0.238) while, number of tillers per plant (-0.250) and LBR (-0.244) exhibited significant negative correlation (Table 5).

The Interrelation studies have great significance to disclose the importance of association between yield and its component traits in any breeding programme. In present investigation the pooled correlation analysis showed that the magnitude of genotypic correlation is greater than the phenotypic correlation coefficient which suggested characters are genetically more similar (Soharu and Pandey, 2018). Ratna *et al.* (2015) also found the same results for tillers per plant. The ultimate goal of applying continuous selection, amelioration, enhancing and nourishing other related yield traits is to generate new rice cultivars with more genetic potential to boost grain output. Our results recommended that the characters like DM, F % and M % are principal yield related attributes and selection of these traits may be considered for enhancing grain yield in North-western Himalayan region. Results are in agreement with the findings of Maurya *et al.* (2018) for days to maturity and fertility percentage. These results agree with previous studies such as Bhutta *et al.* (2019), Chhangte and Devi (2019) and Panda *et al.* (2019).

Path analysis

Through splitting the coefficient of correlation into components of direct and indirect effects, path coefficient analysis allows for a complete comprehension of the contribution of various features (Devi *et al.*, 2017). The pooled investigation disclosed that the attributes like DM, NOT, F%, M% and LBR showed significant association with grain yield. The pooled outcome of the

Table 5: Phenotypic (upper diagonal) and genotypic (lower diagonal) correlation for studied traits in rice germplasm

Character	Environment	DM	PH	NOT	F%	HI	TW	M%	LBR	GYP
DM	Sundernagar	**1.000**	0.037	0.101	-0.079	-0.132	0.158	0.128	0.008	0.023
	Dhaulakuan	**1.000**	0.078	-0.364**	0.094	0.169	0.279**	0.113	0.186	0.286**
	Una	**1.000**	0.069	0.158	-0.118	0.133	0.004	0.262*	0.135	0.373**
	Palampur	**1.000**	0.087	0.058	-0.191	0.191	0.127	0.068	0.230*	0.007
	Malan	**1.000**	0.084	0.163	0.111	-0.044	0.083	0.005	-0.039	0.216*
	Pooled	**1.000**	0.061	0.047	-0.059	0.011	0.206	0.165	0.194	**0.316****
PH	Sundernagar	0.037	**1.000**	-0.100	-0.053	0.13	-0.379**	0.001	-0.239*	0.350**
	Dhaulakuan	0.083	**1.000**	-0.109	0.244*	-0.411**	-0.265*	-0.197	-0.16	0.042
	Una	0.085	**1.000**	0.03	0.11	-0.375**	-0.277**	0.022	-0.167	0.025
	Palampur	0.143	**1.000**	0.05	0.183	0.116	-0.237*	0.167	-0.407**	-0.176
	Malan	0.105	**1.000**	-0.016	0.310**	-0.428**	-0.365**	-0.109	-0.104	0.113
	Pooled	0.065	**1.000**	-0.026	0.261*	-0.331**	-0.358**	-0.11	-0.297**	**0.110**
NOT	Sundernagar	0.128	-0.128	**1.000**	0.08	-0.245*	0.07	0.026	0.255*	-0.179
	Dhaulakuan	-0.539**	-0.039	**1.000**	-0.196	-0.107	-0.01	-0.104	0.204	0.192
	Una	0.231*	0.056	**1.000**	-0.243*	0.112	0.216*	0.052	0.361**	-0.253*
	Palampur	0.180	0.056	**1.000**	-0.222*	0.491**	0.207*	-0.037	0.103	0.092
	Malan	0.325**	-0.064	**1.000**	-0.047	-0.051	0.002	-0.055	0.215*	-0.166
	Pooled	0.055	-0.016	**1.000**	-0.241*	0.023	0.114	-0.012	0.325**	**-0.162**
F%	Sundernagar	-0.071	-0.053	0.199	**1.000**	0.216*	0.202	-0.18	0.119	-0.093
	Dhaulakuan	0.136	0.321**	-0.362**	**1.000**	0.224*	-0.062	0.230*	0.044	0.1
	Una	-0.117	0.109	-0.341**	**1.000**	-0.04	-0.113	0.137	-0.134	0.002
	Palampur	-0.275**	0.245*	-0.244*	**1.000**	-0.210*	-0.148	0.295**	-0.337**	0.232*
	Malan	0.155	0.349**	-0.102	**1.000**	-0.189	-0.068	-0.147	-0.098	0.231*
	Pooled	-0.050	0.292**	-0.300**	**1.000**	0.159	-0.082	0.193	-0.153	**0.245***
HI	Sundernagar	-0.137	0.167	-0.276**	0.297**	**1.000**	-0.168	0.1	-0.287**	0.495**
	Dhaulakuan	0.169	-0.488**	-0.184	0.390**	**1.000**	0.082	0.155	0.151	-0.092
	Una	0.164	-0.481**	0.213*	-0.035	**1.000**	0.177	0.188	0.031	0.028
	Palampur	0.289**	0.142	0.701**	-0.249*	**1.000**	0.109	-0.137	0.227*	0.460**
	Malan	-0.034	-0.474**	-0.01	-0.251*	**1.000**	-0.069	0.109	-0.132	0.287**
	Pooled	0.009	-0.382**	0.061	0.212*	**1.000**	-0.039	0.198	-0.109	**0.236***

Contd. ...

Table 5 Contd. ...

Character	**Environment**	**DM**	**PH**	**NOT**	**F%**	**HI**	**TW**	**M%**	**LBR**	**GYP**
TW	Sundernagar	0.172	-0.422**	0.134	0.436**	-0.279**	**1.000**	-0.13	0.218*	-0.091
	Dhaulakuan	0.282**	-0.285**	-0.032	-0.062	0.085	**1.000**	0.084	0.211*	0.194
	Una	0.002	-0.289**	0.292**	-0.147	0.236*	**1.000**	0.015	0.498**	0.154
	Palampur	0.185	-0.255*	0.271**	-0.145	0.132	**1.000**	-0.01	0.349**	-0.098
	Malan	0.088	-0.400**	0.021	-0.081	-0.065	**1.000**	0.178	0.304**	0.007
	Pooled	0.211*	-0.367**	0.148	-0.078	-0.046	**1.000**	-0.007	0.408**	**0.031**
M%	Sundernagar	0.206	0.028	0.095	-0.209*	0.214*	-0.300**	**1.000**	-0.323**	0.033
	Dhaulakuan	0.215*	-0.370**	-0.112	0.179	0.286**	0.185	**1.000**	0.01	0.210*
	Una	0.512**	0.005	-0.067	0.462**	0.362**	0.031	**1.000**	-0.076	0.192
	Palampur	0.004	0.281**	-0.036	0.366**	-0.220*	0.008	**1.000**	0.01	0.035
	Malan	-0.008	-0.174	-0.288**	-0.186	0.278**	0.283**	**1.000**	-0.174	0.201
	Pooled	0.295**	-0.146	0.009	0.308**	0.376**	0.001	**1.000**	-0.027	**0.131**
LBR	Sundernagar	0.011	-0.254*	0.346**	0.176	-0.376**	0.235*	-0.658**	**1.000**	-0.18
	Dhaulakuan	0.205	-0.213*	0.342**	0.043	0.210*	0.225*	0.071	**1.000**	0.188
	Una	0.145	-0.192	0.475**	-0.203	0.077	0.551**	-0.11	**1.000**	-0.186
	Palampur	0.256*	-0.439**	0.139	-0.361**	0.233*	0.375**	0.035	**1.000**	0.349**
	Malan	-0.043	-0.119	0.464**	-0.147	-0.197	0.317**	-0.226*	**1.000**	-0.318**
	Pooled	0.193	-0.311**	0.371**	-0.184	-0.117	0.418**	-0.02	**1.000**	**-0.201**
GYP	Sundernagar	0.055	0.472**	-0.263*	-0.137	0.370**	-0.182	-0.066	-0.279**	**1.000**
	Dhaulakuan	0.295**	0.041	0.180	0.150	-0.224*	0.206	0.417**	0.246*	**1.000**
	Una	0.461**	0.049	-0.342**	0.058	-0.067	0.187	0.417**	-0.190	**1.000**
	Palampur	-0.028	-0.203	0.130	0.278**	0.315**	-0.106	0.015	0.376**	**1.000**
	Malan	0.322**	0.179	-0.393**	0.333**	0.238*	0.033	0.217*	-0.462**	**1.000**
	Pooled	**0.378****	**0.153**	**-0.250***	**0.326****	**0.113**	**0.031**	**0.238***	**-0.244***	**1.000**

*$p < 0.05$; ** $p < 0.01$

Table 6: Genotypic path coefficient among studied traits against GYP in rice germplasm

Character	Environment	DM	PH	NOT	F%	HI	TW	M%	LBR	GYP
DM	Sundernagar	**0.121**	0.015	0.014	0.030	-0.071	0.038	-0.088	-0.003	0.055
	Dhaulakuan	**0.949**	-0.067	-0.509	0.134	-0.164	-0.024	0.033	-0.056	0.295**
	Una	**0.525**	0.002	-0.103	0.015	-0.037	0.001	0.105	-0.047	0.461**
	Palampur	**-0.019**	-0.034	0.007	-0.166	0.111	-0.062	0.000	0.135	-0.028
	Malan	**0.364**	0.034	-0.126	0.034	-0.015	0.023	0.000	0.009	0.322**
	Pooled	**0.417**	0.002	-0.006	-0.013	0.000	0.021	0.007	-0.051	**0.378****
PH	Sundernagar	0.004	**0.406**	-0.014	0.022	0.087	-0.093	-0.012	0.071	0.472**
	Dhaulakuan	0.078	**-0.815**	-0.037	0.315	0.474	0.025	-0.057	0.059	0.041
	Una	0.044	**0.025**	-0.025	-0.014	0.109	-0.154	0.001	0.063	0.049
	Palampur	-0.003	**-0.239**	0.002	0.148	0.055	0.085	-0.019	-0.231	-0.203
	Malan	0.038	**0.323**	0.025	0.077	-0.210	-0.103	0.006	0.024	0.179
	Pooled	0.027	**0.023**	0.002	0.073	-0.014	-0.037	-0.003	0.083	**0.153**
NOT	Sundernagar	0.016	-0.052	**0.108**	-0.083	-0.144	0.029	-0.041	-0.096	-0.263*
	Dhaulakuan	-0.512	0.032	**0.945**	-0.355	0.178	0.003	-0.017	-0.094	0.180
	Una	0.121	0.001	**-0.446**	0.043	-0.048	0.156	-0.014	-0.156	-0.342**
	Palampur	-0.003	-0.013	**0.039**	-0.147	0.269	-0.090	0.002	0.073	0.13
	Malan	0.118	-0.020	**-0.386**	-0.023	-0.004	0.006	0.010	-0.093	-0.393**
	Pooled	0.023	0.000	**-0.117**	-0.075	0.002	0.015	0.000	-0.098	**-0.250***
F%	Sundernagar	-0.009	-0.021	0.022	**-0.419**	0.155	0.096	0.090	-0.049	-0.137
	Dhaulakuan	0.129	-0.262	-0.342	**0.981**	-0.378	0.005	0.028	-0.012	0.150
	Una	-0.061	0.003	0.152	**-0.127**	0.008	-0.078	0.095	0.067	0.058
	Palampur	0.005	-0.059	-0.010	**0.603**	-0.096	0.048	-0.025	-0.190	0.278**
	Malan	0.056	0.112	0.040	**0.221**	-0.111	-0.021	0.007	0.029	0.333**
	Pooled	-0.021	0.007	0.035	**0.249**	0.008	-0.008	0.007	0.049	**0.326****
HI	Sundernagar	-0.017	0.068	-0.030	-0.125	**0.522**	-0.061	-0.092	0.105	0.370**
	Dhaulakuan	0.161	0.398	-0.174	0.383	**-0.970**	-0.007	0.044	-0.058	-0.224*
	Una	0.086	-0.012	-0.095	0.005	**-0.226**	0.126	0.075	-0.025	-0.067
	Palampur	-0.006	-0.034	0.028	-0.150	**0.384**	-0.044	0.015	0.123	0.315**
	Malan	-0.012	-0.153	0.004	-0.056	**0.442**	-0.017	-0.010	0.039	0.238*
	Pooled	0.004	-0.009	-0.007	0.053	**0.037**	-0.005	0.009	0.031	**0.113**

Contd. ...

Table 6 Contd. ...

Character	Environment	DM	PH	NOT	F%	HI	TW	M%	LBR	GYP
TW	Sundernagar	0.021	-0.172	0.015	-0.183	-0.145	**0.220**	0.128	-0.065	-0.182
	Dhaulakuan	0.267	0.233	-0.031	-0.061	-0.083	**-0.086**	0.029	-0.062	0.206
	Una	0.001	-0.007	-0.130	0.019	-0.053	**0.533**	0.006	-0.181	0.187
	Palampur	-0.004	0.061	0.011	-0.087	0.051	**-0.334**	-0.001	0.197	-0.106
	Malan	0.032	-0.129	-0.008	-0.018	-0.029	**0.258**	-0.010	-0.063	0.033
	Pooled	0.088	-0.008	-0.017	-0.019	-0.002	**0.101**	0.000	-0.111	**0.031**
M%	Sundernagar	0.025	0.011	0.010	0.088	0.112	-0.066	**-0.429**	0.183	-0.066
	Dhaulakuan	0.204	0.301	-0.106	0.176	-0.277	-0.016	**0.154**	-0.020	0.417**
	Una	0.268	0.000	0.030	-0.059	-0.082	0.016	**0.206**	0.036	0.417**
	Palampur	0.000	-0.067	-0.001	0.221	-0.084	-0.003	**-0.069**	0.018	0.015
	Malan	-0.003	-0.056	0.111	-0.041	0.123	0.073	**-0.035**	0.045	0.217*
	Pooled	0.123	-0.003	-0.001	0.077	0.014	0.000	**0.024**	0.005	**0.238***
LBR	Sundernagar	0.001	-0.103	0.038	-0.074	-0.196	0.052	0.282	**-0.278**	-0.279**
	Dhaulakuan	0.194	0.174	0.323	0.042	-0.204	-0.019	0.011	**-0.275**	0.246*
	Una	0.076	-0.005	-0.212	0.026	-0.017	0.293	-0.023	**-0.328**	-0.19
	Palampur	-0.005	0.105	0.005	-0.218	0.090	-0.125	-0.002	**0.526**	0.376**
	Malan	-0.016	-0.038	-0.179	-0.032	-0.087	0.082	0.008	**-0.200**	-0.462**
	Pooled	0.080	-0.007	-0.044	-0.046	-0.004	0.042	0.000	**-0.265**	**-0.244***

path analysis revealed that DM had highest positive effect followed by F% and M% on grain yield, while NOT and LBR possessed negative direct effect on grain yield. The DM exhibited significant positive correlation with GYP chiefly through its direct effect and at small amount indirectly via TW, M% and PH. On the same token, F% had significant positive association with GYP mainly via its direct effect and indirectly through LBR, NOT, HI, M% and PH. M% possessed significant positive correlation with GYP through its direct effects as well indirect effect via traits like DM, F%, HI and LBR. Whereas, significant negative correlation of NOT with GYP was primarily through its negative direct effect and negative indirect effects via traits like F% and LBR. Similarly, significant negative inter-relationship of LBR with grain yield was chiefly the outcome of its negative direct effect and indirectly through PH, NOT, F% and HI (Table 6).

The path analysis of individual environment disclosed that at Dhaulakuan DM pertained positive significant association mainly through its direct effect and indirectly through M% with the GYP, likewise at Una the significant positive correlation of DM with GYP was again through its direct effect and indirectly via PH, F%, M% and TW.

Only at one location *i.e*. Sundernagar PH exhibited positive correlation with GYP which was the outcome of its direct effect as well its indirect effects via traits like HI, LBR, F% and DM. The NOT had significant negative inter-relationship with GYP at Sundernagar mainly due to its indirect effect *i.e*. PH, F%, HI, M% and LBR, while, at Una it possessed significant negative association through its direct effect and indirectly through HI, M% and LBR with the GYP. Similarly at Malan the significant negative correlation of NOT with GYP was chiefly through its negative direct effect and indirectly via PH, F% and LBR.

F% exhibited positive significant association with GYP at two locations. At Palampur primarily through its positive direct effect and indirectly via DM and TW, similarly at Malan through its direct effect and indirectly via DM, PH, NOT, M% and LBR. For HI significant positive as well as negative correlation with GYP was observed at four locations. at Sundernagar significant positive association of HI with GYP was revealed mainly through its direct effect as well as indirectly via the traits like PH and LBR, while at Dhaulakuan significant negative inter-relationship of HI was discovered via its direct effect and indirect effect through traits like NOT, TW and LBR with GYP. At Palampur significant positive correlation of HI was exhibited mainly through its direct effect and indirectly through NOT, M% and LBR, likewise at Malan the positive association was through its direct effect as well as indirectly via NOT and LBR.

Milling percentage (M %) proclaimed significant positive correlation with GYP at three locations. At Dhaulankuan the positive significant association was chiefly through its direct effect as well as indirectly via DM, PH and F%, likely at Una significant positive correlation was noticed via its direct effect and indirectly through DM, NOT, TW and LBR, whilst at Malan significant positive inter-relationship was seen via its direct effect and indirectly through NOT, HI, TW and LBR with GYP.

Length breadth ratio (LBR) possessed significant positive as well as negative association with GYP at four locations out of five locations. At Sundernagar the negative correlation was mainly through its direct effect and indirectly through PH, F% and HI, unlikely at Dhaulakuan the significant positive correlation was noticed via its indirect effects of traits like DM, PH, NOT, F% and M%, whereas at Palampur significant positive association of LBR was observed primarily through its direct effect and indirectly via PH, NOT and HI, however at Malan significant negative correlation was discovered its negative direct effect and indirectly through DM, PH, NOT, F% and HI.(Table 6).

Identifying the relationship between yield components using correlation is a crucial step (Akhtar *et al*., 2011), but isolating the influence of traits into direct and indirect effects by path analysis is more crucial for the selection of yield influencing traits (Dhavaleshvar *et al*., 2019). In individual environment, positive correlation for grain yield per plant was because of positive direct effects of concerned trait and also due positive value of indirect effect via concerned trait. In pooled environmental condition, the direct effect of days to 75 % maturity and fertility percentage reflects the real relationship with grain yield per plant causes of the positive correlation while the indirect effect of days to 75 % maturity via other traits mainly fertility percentage then harvest index and direct effect with of milling percentage were cause positive correlation with grain yield per plant. The same result was indicated for number of tillers per plant, in which the direct effect was negative and almost half to the negative correlation because of its indirect effects on grain yield per plant via other studied traits. These agree with the findings of other researchers (Harimansis *et al*., 2013 and Sarwar e*t al*., 2015). Our results of path analysis are in agreement with the findings of Bhutta *et al*. (2019), who revealed that the direct effect of days to maturity on grain yield was positive and greater therefore, this trait can be selected for further grain yield improvement in rice. Enhanced attention in the breeding program on days to 75 % maturity, fertility percentage and milling percentage as selection criteria is crucial to improve rice grain yield.

Our results obtained from thirty rice germplasms over five diverse locations of Himachal Pradesh showed sufficient genetic variability among all the studied traits. Grain yield per plant was positively and significantly correlated with days to 75 % maturity, plant height, and milling percentage. Path analysis indicated that the direct positive effects of the three traits were associated with positive correlations with the grain yield per plant. Since milling percentage showed low heritability with low genetic advance so that this can be neglected as selection criteria in this population however, recurrent selection or other population improvement method can be applied to improve heritability furthermore it can be considered as selectable trait of interest (Cobb *et al.*, 2019). In Malan location, traits days to 75 % maturity, harvest index, fertility percentage and milling percentage, in Sundernagar, traits plant height and harvest index, in Palampur location, harvest index, fertility percentage and length breadth ratio, in Una location, days to 75 % maturity and milling percentage while, in Dhaulakuan location, days to 75 % maturity and fertility percentage can be used as selection criteria. However, in pooled environments, days to 75 % maturity, plant height and milling percentage can be used as selection criteria to improve grain yield in rice genotypes.

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