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Study on Correlation and Path coefficient analysis for yield related traits in Ricebean (*Vigna umbellata*)

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ABSTRACT

Rice bean (*Vigna umbellata*) is a pulse crop, mainly grown in the kharif season. It is having potential to resist pest and diseases and also rich source of proteins and minerals. Twenty genotypes were evaluated to study the correlation and path analysis in the present research work. The experiment was conducted in crop research centre, ITM University, Gwalior, M.P. in kharif season 2022. Correlation analysis showed that seed yield per plot had positive and highly significant association between days to maturity, clusters per plant, number of pods per plant and hundred seed weight. The genotypic correlation results are slightly greater than the phenotypic path analysis. Path analysis of the present investigation revealed that the characters like number of seeds per pod exhibits positive and direct effect on the seed yield per plot at both genotypic and phenotypic level. Selection of these traits could be helpful in enhancing the seed yield.

Key words: *Seed yield, Correlation and Path analysis.*

Introduction

Rice bean [*Vigna umbellate* (Thunb.) Ohwi and Ohashi], 2n=2x=22 is also known as red bean, oriental bean and climbing mountain bean and it belongs to family *Fabaceae*. It is a kharif season crop having an average height of 30 cm to 100 cm and grown upto almost 200 cm. Flowers are yellow in colour and trifoliate leaves bearing 6 to 9 cm long leaflets. The temperature is ranging 18 to 37°C having annual rainfall 1500 to 2000 mm. It grows on all type of soils with having good drainage system. But avoid cultivation of ricebean crop in light soils as it causes root-knot nematodes problem to the crop. Sowing time of ricebean crop in the first to third week of july month. Depending on plant growth habit the spacing should be row to row 30 cm and plant to plant 15cm by sowing in the depth of 3 to 4 cm. Rice bean is a multipurpose legume which is used as fodder and young stage or after harvesting the seed the remaining stems, leafy portions and empty pods is used for concentrated feed for livestocks and seeds is used to make dal. It is also used for green manure crop and fences as vegetative barriers. Rice bean is having good amount protein is about 14-25%, 3-4% fat, 5-7% crude fibre, 61-67% carbohydrates, 11-12% aspartic acid, 17-18% glutamic acid. Production of ricebean crop is mostly in the areas of Indo-China, Southern China, Nepal, Bangladesh and India. In India it is grown in areas of Himachal Pradesh, Uttaranchal, Assam, Manipur, Meghalaya, Mizoram, Nagaland, Sikkim, Tripura, Madhya Pradesh and Chattisgarh.

Rice beans, a kind of grain legume, have several uses. They may be consumed, used as animal feed, or even composted for fertilizer. “Some of the most important sites in the North Eastern Region for cultivating rice bean in rain-fed circumstances include

the states of Assam, Meghalaya, Manipur, Mizoram, Arunachal Pradesh, and Nagaland, as well as the hill area of North Bengal and Sikkim". The distribution pattern of rice beans exhibits outstanding adaptive polymorphism for a broad variety of environments, with a range that encompasses humid tropical, sub-tropical, and sub-freezing regions. North Eastern India's 1.7 million acres of movable farmland are essential to elevating the region's farmers to a more stable economic footing (Sarma *et al.*, 1995). When it comes to rice beans, Nagaland is quite specific. It's wonderful and is known as Naga dal. As not enough land is being used for farming, yields and productivity are low compared to other types of agriculture. The majority of the harvest is stored for later consumption, but any surplus is sold at market when available. Rice beans are a staple food in the local diet, either cooked as dal or eaten raw as sprouts in salads. Yet, nothing has been done to improve this crop despite its immense potential. "Accurate measurement of genetic variability owing to genetic and non-genetic variables and other genetic features is necessary for the selection of better genotype for use in hybridization programmes to use in the development of enhanced varieties". The major goal of this research was to identify the role that environmental factors play in explaining the heritability of important economic traits across a range of rice bean genotypes cultivated under different settings (Shukla *et al.*, 2012).

Materials and Methods

The experiment was conducted by using randomized block design method with three replications during kharif season 2022-23. Total area was 139.5 square meters with sixty plots each genotype was accommodated in three blocks. The spacing of 12x30 cm was allocated. The intercultural operations were carried out during the crop duration. Randomly five plants selected in each plot for recording observations. The experimental material was collected from NBPGR, New Delhi. Path coefficient analysis was made Dewy and Lu (1959).

Results and Discussion

The findings of the research work was recorded for 10 characters like days to 50 percent flowering, days to maturity, stem thickness, pod length, clusters per plant, pods per cluster, number of pods per plant, number of seeds per pod, hundred seed weight, seed yield per plot.

Correlation coefficient analysis

Genotypic and Phenotypic coefficient of correlation

Table 1. Experimental material

S. No.	Genotypes	S. No	Genotypes
1	IC – 342220	11	IC – 361363
2	IC – 342238	12	IC – 361365
3	IC – 342372	13	IC – 362094
4	IC – 342375	14	IC – 521117
5	IC – 342376	15	IC – 521131
6	IC – 342379	16	IC – 551643
7	IC – 345658	17	IC – 551626
8	IC – 360608	18	IC – 551649
9	IC – 360616	19	IC – 551697
10	IC – 360622	20	IC – 551699

The resultant genotypic coefficient of correlation for seed yield per plot showed positive and highly significant association with days to maturity (0.368**), clusters per plant (0.589**), number of pods per plant (0.677**) and positively significant association with days to 50 percent flowering (0.327*). The resultant phenotypic coefficient of correlation for seed yield per plot showed positive and highly significant association clusters per plant (0.384**), number of pods per plant (0.363**) and positively significant association fordays to maturity (0.306*).

In the present investigation the values obtain in the genotypic coefficient of correlation was slightly greater than the phenotypic coefficient of correlation for all the significant characters except for the stem thickness values. Dodake *et al.* (2011) for the characters number of pods per plant, number of seeds per pod and pod length, Narasimhulu *et al.* (2013) in mungbean characters like number of pods per plant and number of seeds per pod. These were some of the similar observations.

Path coefficient analysis

Path analysis of present investigation revealed that the characters like number of seeds per pod (2.08323), days to maturity (1.44850), pods per cluster (1.10996), hundred seed weight (0.18752) exhibits positive direct effect on the seed yield per plot atgenotypic level. While, the characters like number of seeds per pod (0.47388), number of pods per plant

Table 2. Genotypic character association among yield and yield contributing traits in Rice bean

	DFF	DM	ST	CPP	PPC	PL	NPPP	NSPP	HSW	SYPP
DFF	1.000	0.9627**	0.093	0.194	-0.068	-0.408**	0.225	-0.538**	0.278*	0.327*
DM	0.9627**	1.000	0.164	0.368**	-0.092	-0.370**	0.358**	-0.481**	0.358**	0.368**
ST	0.093	0.164	1.000	-0.164	0.760**	0.392**	0.590**	0.319**	0.661**	0.098
CPP	0.194	0.368**	-0.164	1.000	-0.109	0.125	0.623**	0.129	0.397**	0.589**
PPC	-0.068	-0.092	0.760**	-0.109	1.000	0.369**	0.834**	0.175	0.489**	0.078
PL	-0.408**	-0.370**	0.392**	0.125	0.369**	1.000	0.401**	0.893**	-0.031	-0.089
NPPP	0.225	0.358**	0.590**	0.623**	0.834**	0.401**	1.000	0.317*	0.261*	0.677**
NSPP	-0.538**	-0.481**	0.319*	0.129	0.175	0.893**	0.317*	1.000	0.054	0.065
HSW	0.278*	0.358**	0.661**	0.397**	0.489**	-0.031	0.261*	0.054	1.000	0.341**
SYPP	0.327*	0.368**	0.098	0.589**	0.078	-0.089	0.677**	0.065	0.341**	1.000

* and ** Significant at 0.05 and 0.01 levels of probability, DFF: Days to 50% flowering, DM: Days to maturity, ST: Stem thickness, CPP: Cluster per plant, PPC: Pods per cluster, NPPP: Number of pods per plant, NSPP: Number of seeds per pod, PL: Pod length, HSW: 100 seed weight, SYPP: Seed yield per plot.

Table 3. Phenotypic character association among yield and yield contributing traits in Rice bean

	DFF	DM	ST	CPP	PPC	PL	NPPP	NSPP	HSW	SYPP
DFF	1.000	0.936**	0.071	0.141	-0.014	-0.289*	0.090	-0.397**	0.103	0.248
DM	0.936**	1.000	0.074	0.206	0.015	-0.246	0.104	-0.347**	0.152	0.306*
ST	0.071	0.074	1.000	0.068	0.355**	0.263*	0.259*	0.179	0.069	0.050
CPP	0.141	0.206	0.068	1.000	0.034	0.035	0.445**	0.046	0.148	0.384**
PPC	-0.014	0.015	0.355**	0.034	1.000	0.241	0.447**	0.039	0.157	0.079
PL	-0.289*	-0.246	0.263*	0.035	0.241	1.000	0.256*	0.861**	-0.016	-0.089
NPPP	0.090	0.104	0.259*	0.445**	0.447**	0.256*	1.000	0.200	0.076	0.363**
NSPP	-0.397**	-0.347**	0.179	0.046	0.039	0.861**	0.200	1.000	-0.005	-0.000
HSW	0.103	0.152	0.069	0.148	0.157	-0.016	0.076	-0.005	1.000	0.211
SYPP	0.248	0.306*	0.050	0.384**	0.079	-0.089	0.363**	-0.000	0.211	1.000

* and ** Significant at 0.05 and 0.01 levels of probability, DFF: Days to 50% flowering, DM: Days to maturity, ST: Stem thickness, CPP: Cluster per plant, PPC: Pods per cluster, NPPP: Number of pods per plant, NSPP: Number of seeds per pod, PL: Pod length, HSW: 100 seed weight, SYPP: Seed yield per plot.

(0.25721), clusters per plant (0.19722), days to maturity (0.14773), hundred seed weight (0.11021), days to 50% flowering (0.10015) and pods per cluster (0.05771) exhibits positive direct effect on the seed yield per plot at phenotypic level. The genotypic path coefficient analysis results showed positive and

Table 4. Genotypic path coefficient analysis among yield and yield contributing traits in Rice bean

	DFF	DM	ST	CPP	PPC	PL	NPPP	NSPP	HSW	SYPP
DFF	-0.37253	1.39452	-0.09769	-0.03536	-0.07511	0.58400	-0.00122	-1.12142	0.05216	0.327*
DM	-0.35865	1.44850	-0.07023	-0.07876	-0.14076	0.62014	-0.00169	-1.11880	0.04368	0.368**
ST	-0.03409	0.09528	-1.06761	0.03042	0.85087	-0.56414	-0.00321	0.66982	0.12394	0.098
CPP	-0.07223	0.62561	0.17806	-0.18237	-0.12091	-0.17835	-0.00337	0.26774	0.07452	0.589**
PPC	0.02521	-0.18370	-0.81841	0.01987	1.10996	-0.52779	-0.00452	0.36542	0.09176	0.078
PL	0.15202	-0.62766	-0.42084	-0.02273	0.40934	-1.43113	-0.00217	1.85955	-0.00576	-0.089
NPPP	-0.08391	0.45270	-0.63372	-0.11358	0.92587	-0.57417	-0.00541	0.66043	0.04893	0.677**
NSPP	0.20054	-0.77792	-0.34327	-0.02344	0.19470	-1.27747	-0.00172	2.08323	0.01008	0.065
HSW	-0.10363	0.33743	-0.70562	-0.07247	0.54314	0.04399	-0.00141	0.11197	0.18752	0.341**
Residual	0.4306									

* and ** Significant at 0.05 and 0.01 levels of probability, DFF: Days to 50% flowering, DM: Days to maturity, ST: Stem thickness, CPP: Cluster per plant, PPC: Pods per cluster, NPPP: Number of pods per plant, NSPP: Number of seeds per pod, PL: Pod length, HSW: 100 seed weight, SYPP: Seed yield per plot.

Table 5. Phenotypic path coefficient analysis among yield and yield contributing traits in Rice bean

	DFF	DM	ST	CPP	PPC	PL	NPPP	NSPP	HSW	SYPP
DFF	0.10015	0.13160	-0.00169	0.02778	-0.00080	0.14508	0.02302	-0.18806	0.01133	0.248
DM	0.08921	0.14773	-0.00099	0.05042	-0.00169	0.15075	0.02613	-0.19285	0.02109	0.306*
ST	0.00708	0.00613	-0.02393	0.01324	0.02048	-0.13313	0.06680	0.08619	0.00724	0.050
CPP	0.01410	0.03776	-0.00160	0.19722	0.00199	-0.01777	0.11438	0.02165	0.01627	0.384**
PPC	-0.00138	-0.00433	-0.00848	0.00681	0.05771	-0.12158	0.11500	0.01820	0.01736	0.079
PL	-0.02894	-0.04436	-0.00634	0.00698	0.01399	-0.50220	0.06587	0.40788	-0.00177	-0.089
NPPP	0.00896	0.01501	-0.00621	0.08773	0.02582	-0.12856	0.25721	0.09467	0.00837	0.363**
NSPP	-0.03975	-0.06013	-0.00435	0.00902	0.00222	-0.43212	0.05139	0.47388	-0.00056	-0.000
HSW	0.01030	0.02826	-0.00157	0.02912	0.00910	0.00808	0.01952	-0.00242	0.11021	0.211
Residual	0.6922									

* and ** Significant at 0.05 and 0.01 levels of probability, DFF: Days to 50% flowering, DM: Days to maturity, ST: Stem thickness, CPP: Cluster per plant, PPC: Pods per cluster, NPPP: Number of pods per plant, NSPP: Number of seeds per pod, PL: Pod length, HSW: 100 seed weight, SYPP: Seed yield per plot.

direct effect of the characters which are slightly greater than the phenotypic path coefficient values. Dodake *et al.* (2011) for the characters number of pods per plant, number of seeds per pod and pod length, Narasimhulu *et al.* (2013) in mungbean characters like number of pods per plant and number of seeds per pod were some of the similar studies with similar results.

Conclusion

In the present research work the findings that characters like days to maturity, clusters per plant, number of pods per plant and hundred seed weight showed positive highly significant correlation with seed yield per plot in genotypic level. Clusters per plant and number of pods per plant showed positive highly significant correlation with seed yield per plot in phenotypic level. These are helpful in selecting the combination of the characters in the genotypes.

The characters like days to maturity, pods per cluster, number of seeds per pod and hundred seed weight were the characters reported with positive and direct effect on seed yield per plot. Improving the characters mentioned above are useful in the future breeding programme.

Conflict of Interest- None

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