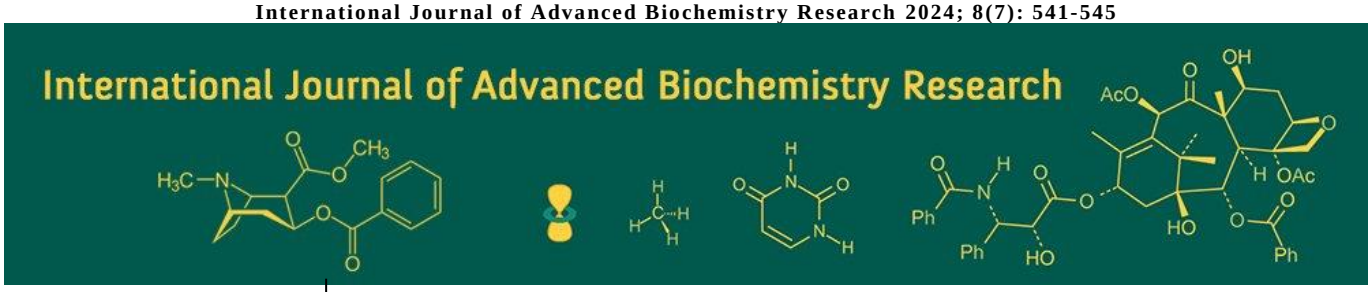

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S Prabakaran
Ph.D. Scholar, Division of Plant Genetic Resources, ICAR-Indian Agricultural Research Institute, New Delhi, India

R Sowmyapriya
Ph.D. Scholar, Division of Molecular biology and Biotechnology, ICAR-Indian Agricultural Research Institute, New Delhi, India

Veena Gupta
Principal scientist, Division of Germplasm Conservation, ICAR-National Bureau of Plant Genetic Resources, New Delhi, India

Corresponding Author:
S Prabakaran
Ph.D. Scholar, Division of Plant Genetic Resources, ICAR-Indian Agricultural Research Institute, New Delhi, India

Correlation and path coefficient analysis of yield and its component traits among different accessions of the tribal pulse, *Abrus precatorius* L

S Prabakaran, R Sowmyapriya and Veena Gupta

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Abstract
The Genebank of National Bureau of Plant Genetic Resources (NBPGR) conserves 152 accessions of Jequirity bean. Experimental trials were conducted with 99 accessions (95 entries + 4 checks) at two locations i.e. Issapur farm of NBPGR (Located at south west Delhi) and NBPGR regional station, Ranchi. The data was recorded using the minimal descriptors developed by NBPGR. The experimental design used was Augmented Block Design (ABD). After correlation analysis, it was observed the association between the morphological traits viz. number of inflorescence per plant (NIF_P) and number of pod cluster per plant (NPC_P) and also between days to flower initiation (DFI) and days to complete pod maturity (DM) was highly significant and with very strong positive correlation. Based on the path coefficient analysis, it was noted that the effect of number of pods per cluster (NP_C), number of pod cluster per plant (NPC_P) and number of seeds per pod (NS_P) over the dependent variable seed yield per plant (SYP) was high. Selection for these traits by a plant breeder will result in the yield improvement of Jequirity bean.

Keywords: Jequirity bean, tribal pulse, *Abrus precatorius*, correlation, regression analysis

Introduction
The tribal population of the world consumes foods which were unique depending on the region where they inhabit and markedly different from rest of the population. *Abrus precatorius* L. was commonly known as Jequirity bean, belongs to the family fabaceae (Prenner *et al*., 2013) [1]. The boiled seeds of Jequirity bean were consumed for protein source by the Onges tribe of Andaman and Nicobar. It was reported that the seeds were rich in almost all the amino acids which were essential to humans except threonine and cysteine (Rajaram *et al*., 1992) [2]. In the African region, the leaves of *Abrus precatorius* subsp. *africanus* was used as vegetable (Tchatchouang *et al*., 2017) [3]. The seed contains highly toxic albuminous protein, abrin and other antinutritional factors which will cause lethality in humans on raw consumption (Dickers *et al*., 2003) [4]. Various techniques to detoxify the seeds were mentioned in the ancient texts of India (Roy *et al*., 2012; Mansi *et al*., 2011; Brave *et al*., 2013) [5-7]. The plant was also known for its medicinal value in Ayurvedic, Siddha and Unani system of medicine (Chakradhari *et al*., 2019) [8]. Its seed was traditionally used for weighing the precious stones and gold (Boddupalli *et al*., 2020) [9]. The plant was reported to have various therapeutic properties like antihelmintic activity, anti-malarial activity, anti-diabetic activity and nephroprotective activity (Molgaard *et al*., 2001; Menan *et al*.,2006; Globade *et al*., 2009; sohn *et al*.,2009) [10-13]. Despite the crop was native to India, no earlier work was conducted with respect to its morphological characterization.

Materials and Methods
1. Source of experimental material
The Indian National Genebank of National Bureau of Plant Genetic Resources (NBPGR), New Delhi conserves 152 Jequirity bean accessions. All those accessions were Indigenous collections (IC). From this, 99 accessions (95 entries + 4 checks) were chosen on the basis of availability of required seed quantity and seed viability (%). IC0306236, IC376080, IC0469931 and IC0418097 were grown as checks. The field trial experiment was conducted

by raising crops at two sites i.e. Issapur farm of NBPGR (Located at south west Delhi) and NBPGR regional station, Ranchi.

2. Experimental Design

The plants were raised as a sole crop at Issapur farm whereas at Ranchi station it was intercropped with Bael (*Aegle marmelos*). In the Genebank, only limited quantities of seeds were available. To overcome such constraints, Augmented Block Design (ABD) was chosen as the experimental design. NBPGR minimal descriptors were used for characterizing those accessions and set of 14 quantitative traits were recorded in both the locations. These traits were listed in the Table 1.

Table 1: List of quantitative traits and their corresponding code used in the characterization of 95 accessions of Jequirity bean.

Code used	Quantitative traits
DFI	Days to flower initiation
IL	Inflorescence length (cm)
NIF_P	Number of inflorescence / plant
NF_IF	Number of Flowers / inflorescence
DM	Days to complete pod maturity
NP_C	Number of pods / cluster
NPC_P	Number. of pod cluster / plant
PL	Pod length (cm)
PW	Pod width (cm)
NS_P	Number of seeds / pod
SL	Seed length (mm)
SW	Seed width (mm)
1000SW	1000 seed weight (g)
SYP	Seed yield per plant (g)

3. Statistical analysis

The correlation study, regression and path coefficient analysis (the effect of various traits on yield) were done by using the software R studio version 3.3.2. The scale used in the correlation and regression study was based on Searle (1965) and Lenka and Mishra (1973) [14, 15].

Results and Discussion

1. Correlation study

The result of correlation analysis was shown in Table 2 and Figure 1. The scale used in the analysis was based on Searle (1965) [14]. From the results, it was observed that the association between number of inflorescence per plant (NIF_P) and number of pod cluster per plant (NPC_P) was highly significant, very strong and positive relation. Similarly, there exists highly significant, very strong positive association was found between days to flower initiation (DFI) and days to complete pod maturity (DM). Significant moderately strong positive association was found between pod length (PL) and pod width (PW) and also between number of pods per

Table 2: Correlation coefficient among different quantitative traits in *Abrus precatorius* (L.)

X1000SW													0.171
SW												0.119	-0.102
SL											0.353	0.268	-0.120
NS_P										0.036	-0.180	0.005	0.451
PW									-0.012	-0.108	0.003	-0.194	-0.119
PL								0.520*	-0.136	-0.047	-0.041	-0.186	-0.081
NPC_P							-0.060	0.022	-0.075	-0.108	-0.072	-0.023	0.291
NP_C						-0.151	0.057	-0.159	-0.272	-0.118	0.064	0.072	0.540*
DM					0.007	-0.141	0.044	0.175	-0.083	-0.126	-0.075	-0.080	-0.034
NF_IF				0.068	0.326	0.064	0.115	0.101	-0.052	0.023	-0.046	-0.022	0.201
NIF_P			-0.039	0.012	-0.183	0.878**	-0.114	-0.025	0.026	-0.131	-0.166	-0.056	0.281
IL		0.007	0.028	-0.138	0.025	-0.003	0.094	-0.091	0.019	0.007	-0.181	0.032	0.007
DFI	-0.197	0.023	0.007	0.866**	-0.019	-0.106	0.067	0.146	-0.034	-0.088	-0.013	-0.037	0.024
	IL	NIF_P	NF_IF	DM	NP_C	NPC_P	PL	PW	NS_P	SL	SW	X1000SW	SYP

cluster (NP_C) and seed yield per plant (SYP). All the remaining associations were non-significant and very weak or moderately weak. Lekshmanan and Vahab (2018) have observed that seed yield was having positive association with pod length, pod weight, pod girth, plant height, pods per plant,100 seed weight, pod cluster per plant and shelf life in Cluster bean [*Cyamopsis tetragonoloba* (L.)]. Ahmad and Belwal (2020) have observed that the seed yield was having highly significant and positive association with number of branches, number of pods per plant, seed density, pod diameter, pod wall thickness, pod length, seed diameter, 100 seed weight, seed length, number of cluster, plant height and number of leaves in Mungbean [*Vigna radiata* (L.)].

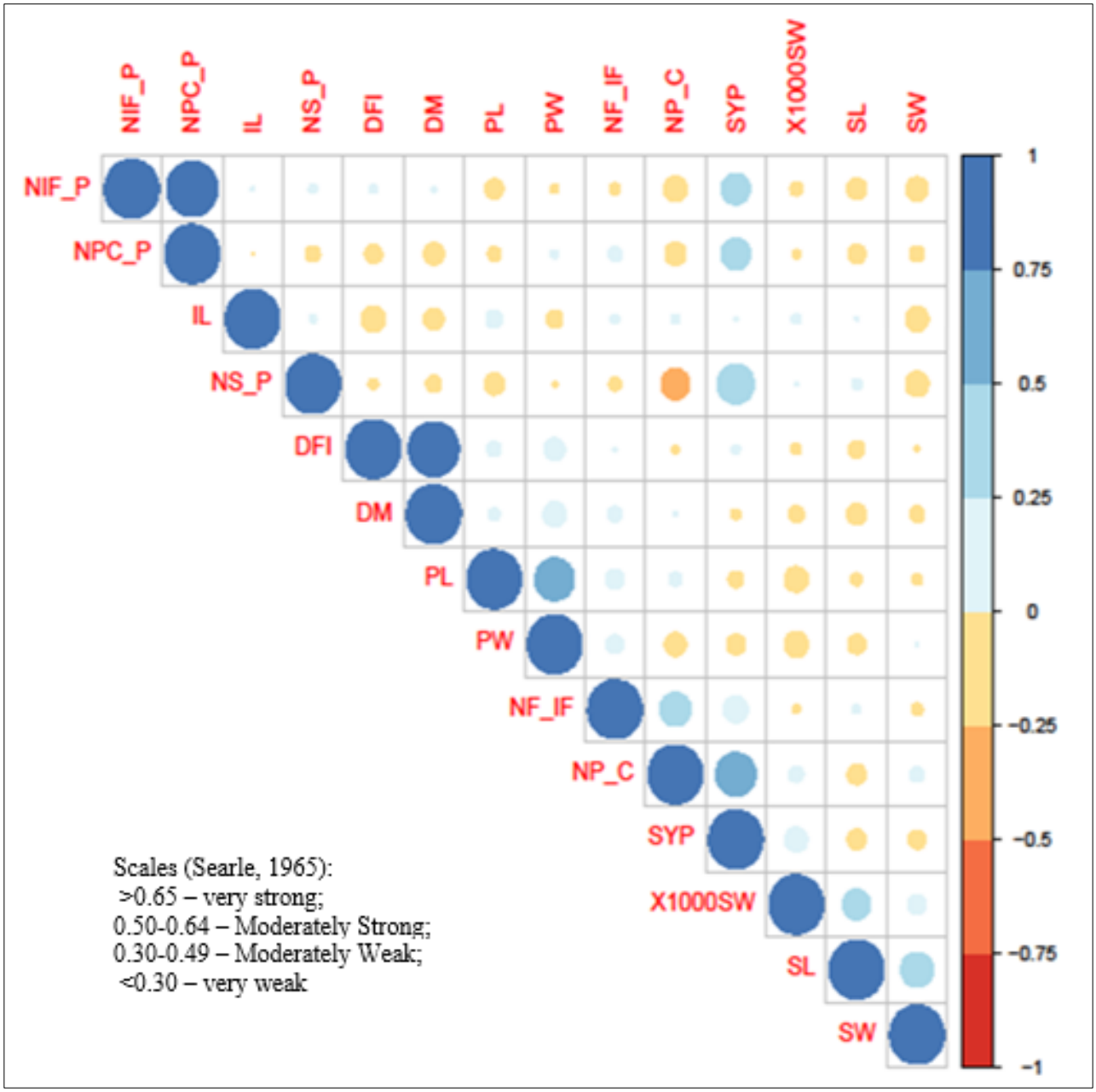

Fig 1: Correlogram depicting the association between various quantitative traits in *Abrus precatorius* (L.)

2. Regression analysis

The result of regression analysis was represented in Table 3. In the analysis, seed yield per plant (SYP) was considered as dependent variable and all the other quantitative traits were considered as independent variable. The residual effect of 0.3124 indicated that the traits accounted for 68.76% to the variability in seed yield per plant. It shows that few other traits which were not studied in this study should be included in the analysis to account fully for the variation in seed yield per plant. It was observed that the effect of variables like number of pods per cluster (NP_C), number of pod cluster per plant (NPC_P) and number of seeds per pod (NS_P) over the seed yield per plant (SYP) was highly significant and the effect was positive and high. Whereas the effect of 1000 seed weight (1000SW) on the seed yield per plant (SYP) was highly significant but low. The effect of all the remaining traits over the seed yield per plant (SYP) was non-significant.

The result of path coefficient analysis was displayed in figure 2. The scale used in this analysis was based on Lenka and Mishra (1973) [15]. The thickness of the arrow depicts the amount of effect over the seed yield per plant (SYP). It was observed that the effect of number of pods per cluster (NP_C), number of pod cluster per plant (NPC_P) and number of seeds per pod (NS_P) over the dependent variable seed yield per plant (SYP) was high. The remaining traits have low or negligible effect over the seed yield per plant (SYP). Based on path coefficient analysis, Lekshmanan and Vahab (2018) [16] reported in cluster bean that pod clusters per plant, pod length, plant height and pods per plant were the important traits that influence pod yield. Similarly, Ahmad and Belwal (2020) [17] mentioned that the traits 100 seed weight and number of pods per plant were having maximum effect on seed yield in Mungbean.

Table 3: Regression analysis of various independent variables over the dependent variable i.e. seed yield per plant (SYP)

	Estimate	Std. Err.	z-value	P(>|z|)
Seed yield per plant (g):(Dependent variable)				
Days to flower initiation	0.128	0.060	2.151	0.032
Inflorescence length (cm)	-0.004	0.030	-0.143	0.886
No. of inflorescence / plant	-0.065	0.068	-0.958	0.338
No. of Flowers / inflorescence	-0.067	0.033	-2.051	0.040
Days to complete pod maturity	-0.005	0.062	-0.088	0.930
No. of pods / cluster	0.820**	0.034	24.012	0.000
No. of pod cluster / plant	0.544**	0.069	7.872	0.000
Pod length (cm)	0.012	0.036	0.323	0.746
Pod width (cm)	0.014	0.036	0.371	0.711
No. of seeds / pod	0.716**	0.032	22.432	0.000
Seed length (mm)	-0.016	0.033	-0.478	0.632
Seed width (mm)	-0.010	0.033	-0.299	0.765
1000 seed weight (g)	0.131**	0.031	4.259	0.000

***** Significant at 5% level of significance; ****** Significant at 5% level of significance; Residual effect = 0.3124.

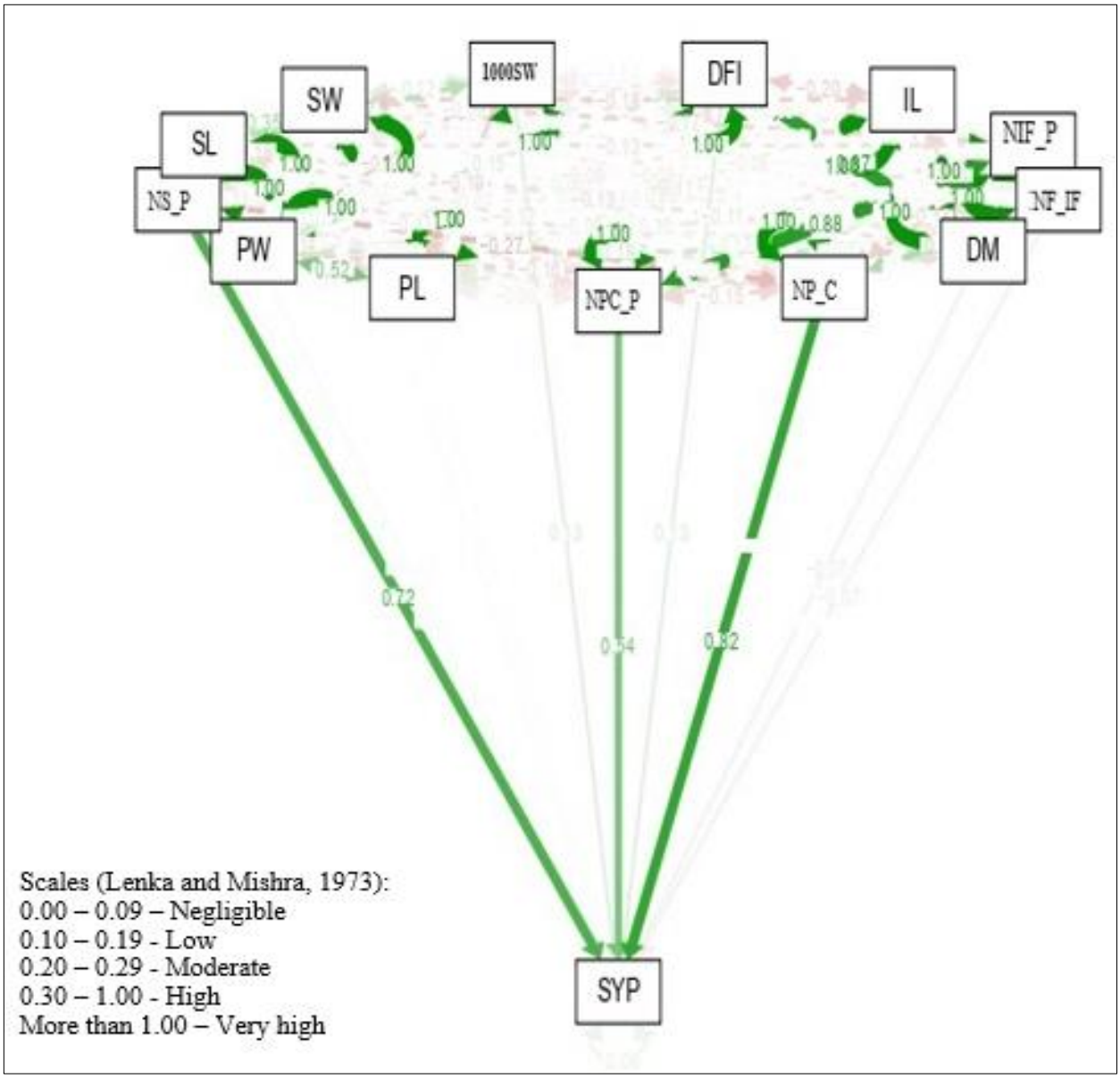

Fig 2: Path analysis depicting the effect of various independent variables over the dependent variable i.e. seed yield per plant (SYP)

Conclusion

Positive correlation between desirable traits was favorable to a breeder because it paves way for the simultaneous improvement of both the traits. The improvement in one trait will result in the improvement of correlated trait also. Based on the regression and path coefficient analysis, selection for traits like number of pods per cluster, pod cluster per plant and number of seeds per pod (independent variable) will help in yield improvement (dependent variable). Hence, a plant breeder can make selection of these morphological traits to increase the yield of Ratti genotypes.

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Conflict of Interest
All authors declare that there is no conflict of interest. The co-author have seen an agreement with the contents of the manuscript and we certify that the submission is original work and is not under review at any other publication.

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