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CORRELATION AND PATH ANALYSIS FOR YIELD AND ITS ATTRIBUTING TRAITS IN PIGEONPEA [*CAJANUS CAJAN* (L.) MILL SP.]

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ABSTRACT

Tasar silkworm *Antheraea mylitta* (D.) wild sericigenous insect which produces tropical tasar silk. It reared outside in wild conditions which attracts lots of pests and predators and among them, predatory wasps have become more significant over the past 3-4 years and have been observed in major tasar growing areas like Bankura and Patel Nagar (Suri) in West Bengal, Kathikund, Dumka, and Kharsawan in Jharkhand, as well as Baripada region in Odisha. The major predatory wasps of tasar silkworm are *Polistes olivaceus*, *P. stigma*, and *P. strigosus*. They are among the commonly observed species in the tasar ecosystem, and they pose a substantial threat to the well-being of the tasar silkworm if left uncontrolled. The *Polistes* wasps are social insects that reside in colonies comprising drones, workers, and egg-laying queens. They construct paper nests using wood fibers or coarse, papery materials and communicate through the use of pheromones. *Polistes* wasps exhibit remarkable efficiency and intelligence as versatile predators, covering long distances to find prey and employing a combination of hovering and walking on plants to locate their quarry. They are attracted to plants emitting frass odours and those that have been subjected to herbivore-induced damage. The article provides an overview of the management and challenges associated with controlling predatory wasps in tasar sericulture and it is concluded by emphasizing the need for further research to develop effective management strategies for controlling predatory wasps in tasar sericulture.

Keywords: Tasar silkworm, Predatory wasps, Behaviour and Hibernation

Introduction

Pigeonpea [*Cajanus cajan* (L.) Mill sp.] is a multiusage legume crop and is well adapted even in surplus lands (Joshi *et al.*, 2009). It has been acknowledged as a great source of vegetarian protein especially in developing countries like India where majority of the population depends on the affordable vegetarian foods. Pigeonpea plays a vital role in vegetarian diet as its seeds constitute protein (21–28%), vitamins, and mineral elements such as phosphorus (0.56-0.72 %), zinc (2.3- 2.5%), potassium and magnesium and it is also a good source of carbohydrate (57.3 - 58.7%), crude fibers (1.2 - 8.1%) and lipid (0.6 – 3.8%) (Phatak *et al.*, 1993). Pigeonpea

seeds provide crucial amino acids like lysine, tyrosine and arginine, whereas cystine and methionine contents are low (Saxena *et al.*, 2010).

According to FAO statistics (2019), worldwide pigeonpea is cultivated in about 4.5 million hectares area yielding approximately 3.68 million tons with an average yield of 832 kg/ha. Despite the substantial area under pigeonpea, productivity across the world is low and slacking as compared to other cereals. This low productivity can be attributed to the lack of effective selection indices for yield improvement while selecting parents for varietal development. Yield is a polygenic character and is the outcome of the direct or indirect association of several component characters. It is

significantly impacted by the environment and has a low heritability in general (Luz *et al.*, 2011; Mukherjee *et al.*, 2016). Since direct selection for yield is less efficient, improvement in contributing traits is imperative. Knowledge of the extent and nature of association among yield and yield contributing traits are important for efficient selection for yield improvement (Baye *et al.*, 2020; Gaur *et al.*, 2020). Thus, through correlation and path coefficient analysis, it would be possible to illuminate the most important characters that would aid in attaining progress under selection.

The objective of the present studies was to study the association of different yield attributing traits and their relative level of correlation with the yield that facilitates breeder to select superior high yielding genotype.

Materials and Methods

The experimental materials include 43 germplasm lines along with six checks (C.G. Arhar-2, BDN-716, CORG-9701, UPAS-120, PT-0012 and KRG-33); for alpha lattice with 2 replications in *kharif* 2022-23, obtained from AICRP on pigeonpea, Department of Genetics & Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur. The observation was recorded on five arbitrarily selected plants in each plot for the traits *viz.*, days to 50% flowering, numbers of flowers at 50 % flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, number of pods per cluster, number of seeds per pod, 100 seed weight (g), days to 1st pod formation, days to 100 % pod formation, seed yield per plant (g).

The phenotypic correlation coefficient was computed using the formula proposed by Singh and Chaudhary, 1979. the path coefficient analysis was conducted as delineated by Dewey and Lu (1959).

Results and Discussion

Correlation between seed yield per plant and other traits were conferred in table 1 for forty- nine genotypes at genotypic and phenotypic level proportionately. Seed yield per plant showed high significant and positive correlation with number of pods per plant (0.694, 0.697) followed by number of branches per plant (0.463, 0.465) and 100 seed weight (0.394, 0.393). Significant and positive correlation with number of seeds per pod (0.298, 0.296) and number of flowers at 50 % flowering (0.238, 0.236) whereas, highly significant and negative correlation with days to 50 % flowering (-0.343, 55 -0.345) and significant and negative correlation with days to 1st podding (-0.269, -0.270) at genotypic and phenotypic

level respectively. The seed yield per plant showed highly significant and positive association with number of pods per plant, number of branches per plant and hundred seed weight.

Kandarkar *et al.*, (2020), Tharageshwari *et al.*, (2020), Chauhan *et al.*, (2021), Devi *et al.*, (2020), Narayan *et al.*, (2018), Meena *et al.*, (2017), Singh and Singh (2016), Pushpavalli *et al.*, (2015), Birhan *et al.*, (2013) and Syamala *et al.*, (2019) proclaimed the similar results for trait number of pods per plant. Kandarkar *et al.*, (2020), Meher *et al.*, (2020), Devi *et al.*, (2020), Pushpavalli *et al.*, (2015) and Syamala *et al.*, (2019) had similar findings for trait number of branches per plant.

Chauhan *et al.*, (2021), Meena *et al.*, (2017) and Pushpavalli *et al.*, (2015) corroborated same results for hundred seed weight. Kandarkar *et al.*, (2020), Chauhan *et al.*, (2021) and Syamala *et al.*, (2019) found similar results for number of seeds per pod. Meena *et al.*, (2017) corroborated same results for days to 50 % flowering.

Path coefficient analysis was performed to determine the direct and indirect contribution of different traits towards seed yield per plant. The results were given in Table 2. Residual effect was recorded to be 0.232, which indicated that the characters under study were devoted to 76.8 % of total variation. Hence, selection on these studied characters might be useful in genetic improvement for yield. Path coefficient analysis revealed maximum positive direct effect was obtained for number of pods per plant (0.555) followed by 100 seed weight (0.214), number of branches per plant (0.098). Days to 100% podding (0.060) and number of seeds per pod (0.0126) had positive and negligible direct effect on seed yield per plant. Whereas, negative direct effect was obtained *via* days to 50% flowering (-0.143), number of pods per plant (-0.083), days to 1st podding (-0.074), plant height (-0.071). Negative and negligible direct effect on seed yield per plant was obtained by number of flowers at 50% flowering (-0.053) and days to maturity (-0.008).

Similar research proofs were discussed by Kandarkar *et al.*, (2020), Chauhan *et al.*, (2021), Rajamani *et al.*, (2022), Tharageshwari *et al.*, (2020), Devi *et al.*, (2020) and Narayan *et al.*, (2018) for trait number of pods per plant. Meher *et al.*, (2020), Rajamani *et al.*, (2022) corroborated similar findings for hundred seed weight. Meher *et al.*, (2020) Rajamani *et al.*, (2022) Devi *et al.*, (2020) and Kandarkar *et al.*, (2020) found alike results for trait number of branches per plant.

Devi *et al.*, (2020) corroborated similar results for trait days to 50 % flowering. Meher *et al.*, (2020) found similar results for number of pods per plant. Kandarkar *et al.*, (2020) and Narayan *et al.*, (2018) found similar contribution of trait plant height. Kandarkar *et al.*, (2020) Narayan *et al.*, (2018) found similar results for trait days to maturity.

Significant and positive correlation along with positive direct effect with seed yield per plant was exhibited by traits such as number of pods per plant followed by number of branches per plant, 100 seed weight and number of seeds per pod. It signifies strong association between them and these traits should be prioritized while breeding for increment in seed yield per plant (g).

Table 1 : Genotypic and phenotypic correlation analysis for yield and its attributing traits in pigeonpea [*Cajanus cajan* (L.) Mill sp.]

Characters		DTM	DTFP	DTHP	NFFF	PH	NBP	NPP	NPC	NSP	HSW	SYP
DFF	G	0.474**	0.551**	0.568**	-0.423**	0.401**	-0.611**	-0.269*	-0.0808	0.1775	0.0817	-0.343**
	P	0.476**	0.551**	0.568**	-0.425**	0.408**	-0.611**	-0.268*	-0.0800	0.1749	0.0791	-0.345**
DTM	G		0.333**	0.478**	-0.312*	0.339**	-0.203*	0.0003	-0.0659	0.260*	0.321*	-0.0215
	P		0.335**	0.479**	-0.311*	0.335**	-0.205*	-0.0015	-0.0672	0.267*	0.326*	-0.0196
DTFP	G			0.528**	-0.425**	0.379**	-0.483**	-0.235*	-0.1460	0.1511	0.1128	-0.269*
	P			0.528**	-0.427**	0.385**	-0.483**	-0.234*	-0.1455	0.1490	0.1109	-0.270*
DTHP	G				-0.439**	0.547**	-0.611**	-0.1195	-0.1653	0.327*	0.309*	-0.1220
	P				-0.439**	0.550**	-0.612**	-0.1198	-0.1655	0.329**	0.311*	-0.1219
NFFF	G					-0.1721	0.491**	0.344**	0.240*	0.0178	-0.0449	0.238*
	P					-0.1689	0.494**	0.346**	0.241*	0.0138	-0.0484	0.236*
PH	G						-0.368**	0.1207	0.0704	0.389**	0.241*	-0.0357
	P						-0.375**	0.1175	0.0682	0.406**	0.253*	-0.0317
NBP	G							0.507**	0.1780	0.0214	0.0389	0.463**
	P							0.507**	0.1772	0.0257	0.0423	0.465**
NPP	G								0.1504	0.472**	0.341**	0.694**
	P								0.1497	0.478**	0.345**	0.697**
NPC	G									0.0300	-0.0109	0.0113
	P									0.0327	-0.0089	0.0122
NSP	G										0.333**	0.298*
	P										0.328**	0.296*
HSW	G											0.394**
	P											0.393**

Table 2 : Path coefficient analysis matrix of direct and indirect effects of seed yield and its attributing traits in pigeonpea [*Cajanus cajan* (L.) Mill sp.]

S. No.	Characters	DFF	DTM	DTFP	DTHP	NFFF	PH	NBP	NPP	NPC	NSP	HSW	Correlation with SYP
1.	DFF	-0.1431	-0.0677	-0.0789	-0.0812	0.0605	-0.0574	0.0875	0.0385	0.0116	-0.0254	-0.0117	-0.343**
2.	DTM	-0.0038	-0.0080	-0.0027	-0.0038	0.0025	-0.0027	0.0016	0.0000	0.0005	-0.0021	-0.0026	-0.0215
3.	DTFP	-0.0412	-0.0249	-0.0748	-0.0395	0.0318	-0.0284	0.0361	0.0175	0.0109	-0.0113	-0.0084	-0.269*
4.	DTHP	0.0345	0.0290	0.0320	0.0607	-0.0266	0.0332	-0.0371	-0.0073	-0.0100	0.0198	0.0188	-0.1220
5.	NFFF	0.0225	0.0166	0.0226	0.0234	-0.0533	0.0092	-0.0262	-0.0183	-0.0128	-0.0009	0.0024	0.238*
6.	PH	-0.0285	-0.0240	-0.0269	-0.0388	0.0122	-0.0710	0.0261	-0.0086	-0.0050	-0.0276	-0.0171	-0.0357
7.	NBP	-0.0604	-0.0200	-0.0477	-0.0604	0.0486	-0.0363	0.0988	0.0501	0.0176	0.0021	0.0038	0.463**
8.	NPP	-0.1494	0.0002	-0.1305	-0.0664	0.1912	0.0671	0.2820	0.5559	0.0836	0.2621	0.1896	0.694**
9.	NPC	0.0067	0.0055	0.0121	0.0137	-0.0199	-0.0059	-0.0148	-0.0125	-0.0831	-0.0025	0.0009	0.0113
10.	NSP	0.0022	0.0033	0.0019	0.0041	0.0002	0.0049	0.0003	0.0059	0.0004	0.0126	0.0042	0.298*
11.	HSW	0.0175	0.0686	0.0242	0.0662	-0.0096	0.0517	0.0083	0.0730	-0.0023	0.0714	0.2141	0.394**

Residual = 0.232

1. DFF = Days to 50% flowering
2. DTM = Days to maturity
3. DTFP = Days to first podding

4. DTHP = Days to 100% podding
5. NFFF = No. of flowers at 50% flowering
6. PH = Plant height

7. NBP = No. of branches per plant
8. NPP = No. of pods per plant
9. NPC = No. of pods per cluster

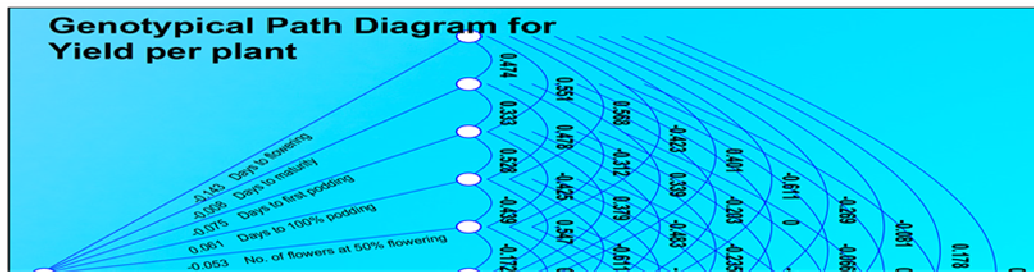


Fig. 1 : Path diagram showing effects of independent traits on seed yield per plant

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