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Assessment of pigeonpea seed traits for resistance to podfly, *Melanagromyza obtusa* (Malloch)

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Abstract

Assessment of pigeonpea seed traits for resistance to podfly, *Melanagromyza obtusa* in pigeonpea was studied at Regional Agricultural Research Station, Lam, Guntur, Andhra Pradesh during *kharif*, 2016. The study revealed that, test weight, seed length, seed width, no. of seeds damaged per pod and protein content had a significant positive correlation with podfly infestation. Whereas, phenol content had a significant negative correlation with podfly infestation. Therefore, these traits can be used as phenotypic and biochemical markers to identify pigeonpea genotypes with resistance to *M. obtusa*, and use in podfly resistance breeding program.

Keywords: *Melanagromyza obtusa*, phenols, pigeonpea, proteins and test weight

1. Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is one of the major grain legumes in the semi-arid tropics (SAT) (Nene and Sheila 1990) ^[10]. It provides a significant proportion of the daily protein requirements of people living in the SAT. It is grown in over 50 countries in Asia, East and southern Africa, and the Caribbean for food, fodder, fuel wood, rearing lac insects, hedges, windbreaks, soil conservation, green manuring, and roofing (Sharma *et al.* 2003) ^[15]. Yields of pigeonpea in the farmer's fields have become stagnant for the past four decades, largely because of insect pest damage. More than 200 insect species have been reported to feed on pigeonpea from germination to harvest, of which podfly, *Melanagromyza obtusa* (Malloch) (Agromyzidae: Diptera) is one of the most important yield reducing factors (Shanower *et al.* 1999) ^[14]. It causes an average of 34.5% pod damage, which in turn results in 29.8% grain loss (Srivastava 1972) ^[17]. The losses due to podfly damage have been estimated to be US\$ 256 million annually (ICRISAT 1992) ^[5].

Podfly being an internal feeder, both maggot and pupal stages are present inside the pods. The maggots feed on the developing seed and pupate inside the pod, thus making it unfit for human consumption as well as seed purpose. The podfly infested pods do not show any external symptom of damage until the fully grown maggot chew the pod wall, leaving a thin papery membrane intact called as window, through which adults exit from the pod. The podfly attack remains unnoticed by farmer owing to the concealed mode of life with in the pods and thus it becomes difficult to manage the pest in time. It is an emerging constraint to increase the production and productivity of this crop under subsistence farming conditions. Thus, identification and development of podfly resistant cultivars will provide an equitable and environmentally sound tool in the sustainable management of this insect pest. The morphological and biochemical traits can be used as markers to identify the resistance source against podfly to be used in breeding programme. Therefore, the present investigation was conducted to study the influence of seed characters on the incidence of podfly (*Melanagromyza obtusa*) in pigeonpea.

2. Materials and Methods

A field experiment was conducted with 14 pigeonpea genotypes at Regional Agricultural Research Station, Lam, Guntur, Andhra Pradesh during *kharif*, 2016 in a randomized block design with three replications. Each germplasm accession was accommodated in two rows each of 4 m length. After receipt of sufficient rains, sowing was taken up by adopting 1.8 × 0.2 m inter and intra row spacing, respectively.

Normal agronomic practices were followed for raising the crop. No insecticide was applied in the experimental plots. To identify the component traits associated with resistance to podfly damage, a number of morphological characters (test weight, seed length, seed width, no. of seeds per pod and no. of seeds damaged per pod) and biochemical constituents (phenols, proteins and sugars) of seeds were studied under laboratory conditions.

2.1 Morphological Characters

2.1.1 Test weight (g): A random sample of one hundred healthy, clean, whole dry, well developed seeds from each genotype were counted and weighed per replication.

2.1.2 Seed length and width (mm): Measurement on length and width of seeds was taken with vernier calipers on 10 seeds of each genotype per replication.

2.1.3 Number of seeds per pod: The average number of seeds on ten fully developed, mature, undamaged pods taken at random from each selected plant per replication.

2.1.4 Number of seeds damaged per pod: Ten fully developed, mature pods were taken at random from each genotype and the no. of seeds damaged per pod was recorded per replication and the average value was taken.

2.2 Biochemical Constituents

To study the biochemical constituents, seeds (30 days after opening of the flowers) were selected from previously tagged plants of each replication separately. Such seeds were kept separately in brown paper bags. The seeds were dried in an oven at 60°C for 2–3 days. The dried sample was ground in an electric blender. The ground samples were taken in brown paper bags and kept in oven at 50°C for 1 day to ensure complete drying of the samples. The completely dried sample was used for the estimation of biochemical constituents. The phenol content was estimated as per the method developed by Malick and Singh (1980) [8]. The protein content was estimated as per the method developed by Lowry *et al.* (1951) [7]. Estimation of sugars was done as per the method developed by Hedge and Hofreiter (1962) [4].

3. Results and Discussion

Data on various morphological characters, biochemical constituents and their correlation with pod and grain damage are presented in Table 1.

3.1 Test weight (g): The differences in test weight of the genotypes were significant, which varied from 9.30 g (CO 6) to 12.90 g (ICPL 87119) with a mean of 11.22 g (Table 1). Correlation studies between test weight and podfly infestation resulted a positive relationship, suggesting that the genotypes having bolder seeds with high test weight were more prone to the damage by podfly. However, the effects were significant with pod damage with correlation coefficient value (r) 0.536, whereas the effects were non-significant with grain damage with correlation coefficient value (r) 0.498. The findings were in agreement with Reddy *et al.* (1990) [12], Devi *et al.* (2015) [1] and Revathi *et al.* (2016) [13] who reported that the pigeonpea cultivars with bolder seeds suffered more damage than the small seeded ones due to podfly *i.e.*, positive correlation with test weight.

3.2 Seed length and width (mm): The length and width of

seeds in different genotypes varied significantly from 5.41 mm (WRP 1) to 6.89 mm (ICPL 87119) and 4.63 mm (CO 6) to 5.85 mm (GRG 2013), respectively (Table 1). Seed length and width showed significant positive correlation with podfly infestation. Correlation coefficient value (r) for seed length is 0.620 with pod damage and 0.583 with grain damage. With regard to seed width, correlation coefficient value (r) is 0.648 with pod damage and 0.666 with grain damage. The present finding was in accordance with Durairaj (1999) [3] who reported positive association with grain length and width.

3.3 Number of seeds per pod: Results achieved on number of seeds per pod revealed that their number ranged between 3.63 (BRG 10-2) to 4.07 (LRG 52) with a mean of 3.90 (Table 1). The differences in number of seeds per pod among all the genotypes were found to be non-significant. The relationship between number of seeds per pod and the damage due to podfly showed a non-significant negative correlation with r = -0.325 with pod damage and r = -0.353 with grain damage. It indicates that pods with more no. of seeds suffered less damage due to podfly. The results were in agreement with findings of Durairaj (1999) [3], Devi *et al.* (2015) [1] and Revathi *et al.* (2016) [13] who showed that genotypes having more number of grains per pod had less pod damage.

3.4 Number of seeds damaged per pod: Data recorded on number of seeds damaged per pod showed significant difference among the tested genotypes varying from 0.14 (ICPHaRL 4985-10) to 1.07 (GRG 2013) with a mean of 0.42 damaged seeds per pod (Table 1). The correlation studies showed highly significant positive correlation between number of seeds damaged per pod and podfly infestation in terms of both pod damage (r = 0.947) and grain damage (r = 0.958). These findings were in similar lines with Devi *et al.* (2015) [1] and Revathi *et al.* (2016) [13] who reported positive correlation with podfly infestation.

3.5 Phenols (mg/g): Phenol content in different pigeonpea genotypes varied from 3.62 (Guliyal Local (Red)) to 13.71 mg/g (ICP 11957) with an average of 7.16 mg/g (Table 1). Phenol content showed significant negative correlation with podfly infestation indicating that as phenol content increases infestation by podfly decreases. Correlation coefficient value (r) for phenol content was -0.564 with pod damage and -0.544 with grain damage. The results are in accordance with the findings of Singh (2003) [16], Moudgal *et al.* (2008) [9], Dhakla *et al.* (2010) [2], Pandey *et al.* (2011) [11] and Kumar *et al.* (2015) [6] that the genotypes with more phenol content suffered less damage by podfly *i.e.*, negative correlation.

3.6 Proteins (%): The average protein content was 25.34 percent and it ranged between 21.37 (ICPHaRL 4985-11) to 30.35 percent (Guliyal Local (Red)) (Table 1). Protein content showed significant positive correlation with pod damage (0.718) and grain damage (0.733). Thus, from the present results it was clear that as the protein content increases infestation by the podfly increases. The results of the investigation are in conformity with the findings of Moudgal *et al.* (2008) [9], Dhakla *et al.* (2010) [2] and Kumar *et al.* (2015) [6] who reported that protein content was positively associated with the susceptibility to podfly damage.

3.7 Sugars (%): Sugar content of different genotypes of pigeonpea ranged from 10.57 (ICP 11957) to 15.86 percent (ICPL 87119) with an average of 13.52 percent (Table 1). The

correlation studies indicated a non-significant positive relation between sugar content and podfly infestation. Correlation coefficient value (r) for sugar content was 0.178 with pod damage and 0.159 with grain damage. Thus, it was clear that sugar content of tested genotypes did not play any role in

offering resistance or susceptibility with podfly infestation. Singh (2003) [16] and Kumar *et al.* (2015) [6] also reported that higher sugar content increased the rate of podfly infestation *i.e.*, positive correlation. However, the results are contrary to Dhakla *et al.* (2010) [2] who observed negative correlation.

Table 1: Influence of seed characters on the incidence of podfly (*Melanagromyza obtusa*) in pigeonpea during Kharif, 2016

S. No	Name of the genotype	Test weight (g)	Seed length (mm)	Seed width (mm)	No. of seeds per pod	No. of seeds damaged per pod	Phenols (mg/g)	Proteins (%)	Sugars (%)	Pod damage (%)	Grain damage (%)
1	ICPHaRL 4989-7	11.00	6.27	5.04	3.93	0.23	7.48	22.97	13.48	14.17	7.28
2	ICPHaRL 4985-10	10.60	6.42	5.31	3.97	0.14	8.71	22.50	14.31	13.50	6.94
3	ICPHaRL 4985-11	10.93	6.24	5.37	3.97	0.22	7.04	21.37	14.12	12.17	7.72
4	Guliyal Local (Red)	12.77	6.65	5.71	3.87	0.53	3.62	30.35	15.78	34.33	22.39
5	BRG 10-2	10.83	6.00	5.18	3.63	0.44	6.08	25.90	13.48	23.67	13.00
6	ICP 11957	9.63	5.81	5.26	3.93	0.28	13.71	28.64	10.57	18.75	10.28
7	LRG 52	12.10	6.36	5.22	4.07	0.22	6.69	23.07	14.65	17.67	7.28
8	GRG 2013	11.77	6.65	5.85	3.80	1.07	5.02	29.68	13.36	52.67	36.83
9	ICP 8863	11.10	6.40	5.19	4.00	0.57	4.58	27.13	13.06	41.44	23.22
10	CO 6	9.30	6.13	4.63	3.90	0.30	10.72	26.19	13.25	18.33	9.67
11	WRP 1	9.73	5.41	4.96	3.90	0.21	8.62	25.34	11.36	9.33	4.78
12	ICPL 87119	12.90	6.89	5.83	3.83	0.68	4.85	24.77	15.86	32.67	18.06
13	ICPL 332-WR	11.90	6.56	5.73	3.73	0.65	8.01	25.24	11.97	33.83	19.78
14	LRG 41 (Check)	12.50	6.71	5.65	4.03	0.38	5.11	21.55	14.01	26.50	15.00
	Mean	11.22	6.32	5.35	3.90	0.42	7.16	25.34	13.52	-	-
	F-Test	Sig	Sig	Sig	NS	Sig	Sig	Sig	Sig	-	-
	SEm±	0.17	0.10	0.06	0.08	0.04	0.26	0.77	0.48	-	-
	CD (P=0.05)	0.50	0.28	0.19	0.24	0.11	0.75	2.24	1.39	-	-
	CV (%)	2.66	2.62	2.10	3.67	15.24	6.23	5.28	6.15	-	-
	Correlation coefficient (r) with pod damage	0.536*	0.620*	0.648*	-0.325 ^{NS}	0.947**	-0.564*	0.718**	0.178 ^{NS}	-	-
	Correlation coefficient (r) with grain damage	0.498 ^{NS}	0.583*	0.666**	-0.353 ^{NS}	0.958**	-0.544*	0.733**	0.159 ^{NS}	-	-

**Significant at 1% level (P = 0.01) *Significant at 5% level (P = 0.05) Sig – Significant NS – Non Significant

4. Conclusion

Plant-herbivore interactions are influenced by several physico-chemical plant traits, environmental conditions, and physiological status of the test insects. Morphological characters of plants interfere with oviposition and feeding by the insects, while biochemical constituents confer antibiosis as well as antixenosis mechanisms of resistance to insects. The analysis of the data on different morphological characters revealed that test weight, seed length, seed width and no. of seeds damaged per pod showed the significant positive correlation with podfly infestation. The data on biochemical assay revealed that protein content proved to be an important nutritional factor for damage by the podfly and these were significantly higher in susceptible genotypes. While, phenols proved to be an important anti-nutritional factor for damage by the podfly and these were significantly higher in resistant genotypes. Therefore, these morphological and biochemical seed traits can be used as markers to identify the resistance sources of pigeonpea with different mechanism of resistance against pod fly. This finding can be used very effectively in pod fly resistant breeding programme.

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