

Original Research Article

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Identification of Quantitative Trait Loci for Biochemical Traits Related to Pod Borer Resistance among Recombinant Inbred Lines in Pigeonpea [*Cajanus cajan* (L.) Mills] Paugh.

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ABSTRACT

Pigeonpea [*Cajanus cajan* L. Mill spaugh] is a prominent grain legume crop mainly grown in semi-arid tropics of the world. Pigeonpea pod borer (*Helicoverpa armigera*) is an important insect pest of Pigeonpea which may sometimes lead to 60 -80% losses of yield predominantly in Pigeonpea growing areas. The objective here was to appraise the inheritance of resistance pertaining to pod borer in case of Pigeonpea and to trace out the quantitative trait loci (QTL) governing pod borer resistance for the stimulation of the checking of the pest. 150 recombinant lines of F6-7 derived from the cross 'H2001-4' x 'ICP7035' were used. Out of which 84 lines were randomly chosen for the DNA studies. Single nucleotide polymorphisms were crucial for the generation of high-density linkage maps. The genetic variability studies have shown that there is significant variability for the traits under study in the population and also a wide range of variation in the mean values for the traits. Four characters studied were phenol content in pods (mg/g), reducing sugars (mg/g) and non-reducing sugars (mg/g), and protein content (%) in seeds. Correlation studies were made with respect to percentage of pod damage which depicted the significant correlation with the traits under study. Pigeonpea with early maturing, phenol content greater than 16mg/g with maximum range of 23 mg/g showed reduced percentage of pod damage. Phenol content in pod walls (mg/g) also showed significant negative correlation (-0.9508*), significant positive correlation with protein content (%) (0.8035*), significant positive correlation with non-reducing sugars (mg/g) (0.8631*) and positive correlation of 0.0624 (mg/g) by reducing sugars. The studies pertaining to correlation showed that high phenol content in pod walls resulted in low percentage of pod damage and lines with high amount of protein and reducing and non-reducing sugars showed more percentage of pod damage. After QTL analysis of all traits, QTLs have been identified for two traits i.e., reducing sugar and phenol content. Total number of QTLs identified was five, three for reducing sugars and two for phenol content. Constant QTL has been identified for one trait (Reducing Sugar) in chromosome 5. The consistent QTLs identified were between CSCSP 14826- SCP 6824 respectively on chromosome 5 explaining the variation of 0.12 percent in environment one and 0.14 percent in environment 2 respectively. QTLs have also been identified for phenol content in pod walls but on different chromosomes. The correlation response and the identified QTLs will assist in marker assisted plant breeding practices for the development of cultivars having resistance to pod borer infestation.

Keywords

QTL, *Helicoverpa armigera*, Gram pod borer (Hubner), SNPs, MAS and biochemical traits

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Introduction

Pigeonpea pod borer is a significant insect pest in almost all Pigeonpea growing areas of India and the world (Saxena, 2012). Hubner causes undeviating losses in yield besides quality which in turn leads to reduction in selling price due to damaged seeds (Lal, 1946 and Shrivastava, 1964). Maturity of the

pigeonpea is associated with gram pod borer outbreak (Lal, 1946 and Shrivastava, 1964) as laying of the eggs occur in vegetative phase and development of the larva at reproductive stage. Percentage of damaged seeds may range from 10 to 60 percent. Spraying of insecticides rampantly may lead to ecological and economic issues that will be limiting the usage of them. The genetic transformation of

Pigeonpea with insecticidal proteins from *Bacillus* species resulted in offering striking approach when compared to utilization of pesticides (Ramu *et al.*, 2011). But the legal hurdles for development and marketing of transgenic Pigeonpea has limited this approach further. Hence finding out the resistant genes from available germplasms endogenously is an appreciable approach and also may be considered as a significant method.

Previously for the resistance which is endogenous in nature scientists mainly depended on phenotypic selection of individuals that had been derived from experimental crosses which had been made between experimental lines and elite cultivars (Stubner *et al.*, 2012). Thus, practical appraisal of endogenic resistance to Hubner in Pigeonpea was analytical for selection. Percentage of pod damage is an important constraint for the study of the severity of the infestation of the pest. The other morphological traits related to pod borer resistance were also evaluated as they were considered to be non-preferential and play a pivotal role in offering resistance to Hubner (Acharya *et al.*, 2008). In order to reduce the costs for experimentation some scientists based on the feeding habit and nature of laying eggs certain morphological characters were identified and association analysis was done (Jagtap *et al.*, 2012). Morphological traits correlated include pod length (cm), petiole length (cm), Peduncle length (cm) Leaf thickness (mm), pod wall thickness (mm). Nevertheless, such kind of selection done indirectly may not be efficient up to the mark. Nevertheless, meandering selection may not be highly potential one for achieving remarkable resistance to Hubner. But use of DNA based markers for finding out the chromosomal regions that are contributing for the variation of traits under study assist in achieving reliable results (Allen, 1994). Some

of the important points about MAS is during the early stages of plant growth one can trace out and eliminate the unnecessary plants from the population. Selection can be made for several traits at a time simultaneously and the appreciative expression of the genes governing the quantitative traits can be backcrossed to well adapted genotypes through marker assisted backcross breeding. MAS can significantly improve the selection for traits that are showing low inheritance (resistance to Hubner) with the assistance of high heritable DNA markers.

Ten Pigeonpea genotypes had been utilized for the generation of 150.8 million sequence tags by illumina technology (Dubey *et al.*, 2011). Out of which 2 genotype sequences aligned with the tentative unique sequences that had been found i.e. 127754 with respect to *Cajanuscajan* transcriptome assembly and differences identified to trace out the SNPs with help of Alpheus program of NCGR.23. Number of SNPs identified was 12141. For the discovery of SNPs on a large-scale integrated pipeline utilized and ESTs around 10376 found. Raju *et al.*, (2010) conducted parallel examination and found out the 102 SNPs from 37 contigs out of 871. Asha and UPAS120 were the two varieties from which two pools of RNA had been prepared and transcriptome assembly contigs carefully searched for the SNPs under INDO US AKI project. Alignment of commonly occurring large contigs for stringent comparison to find out the SNPs among 15511, 2304 SNP which are genic nature identified (Singh *et al.*, 2012). Varshney *et al.*, (2012) analysed illumina transcript reads and identified 28104 SNPs from the pool of 12 genotypes of Pigeonpea.

Young *et al.*, (1992) identified the QTL for bruchid resistance and mapped using the RFLP markers in TC1966 and a susceptible mung bean cultivar on linkage group VIII which was 3.6cM away from the closest RFLP

marker. Bulk segregant analysis and quantitative analysis showed the seven RAPD markers that had been linked to the resistance to potato leaf hopper (*Empoasca fabae*) and four to *E. kraemeri* (Murray *et al.*, (2004). In case of soybean resistance for insect pest for antibiosis, pubescence shape and antixenosis showed nature of quantitative inheritance (Terry *et al.*, 2000; Narvel *et al.*, 2001).

For nematode pests, qualitative ((Meksem *et al.*, 2001; Njiti *et al.*, 2002) and quantitative resistance had been identified (Concibido *et al.*, 1996, 1997, 2004) but there are no QTL analysis reports pertaining to pod borer resistance in case of Pigeonpea. Present study focusses upon the identification of QTLs for biochemical traits related to pod borer resistance in Pigeonpea.

Materials and Methods

Chosen plant material and extraction of the DNA

One hundred and fifty recombinant inbred lines of F6:7 generation, which had been derived from the cross H2001-4 (highly susceptible) and ICP 7035 (moderately resistant) (Anita Kumari 2001). Experimentation conducted at IARI research farms New Delhi during the years 2014-2015 and 2015-1016. Augmented plant breeding design used with susceptible parent grown around the field. Out of the hundred and fifty lines, eighty-four lines had been randomly chosen for the DNA studies. Field was left without spraying throughout the season with two rows of susceptible parent grown around the field to bring about the infestation during the season. Percentage of pod borer damage was calculated with the following formula

$$\text{Percent pod damage} = \frac{\text{Number of pods damaged}}{\text{Total number of pods}} \times 100$$

The other characters that had been studied were pod length (cm), petiole length (cm), leaf thickness (mm), pod wall thickness (mm) peduncle length (cm) and biochemical traits like phenol content in pod walls (mg/g), protein content in seed (%), reducing sugars (mg/g), and non-reducing sugars (mg/g). Data was analyzed in each of the two environments for the study of the genetic parameters and for genotypic and phenotypic correlation coefficients. Pods of Pigeonpea were collected at an immature stage and freeze dried in life lyophilizer. Freeze dried pods were ground and analyzed for phenol content in pod walls using suitable method (Sadasivam and Manickam, 1996). Total protein content was estimated using micro kjeldahl method for total nitrogen content has to be further multiplied by 6.25 factor in order to get total protein content (Sadasivam and Manickam, 1996). Reducing and non-reducing sugars were estimated by calculating total sugars (mg/g) and reducing sugars (mg/g) from the sample and subtracting gives the non-reducing sugars from the sample (Sadasivam and Manickam, 1996). Genic SNP chip for genotyping had been developed. A 62 K Pigeonpea SNP genotyping Chip (CcSNPnks, unpublished) was used. For this, good quality Pigeonpea genomic DNA was isolated from seedling using the CTAB method, purified and quantified using Nano-drop spectrophotometer and genomic DNA quality was checked on 1% agarose gel. Chip is holding 62K SNPs from different groups of genes.

Gene titan was used for the validation of the SNPs in the WETLAB by considering 96 RILs and 96 varieties. The individuality of the SNPs and their call representation was determined by axiom analysis suite software. SNP with >0.85 DQC and 0.95% call rates were considered. 852 SNP markers had been used for the construction of linkage map out of which 359 showed polymorphism. The software used was Join Map 4.1v software.

Results and Discussion

Evaluation of the resistance to Pigeonpea pod borer showed continuous frequency distribution indicating that the resistance is controlled by many genes. Minimum percentage of pod damage is 10.63% and maximum of 60.4%. Both the parents H2001-4 (62.15%), ICP 7035 (21.24%) significantly differed in the resistance to pod borer. The kurtosis (-0.836) and skewness (-0.038) recommended that the segregation aptly takes the model of normal distribution. Other traits under the study also showed less skewness and kurtosis (< 1) indicating that those traits too follow normal distribution.

Correlation analysis

Among the morphological traits studied pod length (cm) showed significant negative correlation (-0.3045*) with percentage of pod damage. Peduncle length (cm), showed positive correlation with PPD (0.0596), petiole length (cm) showed positive correlation (0.1201).

Pod wall thickness (mm) (-0.1606) and leaf thickness (mm) (-0.0512) exhibited negative correlation. Biochemical traits studies showed remarkable correlations.

Protein content in seed (%) showed significant positive correlation (0.8035*), reducing sugars (mg/g) (0.0624), non-reducing sugars (0.8631*) showed positive correlation. But the phenol content in pods (mg/g) showed significant negative correlation (-0.9508*) (Table 1)

QTL analysis of the biochemical traits related to pod borer resistance

A total of 852 SNP markers had been used to trace out the polymorphism between the parents, out of which 359 had been shown the

polymorphism (Table 2). They were mapped into the chromosomes. Four biochemical traits were studied out of which five QTLs had been identified for two trait reducing sugars (mg/g) and phenol content in pod walls (mg/g). Consistency in both the environments was shown by the identified QTLqRC5 for reducing sugars (mg/g) upon the chromosome number 5 and between the markers CSCSP 14826 – SCP 6874 (Fig. 1) With a position (cM) 39.7cM-43.4cM in environment-1, and 32.2cM -36.5cM in second environment having a LOD scores of 2.15418 and 3.826276 with an additive effect of 1.1408 and 1.3589 in first and second environments. The traced-out QTL explained the phenotypic variance (%) by 0.125723 percent. In the second environment QTLqRC1 for reducing sugars (mg/g) had been identified on chromosome number 1 and 5.

The QTL on chromosome 1 is between the markers CSCSP 4699- CSCSP 13375 positioning between 42.8cM - 46.5cM, having a LOD score 3.022801 with an additive effect of 1.7065 explaining the phenotypic variation by 0.116026 percent. QTLs for phenol content in pod walls (mg/g) had been identified on chromosome 5 and 1 in the respective first and second environments.

They had been positioned between the markers CSCSP14826 -DRDRP696 positioning at 44.0cM - 47.1cM and CSCSP 13375 –CSCSP 11800 positioning at 47.7cM - 50.8cM respectively. The identified QTLs had LOD scores of 1.921824 and 2.760043 with negative additive effect of -2.4354 in first environment and positive additive effect of 2.4844 in the second environment. They had explained the phenotypic variation by 0.084726 percent in first environment and 0.132056 percent remarkably. Based on the fact of explaining the phenotypic variation by low percentage, the identified QTLs were characterized as minor QTLs (Table 3).

Table.1 Phenotypic correlation coefficients at 1% level of significance

Traits	Pod length (cm)	Peduncle length (cm)	Petiole length (cm)	Pod wall thickness (mm)	Leaf thickness (mm)	Protein content (%)	Reducing sugars (mg/g)	Non-reducing sugars content (mg/g)	Phenol content (mg/g)	Pod damage (%)
Pod length (cm)	1	-0.1252	0.0172	0.1000	-0.0235	-0.1823*	0.1756*	-0.1965*	0.2903*	-0.3045*
Peduncle length (cm)		1.0000	-0.0332	-0.0333	0.1516	-0.0096	0.1345	0.0528	-0.1012	0.0596
Petiole length (cm)			1.0000	0.1335	0.1573	0.2304*	-0.0718	0.1933*	-0.0539	0.1201
Pod wall thickness (mm)				1.0000	0.1784*	0.0407	0.2742*	0.0049	0.1817*	-0.1606
Leaf thickness (mm)					1.0000	0.0227	0.0773	-0.0308	0.0864	-0.0512
Protein content (%)						1.0000	0.0714	0.8891*	-0.7563*	0.8035*
Reducing sugars (mg/g)							1.0000	0.0289	0.0153	0.0624
Non-reducing sugar content (mg/g)								1.0000	-0.8228*	0.8631*
Phenol content (mg/g)									1.0000	-0.9508*
Pod damage (%)										1.0000

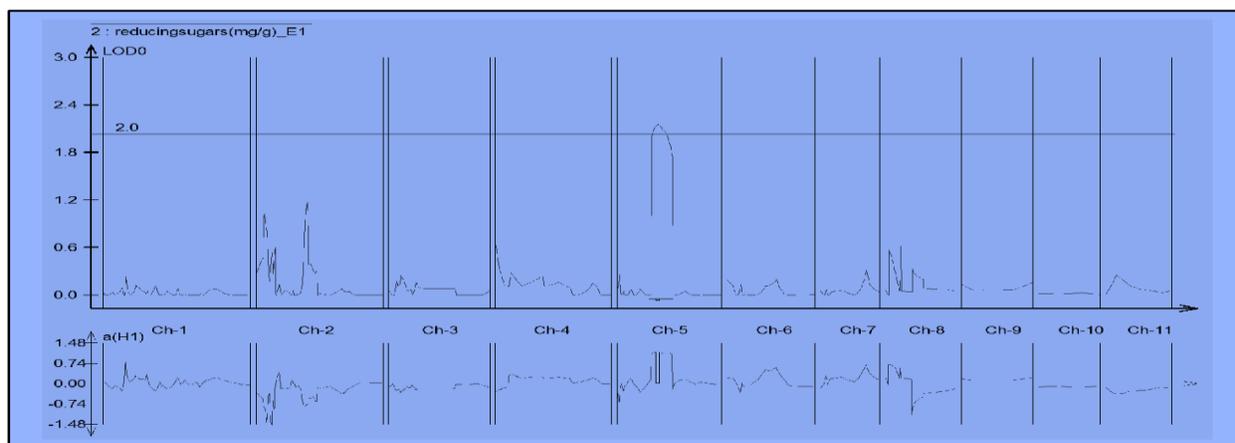
Table.2 Linkage groups and assigned markers

S.no	Chromosome	Markers	Position (cM)
1	LG1	80	150.012
2	LG2	76	129.16
3	LG3	51	102.9
4	LG4	40	117.64
5	LG5	33	106.15
6	LG6	23	89.33
7	LG7	19	60.002
8	LG8	13	72.167
9	LG9	10	72.167
10	LG10	7	72.216
11	LG11	7	62.7
Total	11	359	1028.99cM

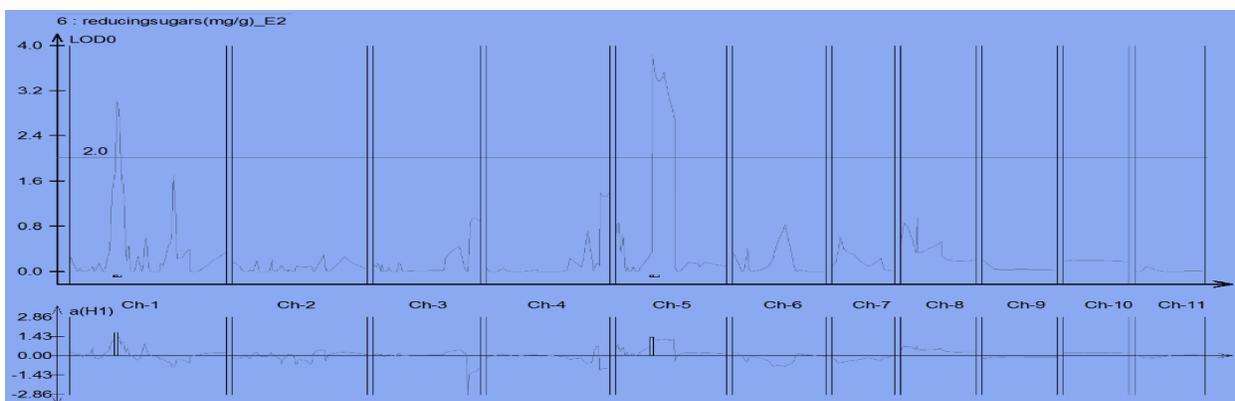
Table.3 Summary of the different QTLs identified for biochemical traits related to Pod borer resistance (*Helicoverpa armigera*)

QTLs for RIL (ENV-1)					
Trait	Chromosome	Position (CM)	LOD	Additive effect	Phenotypic Variance (%)
Reducing Sugars	5	39.7-43.4	2.15418	1.1408	0.125723
Phenol Content	5	44.0-47.1	1.921824	-2.4354	0.084726
QTLs for RIL (ENV-2)					
Trait	Chromosome	Position (CM)	LOD	Additive effect	Phenotypic Variance (%)
Reducing Sugars	1	42.8-46.5	3.022801	1.7065	0.116026
Reducing Sugars	5	32.2-36.5	3.826276	1.3589	0.147826
Phenol Content	1	47.7-50.8	2.760043	2.4844	0.132056

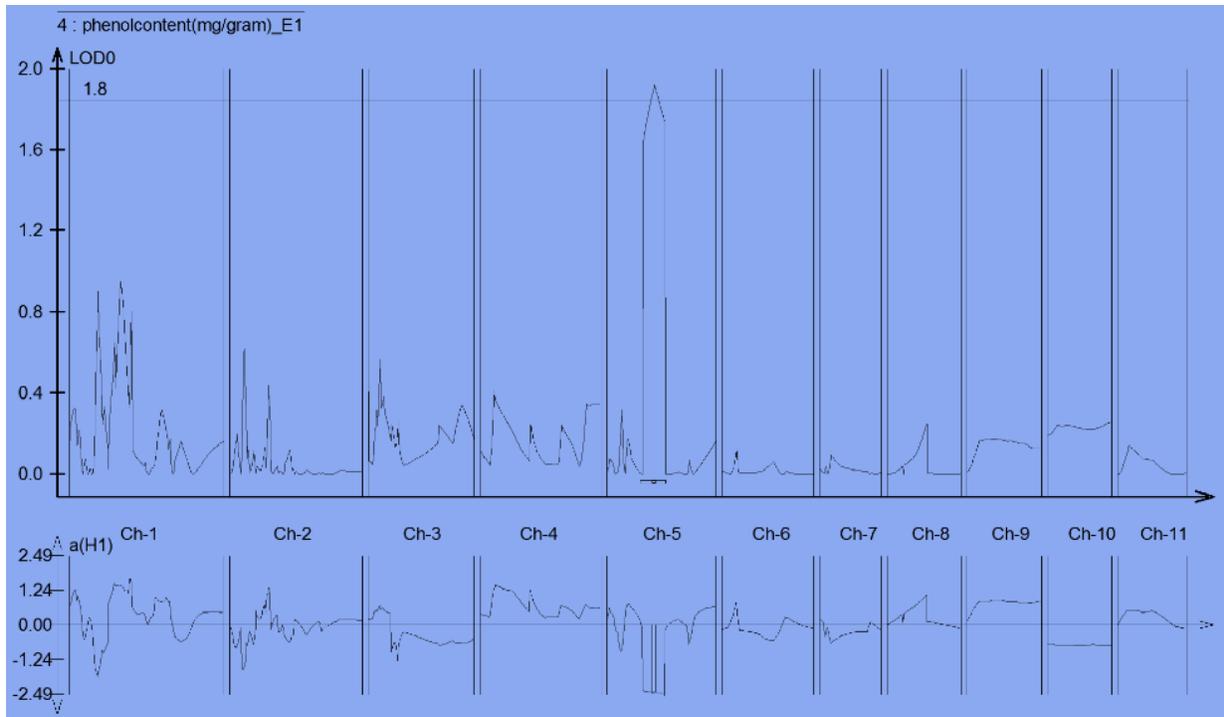
Fig.3 Cartographer generated images for QTL analysis



Cartographer image for Reducing sugars (mg/g) environment -1



Cartographer image for reducing sugars (mg/g) environment -2



Cartographer image for Phenol content (mg/g) in first and second environment.

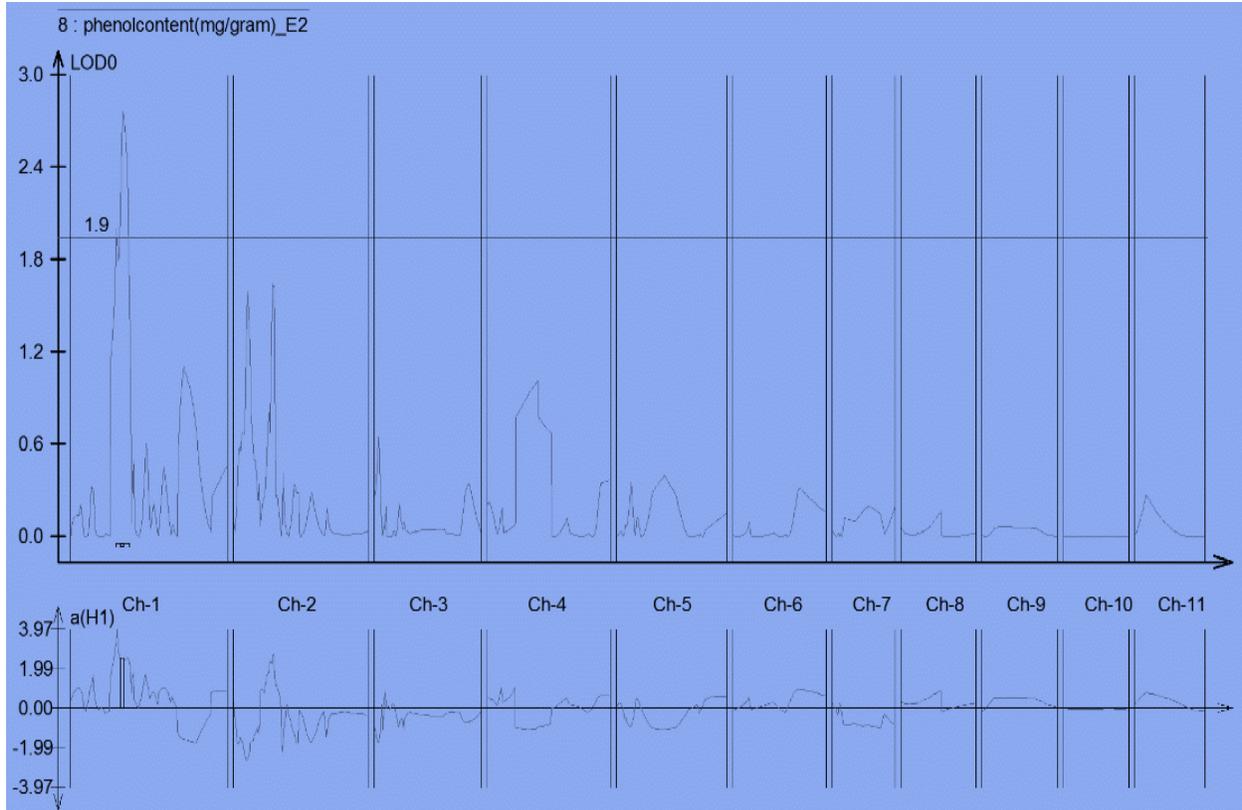
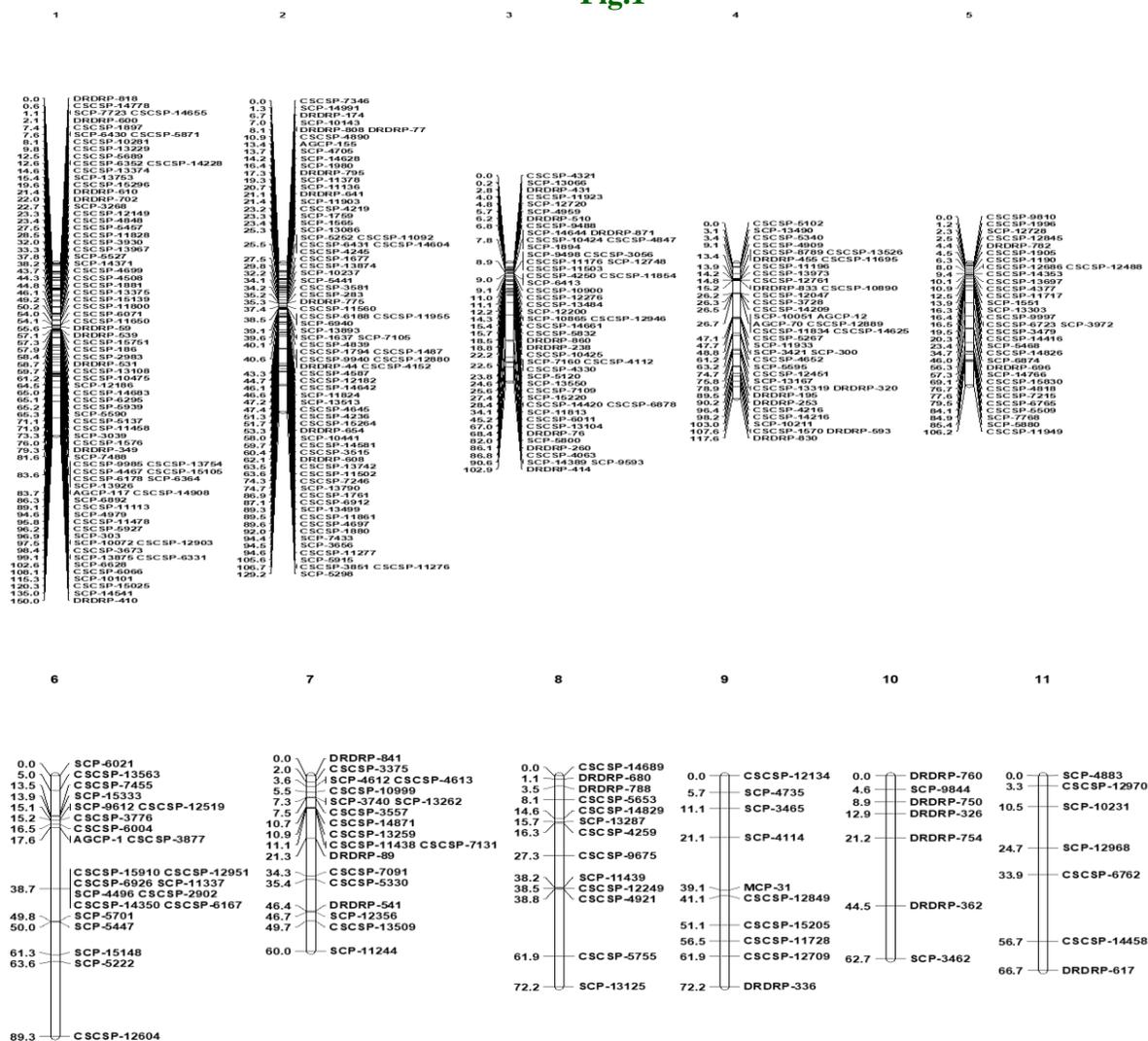


Fig.1



ICP 7035 was reported to be moderately resistant to pod borer by Anita kumari (2005). As it has shown high degree of crossability with the H2001-4 it was used as one of the parents and to get the unambiguous results pertaining to inheritance pattern and other significant genetic parameters which are noteworthy regarding pod borer resistance. Correlation studies depicted that some morphological and biochemical traits offered resistance to pod borer (Jagtap *et al.*, 2012).

Longer pods (cm) with low peduncle length (cm), low petiole length (cm) and high leaf and pod wall thickness (mm) had given a way for the low infestation of insect pest as they had limited the Hubner. Similar results had been found more the protein content (%), and reducing and non-reducing sugars have shown more infestation of the pest. Genotypes with more amount of Phenol content in pod walls (mg/g) had shown high resistance to the infestation of pod borer. Morphological traits

are responsible for inhibition of egg deposition and induce non-preferential nature in the insect pest. Similar results had been reported by Thakur *et al.*, (1989). Peduncle length (cm) and petiole length must be short so that insect will not find opportunity for egg deposition. Pod wall thickness (mm) and leaf thickness (mm) resist the feeding habit of the insect pest. So genotypes with more pod wall thickness and leaf thickness showed low percentage yield loss. Similar results had been reported by Sunitha *et al.*, (2008).

Protein content (%) and total sugars (mg/g) were positively correlated to percentage of pod borer damage indicating that genotypes with more amount of the reducing and non-reducing sugars and protein content (%) will be more susceptible for pod borer infestation. In contrast to this, genotypes with more amount of phenol content in pod walls (mg/g) resisted the pod borer infestation. Similar findings had been reported by Chowdary *et al.*, (2013). Qtls had been identified for two of the four biochemical traits studied. Consistency was found for the QTL associated with reducing sugars (mg/g), (qRS5) and was linked with the intrinsic resistance to pod borer appraised through percentage of pod damage.

Previous reports are not found pertaining to tracing out the QTL for reducing sugars. In both the environments the QTL fall between the marker intervals CSCSP 14826 – SCP 6874 on chromosome 5. Qtls identified for phenol content does not show any consistency in both the environments. QTL found may also significantly code for resistance to other insect pest of pigeonpea. Mapping populations involved with *Cajanus scarabaeoides* that showed resistance to pod borer was developed and research is going on even with transgenics for resistance to pod borer Sharma *et al.*, (2004). The identified QTL can be used as candidate marker in

marker assisted selection. Morphological markers which had exhibited pleiotropic effect must be given lower weightage in the discriminant function analysis in the selection criteria when compared to other traits which are in association with resistance to Hubner. Deploying the marker assisted selection (MAS) may also categorize the genetic factors responsible for morphological as well as biochemical associated with resistance. Further fine mapping leads to the breakage of association between the markers and morphology associated with resistance. Resistance offered by the ICP 7035 cultivar was not directly controlled by the traits considered for study but was strongly supported by the correlation studies with respect to percentage of pod borer damage. Nevertheless loci involved in the correlated traits of percentage of pod damage could be used in selection for hubner resistance. The markers found to be reliable can be used for transferring and evaluating the resistance to pod borer in marker assisted selection into elite cultivars of Pigeonpea. Knowledge about different markers may assist in developing efficient breeding schemes involving different crosses for resistant to pod borer. Till now it's been a tough job to find the promising markers for resistance as it has shown a complex inheritance pattern. The study made will be helpful to dissect the complex trait resistance to pod borer throughout pigeonpea growing areas.

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References

- Acharya S, Tikka SBS and Patel JB (2008) Sui-generis Research in Pigeonpea, Directorate of Research, SDAU, Sardarkrushinagar.
- Allen FL (1994) Usefulness of plant genome mapping to plant breeding. In: Gresshoff P (ed) Plant genome analysis. CRC Press, Boca Raton, pp 11–18.
- Anitha Kumari D (2005) Mechanisms of resistance to *Helicoverpa armigera* (Hubner) in Pigeonpea (*Cajanus cajan* (L.) Mill Sp) Ph. D thesis submitted to Acharya N.G. Ranga Agricultural University, Rajendranagar.
- Arbind K Choudhary, Ranjeet Sharad Raje, Subhojit Datta, Rafat Sultana, Timmanna Ontagodi (2013) Conventional and Molecular Approaches towards Genetic Improvement in Pigeonpea for Insects Resistance. American journal of plant sciences Vol.4 No.2A Article ID: 28451, 14 pages.
- Concibido VC, Denny RL, Lange DA, Orf JH, Young ND (1996). RFLP mapping and marker-assisted selection of soybean cyst nematode resistance in PI 209332. *Crop Sci.*, 36:1643–1650.
- Concibido VC, Diers BW, Arelli PR (2004) A decade of QTL mapping for cyst nematode resistance in soybean. *Crop Sci* 44: 1121–1131.
- Concibido VC, Lange DA, Denny RL, Orf JH, Young ND (1997) Genome mapping of soybean cyst nematode. *Crop Sci.*, 37: 258–264.
- Dubey A, Farmer A, Schlueter J, Cannon SB, Abernathy B, Tuteja R, Woodward J and Shah T (2011) Defining the transcriptome assembly and its use for genome dynamics and transcriptome profiling studies in Pigeonpea (*Cajanus cajan*). *DNA Research*, 18: 153–164.
- Jagtap BR, Acharya S, Patel JB and Bharat L (2012) Character association analysis of resistance to *Helicoverpa armigera* in Pigeonpea [*Cajanus cajan* (L.) millsp.] Patel International Journal of Food, Agriculture and Veterinary Sciences. Vol. 2 (1) January-April, pp.92-100.
- Lai KB (1946) Pest of rabi crops. *PI Pro. Bull.* 1:29-30.
- Meksem K, Pantazopoulos P, Njiti VN, Hyten DL, Arelli PR, Lightfoot DA (2001) ‘Forrest’ resistance to the soybean cyst nematode is bigenic: saturation mapping of the Rhg1 and Rhg4 loci. *Theor Appl Genet* 103:710–717.
- Murray, J.D., T.E. Michaels, K.P. Pauls, C. Cardona & A.W. Schaafsma, 2004b. Yield and insect injury in leafhopper (*Empoasca fabae* Harris and *Empoasca kraemerii* Ross & Moore) infested dry beans in Ontario and Colombia. *Can J Plant Sci* 84: 891–900.
- Narvel JM, Walker DR, Rector BG, All JN, Parrott WA, Boerma RH (2001) A retrospective DNA marker Euphytica (2008) 164:275–282 281 assessment of the development of insect resistant soybean. *Crop Sci* 41: 1931–1939.
- Njiti VN, Meksem K, Iqbal MJ, Johnson JE, Kassem MA and Zobrist KF (2002) Common loci underlie field resistance to soybean sudden death syndrome in Forrest, Pyramid, Essex, and Douglas. *Theor Appl Genet* 104: 294–300.
- Raju NL, Gananesh BN, Lekha P, Jayashree B, Pande S, Hiremath PJ, Byregowda M, Singh NK, Varshney RK (2010) The first set of EST resource for gene discovery and marker development in pigeonpea (*Cajanus cajan* L.) *BMC Plant Biol.*; 10: 45.
- Ramu SV, Rohini S, Keshavareddy G, Gowri Neelima M, Shanmugam NB, Kumar ARV, Sarangi SK, Ananda Kumar P

- and Udaya kumar M Expression of a synthetic cry1AcF gene in transgenic Pigeon pea confers resistance to *Helicoverpa armigera*.
- Sadasivam S and Manickam A (1996) Biochemical methods, 2nd Edition, *New Age International (P) Limited Publisher.*, pp: 193-194.
- Saxena KB (2012) Genetic Improvement of Pigeonpea. *Tropical Plant Biology*, 1: 159-178.
- Sharma HC and Crouch JH (2004) International Research Institute the Semi-Arid Tropics Patancheru 502 AP Molecular Marker-Assisted Selection: A Novel Approach for Host Plant Resistance to Insects in Grain Legumes.
- Shrivastava, A. S. 1964, Pest of gram. Entomological Research Memoir., pp: 51-53.
- Singh NK, Gupta DK, Jayaswal PK, Mahato AK, Dutta S, Singh S (2012) The first draft of the Pigeonpea genome sequence. *J. Plant Biochem. Biotechnol.* 21, 98–112.
- Stuber CW, Lincoln SE, Wolff DW, Helentjaris T, Lander ES (1992) Identification of genetic factors contributing to heterosis in a hybrid from two elite maize inbred lines using molecular markers. *Genetics* 132: 832–839.
- Sunitha V, Rao GVR, Lakshmi KV, Saxena KB, Rao VR and Reddy YVR (2008) Morphological and Biochemical Factors Associated with Resistance to *Maruca vitrata* (Lepidoptera: Pyralidae) in Short duration Pigeonpea. *International Journal of Tropical Insect Science*: Vol. 28, 1, 45-62.
- Terry LI, Chase K, Jarvik T, Orf J, Mansur L, Lark KG (2000) Soybean quantitative trait loci for resistance to insects. *Crop Sci* 40: 375–382.
- Thakur BS, Rawat RR, Verma R and Moitra A (1989) Influence of Shape and Size of Pods of *Cajanus cajan* (L) Millsp. on the Susceptibility to the Pod fly, *Melanagromyza obtusa* Malloch and the Pod bug *Clavigralla gibbosa* Spinola. *Indian Journal of Entomology*: Vol. 51, 2, 159-162.
- Varshney RK (2012). Draft genome sequence of Pigeonpea (*Cajanus cajan*), an orphan legume crop of resource-poor farmers Rajeev K Varshney, Wenbin Chen Scott a Jackson *Nature Biotechnology*, 30, pp 83–89.
- Young ND, Kumar L, Menancio-Hautea D, Danesh D, Talekar NS, Shanmugasundaram S and Kim DH (1992) RFLP mapping of major bruchid resistance gene in mungbean (*Vigna radiata* L. Wilczek). *Theor. Appl. Genet.*, 84: 839-844.
- Sunitha V, Rao GVR, Lakshmi KV, Saxena

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