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Identification of Quantitative Trait Loci for Plant Type and Seed Yield Components among Recombinant Inbred Lines in Pigeon pea [*Cajanus cajan* (L.) Mills] Paugh

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A B S T R A C T

Poor and inconsistent yields of the Pigeonpea cultivation across different environments grown in respective seasons reduce the economic benefits for the farmers. Besides tolerances/ resistance to abiotic and biotic stresses, plant type and seed yield components of Pigeonpea are the principal determinants of the consistent yields. The contemporary research was orchestrated for the identification of QTLs for plant type and seed yield components. Two contrasting parents H2001-4 and ICP 7035 were crossed and advanced to F6: 7 generation for the development of recombinant inbred lines using single seed development method. Correlation studies and assessment of genetic variability parameters in two different environments was made, which provided valuable information about the genetics underlying the traits related to plant type and seed yield components. Consistent QTLs for three traits such as plant height, days to maturity and days to flowering across two environments were identified with the assistance of SNP markers which were mapped unto chromosomes. Positive significant trait-trait correlation had been found stipulating that there may be close linkage between the loci governing the trait or due to pleiotropy. Consistency paves a way for the exploitation of identified QTLs through marker assisted selection. Additionally, fine mapping may also help in tracing out candidate gene markers by employing synteny.

Introduction

Pigeonpea (*Cajanus cajan* L.) is a significant pulse crop mostly grown in semi-arid tropical regions of the world. Pigeonpea used as a substitute for animal protein in developing countries of subtropical and semi-arid regions. Pigeonpea is not only one of the best sources of protein but also enhances the fertility of the soil. Pigeonpea is used as the fuel, fodder, enhancing soil fertility and for the control of soil erosion. Hence it is a multipurpose crop (Janboonme *et al.*, 2007). India is the centre of origin for Pigeonpea, as many wild relatives and a large amount of natural genetic variation is found in India (van der Maesen, 1980).Challenges posed by the market globalization made it necessary to breed for

high productive and high density planting short duration pulse crops that become part of significant cropping systems both in irrigated and dry areas. It is a potential drought tolerant crop, grown as mixed crop and also uncustomary places like parks, roadsides, as border crop to other field crops etc. (Kalaimangal *et al.,* 2008). Generally, pigeonpea is a long duration crop. But now a day's short duration varieties like UPAS 120, PUSA 992, MANAK etc. are becoming substitute for major crop in cropping systems in irrigated areas as they are having good economic returns (Dahiya *et al.,* 2002). Poor and inconsistent yields of the Pigeonpea cultivation across different environments grown in respective seasons reduces the economic benefits for the farmers (Magrini *et al.,* 2016). Plant type includes the morphological traits that are in direct association with yield and the planting density per square meter in the field which represents its spatial arrangement

These parameters are involved in the reflection of striking changes during crop domestication (Cai *et al.,* 2016). Breeding for traits pertaining to plant architecture shown great aftermath on adaptability and overall yield potential of the crop (Busov *et al.,* 2008; Wang and Li 2008). Plant breeding may be benefitted from the novel technologies that had been developed for the plant phenotyping and genotyping. (Maalouf *et al.,* 2015) Genetic maps assist in identification of QTLs linked to the trait of interest and there by selecting the superior genotypes in the population (Ribaut and Hoisington, 1998). Marker assisted selection assist in speeding up the process of selection and also improving the efficiency of selection by selecting genotypes which are superior.Genetic relatedness had been studied for the first time using the RAPD markers by Choudary *et al.,* in the year 2007. Kotresh *et al.,* (2006) identified markers that were closely linked with wilt resistance with Pigeonpea. Bohra *et al.,* (2011) used SSR markers for the characterization of the germplasm lines and to study the diversity of the parental lines, purity analysis of the hybrid lines like ICPH 2671 and ICPH2438.Intraspecific linkage map in Pigeonpea had been developed by Gnanesh *et al.,* (2011). The cross was made between ICP 8863 and ICPL 20097.

Giriraj Kumawat *et al.,* (2012) developed F_2 population and identified QTLs for plant type and earliness in Pigeonpea. It was an intraspecific cross Pusa Dwarf and HDM04 - 1. 107 SNP markers and 28 SSR markers had been used for the genotyping of the population. In the current study, the RIL population was derived by crossing between the two contrasting parents ICP 7035 and H2001-4 and QTLs analysis was made to identify the QTLs for the respective traits.

Materials and Methods

Utilization of plant material and conduction of experiment

Two contrasting parents ICP 7035 and H2001-4 chosen and F_{6-7} recombinant inbred lines were developed in the Division of Genetics. Parents under the study were showing remarkable differences with respect to one another. ICP 7035 was a moderately resistant variety (Anita Kumari *et al.,* 2010). ICP 7035 was a semi-compact medium duration one and show moderate resistance to pod borer, Hubner. But the H2001-4 was having indeterminate plant growth matures early (Table 1). Till 6 generation single seed descent method had been followed for the generation of recombinant inbred lines. 318 recombinant inbred lines were taken for the study over two seasons 2014 and 2015 out of which 96 were randomly chosen. The parental lines H2001-4 and ICP 7035 acted as if anticipated in fulfilment of botanical features.

Experimentation in the field

The field evaluation was carried out during *Kharif*, 2014-15 (Environment-1) and 2015-16 (Environment-2). Around 318 recombinant inbred lines were sown in augmented RBD design (Federer, 1956) in six blocks with parents (ICP 7035 and H2001-4).

Seven checks were used for the assessing the performance of the different inbred lines which were viz., Pusa 992, Pusa 991, Pusa 2001, Pusa 2002, Pusa 2012, Pusa 855 and V114.

Out of which randomly picked 84 lines have been used for SNP analysis for mapping of QTLs governing traits related to plant type and seed yield components.

Plant traits studied

Ten plant traits were studied pertaining to plant type and seed yield components. Ten plants were randomly chosen in each row and mean values for each trait were recorded. The recorded mean values were used for QTL analyses. Plant type traits comprised: Plant height (cm), number of primary branches, number of secondary branches, days to flowering, days to maturity, pod bearing length with main axis (cm), branching angle between the main axis and primary branches (degrees).

Seed yield components comprised: Number of pods per plant, number of seeds per pod, 100 seed weight, (10 pods were chosen randomly from each plant and mean values were recorded. Phenotypic data was statistically analysed by the Windostat version 9.3 Indostat services Hyderabad. Frequency distribution and descriptive statistics were studied which give information about the number of genes governing that particular trait. Pearsons correlation coefficients were also calculated.

The construction of linkage map was done with the help of Join map 4.0 software. A chi square test was performed on the genotyping data to test the goodness of fit with the expected segregation ratio of 1:1 in the RILs. The locus genotyping frequencies of Join map were used to identify markers with aberrant segregation after performing chi square test (p 0.05). Linkage groups were identified by grouping of markers at a minimum LOD threshold of 3 to a maximum of 10 with a step of 0.5. The groups were converted to maps at LOD 3 using the regression algorithm with recombination frequency of 0.20 and performing a ripple after adding 2 loci. Kosambi's mapping function was used to calculate map distance in centimorgan (cM). For the construction of final map only single SNP marker per genes selected for a position in the map because plotting various markers for same gene at same position has no meaning and it will create unnecessary load on the software and will consume more time. QTL analysis for the traits was carried out by combining the phenotypic and genotyping data on 94 RILs using WinQTL Cartographer v2.5. To find out the association of each marker to a trait, composite interval mapping (CIM) using the ZmapQTL standard model 6 with a window size of 10 cM and 2cM walk speed was used. For estimating a genome-wide LOD threshold score for QTL ($p = 0.05$), a 1000-permutation test was performed. The additive effect and the percentage of phenotypic variation explained by each putative QTL were estimated by the Composite interval mapping method (Fig. 2).

Results and Discussion

A total of 22 QTLs had been identified for seven traits under the study across the two environments. Consistent QTLs for three important traits for plant type such as plant height, days to flowering and days to maturity were identified. LOD score value varied for

different QTLs identified. QTLs had been identified for other traits like seeds per pod and branching angle. QTLs for plant height qPH2 and qPH3 in one environment and qPH2 and qPH5 in other environment, the former explained the variation ranging from 7% -13% indicating that they are minor QTLs, having also the additive effect 14.4 and -21.2 and 11.2 and -22.48, respectively. A single QTL for days to flowering qDF5 is having the additive effect -14.2 and -13.46, explaining the phenotypic variation of 12%-13% respectively over the two environments. QTLs for days to maturity were located on chromosomes 4 and 5 qDM4, qDM5 in first environment and second environment. They are having the additive effect ranging from 6.14 to 6.37 and -16.9 to -18.27, explaining the phenotypic variation from 3 -13 percent and are minor QTLs as the R^2value falls below 10. The markers associated with the consistent QTLs can be further used in the marker assisted plant breeding for improving the cultivars.

Correlation analysis

Correlation studies depicted that highest significant correlation was between the days to flowering (DF) and days to maturity (DM) that is 0.942 followed by days to maturity (DM) with the plant height (PH) (0.621) and days to flowering (DF) with plant height (PH) (0.618). Significant correlation was also established between the traits like secondary branches (SB) with primary branches (PB) (0.319) and branching angle with main axis (BA) with secondary branches (0.220) and pod bearing length (PBL), (0.231). The result showed that these traits with significant correlation were with remarkable amount of stability (Table 3). The frequency distribution of the different traits (Fig. 4) and descriptive statistics (Table 4, 5 and 6) shows that the traits are governed by many genes and considerable amount of variability was there in the population. It was observed that the recombinant inbred lines in the two environments were almost fixed at almost all the loci as the heritability of the characters is high. The difference between the PCV and GCV were less indicating the less influence of the environment. All the characters under study showed considerable range of values. Even though sowing was done in different years there is no influence of interaction effects over the years (Table 7 and 8).

QTL analyses

Naming of the QTLs was done based on the character abbreviation followed by chromosome number on which they had been located for the particular trait in the ICP 7035 X H2001-4 RIL population. List of the QTLs that had been found for characters of plant type and seed yield components were given in Table 9 and the cartographer images generated for the consistent QTLs and other QTLs found were depicted in Figure 4.

Plant height (PH)

Total four QTLs had been found on chromosomes 2 and 3 in first environment and on chromosomes 2 and 5 in second environment respectively. But the one which was found on chromosome 2 is the consistent one as it was found on same position in two environments. It explained the phenotypic variation by 10% in first environment and by 7% in second environment indicating that they were minor QTLs. The consistent QTLs of chromosome no 2 showed positive additive effect of 14.4 with 2.79 LOD score and at a position of 0.0 – 0.2 CM in first environment and with positive additive effect of 11.2, having a LOD score of 2.3 identified between 0.0- 0.3CM, though the LOD score was less than genome wide threshold LOD score at less than 0.05 probability (Fig. 1).

Table.1 Phenotypic characters of parental genotypes ICP 7035, H 2001-4

Trait	H-2001- 4 (female)	ICPL 7035 (male)
Plant height (cm)	218	130
No of primary branches	16	6.6
No of secondary branches	3.9	12
Days to flowering	120	96
Days to maturity	160	130
No of pods per plant	165	230
No of seeds per pod	3.5	5.5
Pod bearing length on main axis (cm)	30.5	20.5
100 seed weight (g)	8.5	13.5
Branching angle with main axis of the stem (Degrees)	45	25

Table.2 Number of lines used in two different seasons

Experiment	Environment	Year	Season	Number of RILs evaluated	Number of RILs used for mapping
Evaluation RILs under field	**1**	**2014-15**	**Kharif**	**318**	**84**
Evaluation of RILs under field	**2**	**2015-16**	**Kharif**	**318**	**84**

Table.3 Linkage groups and 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.4 Correlation coefficients table for 10 traits under study among RILs (ICP 7035 X H2001-4)

Variables	PH	PB	SB	DF	DM	NPP	SPP	PBL	SS	BA
PH	1									
PB	-0.025	1								
SB	-0.024	0.319**	1							
DF	0.618**	-0.011	-0.063	1						
DM	0.621**	-0.054	-0.146	0.942**	1					
NPP	0.066	-0.084	0.071	0.062	0.089	1				
SPP	-0.019	-0.093	-0.197	0.057	0.047	0.019	1			
PBL	-0.132	-0.091	0.064	0.080	0.026	- 0.004	0.083	1		
SS	-0.026	0.108	-0.118	0.019	0.057	- 0.061	0.187	-0.037	1	
BA	-0.088	0.081	0.220**	-0.093	-0.101	0.001	0.018	0.231**	-0.161	1

PH: Plant height (cm), PB: Number of primary branches, SB: Secondary branches, DF: Days to flowering, DM: Days to maturity, NPP: Number of pods per plant, SSP: Seeds per pod, PBL: Pod bearing length on main axis (cm), SW: 100 Seed weight (g), BA: branching angle with main stem (Degrees). (**) significant at 1% and 5% level of significance.

Table.5 and Table.6 Descriptive statistics of ten traits among parents and recombinant inbred lines under environment one (E1) and environment two (E2)

S. No	Trait	Parents		RILs	
		ICP 7035	H2001-4	Range	Mean±SD
1	PH	129.71	175.42	92.31-193.62	147.95±23.93
2	PB	8.34	12.77	6.11-15.76	10.68±2.90
3	SB	4.55	3.47	2.04-6.32	4.20±1.08
4	DF	116.63	99.83	79.83-153.32	130.1±16.39
5	DM	149.75	136.33	122-173.4	158.78±17.02
6	NPP	142.99	166.55	110.34-179.11	143.68±12.27
7	SPP	5.11	3.93	2.43-6.3	4.57± 0.90
8	PBL	31.37	21.28	19.88-55.05	34.28±8.48
9	SW	10.85	7.78	5.43-15.94	10.88±2.30
10	BA	23.17	50.80	20.65-56.64	38.51±10.28

S. No	Trait	Parents		RILs	
		ICP 7035	H2001-4	Range	Mean±SD
1	PH	133.17	177.66	94.32-191.42	148.45±23.09
2	PB	8.04	10.17	6.54-15.19	10.77±2.94
3	SB	4.46	3.01	1.82-6.24	4.22±1.14
4	DF	113.63	106.00	80.83-154.26	131.51±16.94
5	DM	151.55	139.03	120.09-174.34	159.96±17.58
6	NPP	142.99	159.14	112.89-170.44	143.12±12.40
7	SPP	4.98	3.72	2.34-6.12	4.52±0.89
8	PBL	30.37	25.92	20.01-56.03	34.54±8.27
9	SW	10.46	7.75	5.51-16.02	11.06±2.27
10	BA	21.17	51.35	21.47-56.22	35.43±11.16

PH: Plant height (cm), PB: Number of primary branches, SB: Secondary branches, DF: Days to flowering, DM: Days to maturity, NPP: Number of pods per plant, SSP: Seeds per pod, PBL: Pod bearing length on main axis (cm), SW: 100 Seed weight (g), BA: Branching angle with main stem (Degrees).

Table.7 and Table.8 Genetic parameters of variation for the traits under study in environment one (E1) and environment two (E2)

Genetic parameters E1												
S. No.	**Characters**	**Mean**	**Range min**	**Range max**	**Pv**	**Gv**	**Ev**	**Gcv (%)**	**Pcv (%)**	**H²**	**GA**	**GA as % of mean**
1	PH	147.27	92.31	193.62	499.67	498.75	0.92	15.16	15.17	0.99	45.58	30.88
2	PB	10.69	6.11	15.76	8.96	8.81	0.15	27.76	28	0.98	6.04	56.5
3	SB	4.2	2.04	6.32	1.38	1.26	0.12	26.72	27.96	0.91	2.02	48.09
4	DF	130.11	79.83	153.02	337.235	336.13	1.1	14.09	14.11	0.99	37.45	28.78
5	DM	158.79	122	173.40	218.92	217.41	1.51	9.28	9.31	0.99	30.17	18.97
6	NPP	143.63	110.34	179.11	177.5	174.5	3	9.19	9.27	0.98	26.89	18.72
7	SPP	4.57	2.43	6.3	0.9	0.83	0.07	19.93	20.75	0.92	1.79	39.16
8	PBL	34.29	19.88	55.05	74.06	73.66	0.4	25.02	25.09	0.99	17.55	51.18
9	SW	10.88	5.43	15.94	10404.1	10404.05	0.05	937	956.25	0.99	208.11	1911.8
10	BA	38.52	20.65	50.08	98.87	99.47	0.4	25.89	25.94	0.99	20.38	73.67

Genetic parameters E2												
S. No.	**Characters**	**Mean**	**Range min**	**Range max**	**Pv**	**Gv**	**Ev**	**Gcv (%)**	**Pcv (%)**	**H²**	**GA**	**GA as % of mean**
1	PH	146.27	94.32	191.42	501.11	491.66	9.45	15.15	15.3	0.98	45.19	30.89
2	PB	11.69	6.54	15.19	8.83	8.26	0.57	24.58	25.41	0.93	5.69	48.67
3	SB	4.24	1.82	6.24	1.32	0.89	0.43	22.24	27.09	0.67	1.58	37.26
4	DF	132.11	80.83	154.26	347.22	342.77	4.45	14.01	14.1	0.98	37.61	28.46
5	DM	159.79	120.09	174.34	226.27	223.81	2.46	9.3	9.4	0.98	30.36	18.99
6	NPP	142.63	112.89	170.44	176.73	152.25	21.48	8.64	9.32	0.86	23.55	16.51
7	SPP	4.37	2.34	6.12	0.89	0.81	0.08	20.5	21.58	0.91	1.76	40.27
8	PBL	33.29	20.01	56.03	76.25	70.56	5.69	25.23	26.23	0.92	16.54	49.68
9	SW	10.48	5.51	16.02	10404.26	10404.15	0.11	972.28	973.29	0.99	208.02	1984.92
10	BA	34.52	21.47	56.22	98.92	96.99	1.93	28.52	28.81	0.98	20.07	58.14

PH: Plant height (cm), PB: Number of primary branches, SB: Secondary branches, DF: Days to flowering, DM: Days to maturity, NPP: Number of pods per plant, SSP: Seeds per pod, PBL: Pod bearing length on main axis (cm), SW: 100 Seed weight (g), BA: branching angle with main stem (Degrees)

Table.9 Summary of QTLs identified in both the environments for plant type and seed yield components

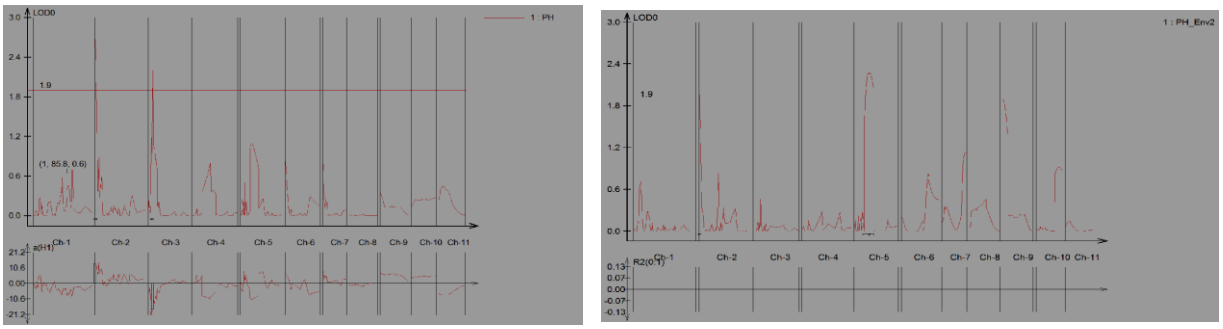
QTLs for RILS					
First Environment					
Trait	**Chromosome No.**	**Position (cM)**	**LOD**	**Additive effect**	**Phenotypic Variance (%)**
PH	**2**	**0-0.2**	**2.79**	**14.4**	**10**
	3	10.8-11.2	2.21	-21.2	7
DF	5	1.8-2.5	2.62	-14.2	13
DM	4	2.8-3.3	1.92	6.14	7
	5	1.9-2.4	2.89	-16.9	3
SPP	3	81.8-82.4	4.44	-1.26	23
	4	93.0-93.5	1.9	-1.1	26
	4	101.8-102.3	4	-0.96	26
BA	2	47.8-48.3	2.4	-12.7	11
	2	59.5-60.3	2.6	-10.6	11
Second Environment					
PH	5	36.5-36.9	2.28	-22.48	13
	2	0-0.3	2.3	11.2	7
DF	5	2.0-2.5	2.75	-13.46	12
DM	4	2.8-3.3	1.9	6.37	8
	5	2.0-2.4	3	-18.27	13
SPP	1	19.2-19.8	3.41	-1.07	17
	2	45.7-46.2	2.09	-0.84	9
	10	8.7-9.1	2.86	0.74	22
PBL	2	29.5-30	2.07	-5.32	9
	4	75.5-76	2.64	7.6	12
	4	0-0.2	2.48	-5.37	12
BA	5	93.3-93.7	2.49	10.7	36

PH: Plant height (cm), DF: Days to flowering, DM: Days to maturity, SPP: seeds per pod, PBL: Pod bearing length (cm), BA: Branching angle with main axis (Degrees).

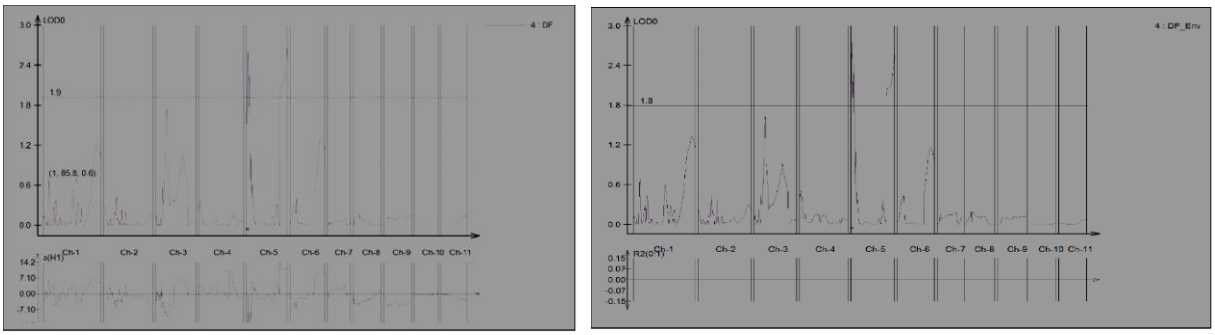
Fig.1-3

Cartographer images for consistent QTLs in both the environment

Plant height first environment and second environment



Days to flowering in the first environment and second environment



Days to maturity in the first and second environment

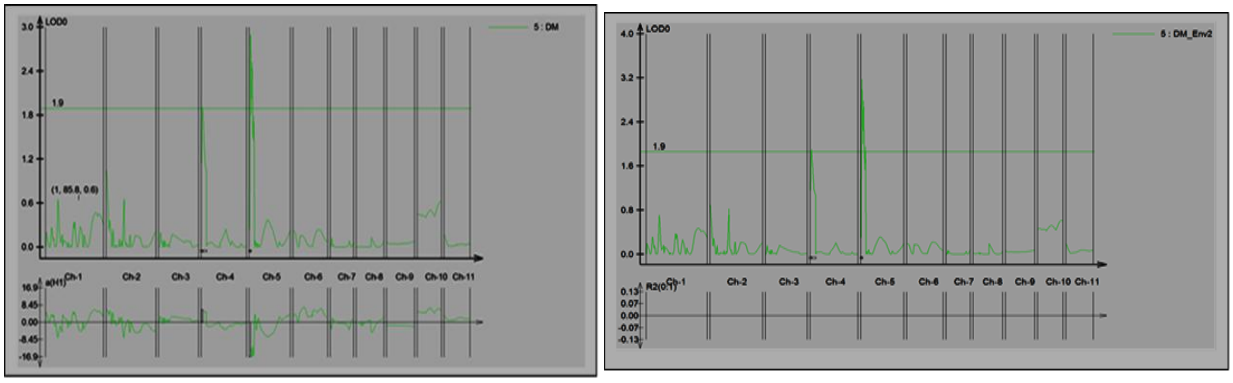
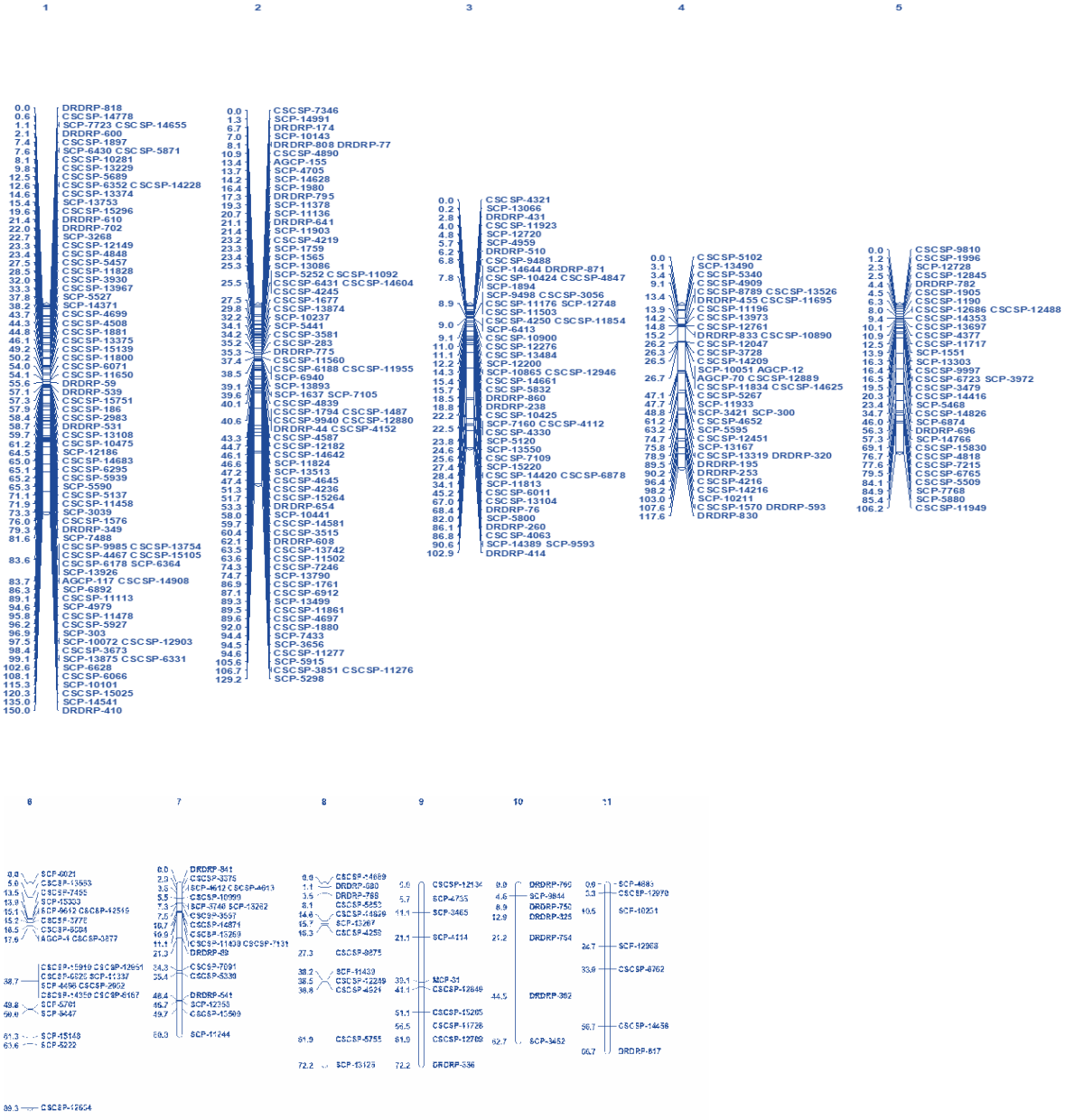


Fig.4 Linkage map of Pigeonpea with 359 polymorphic markers with the location of QTLs



Other QTLs had been found on chromosome 3 and chromosome 5 which are in requirement of validation in other elite mapping populations under different seasons to confirm their fidelity and consistency and they also showed negative additive effect. The region lies between the markers CSCSP 7346 – SCP 14991 on chromosome 2 (Table 9 and Fig. 4).

Days to flowering (DF)

Total of 2 QTLs in two environments have been identified on chromosome 5 with a negative additive effect of -14.2 and -13.46 in first and second environments having the LOD scores of 2.62 and 2.75 respectively (Fig. 2). They explained the phenotypic variation by 13% and 12% in the respective

environments. They are present between the markers CSCSP 9810 – SCP 12728 on chromosome 5. They were regarded as major QTLs as they had explained the phenotypic variation more than 10 per cent (Table 9 and Fig. 4).

Days to maturity (DM)

Four consistent QTLs had been identified on chromosomes 4 and 5 in two different environments whose additive effects were 6.14 and -16.9 in first environment pertaining to chromosome 4 and 5 and 6.37 and -18.27 in second environment (Fig. 3). The positive and negative effects of the QTLs indicate that they are from female and male parents respectively for which selection is to be made for desirable allele. The identified QTLs explained the phenotypic variation by 7% and 3% in first environment and 8% and 13% in second environment. They have been identified with the LOD scores 1.92 and 2.89 of 4 and 5 chromosomes and 1.9 and 3 in second environment. The identified QTLs were between the markers CSCSP 5102 – CSCSP 5340on chromosome 4 and CSCSP 1996 – CSCSP 12845 on chromosome 5 (Table 9 and Fig. 4).

Two environment study made it clear that which QTLs are truly consistent and are not influenced by the factors of the environment. Concerning plant type, four consistent QTLs had been identified. One for plant height (PH), one for days to flowering (DF) and two for days to maturity (DM) as they were detected in same region.

Concerning seed yield components, QTLs had been identified for seeds per pod in two environments but did not showed any consistency. As a result of which validation in different seasons/ environments under different background is necessary for confirmation. Thus, stable QTLs represent striking quarry for marker assisted selection in case of Pigeonpea. Plant height being major agronomic character is associated with total yield potential of the crop. In contrast to the findings of Giriraj *et al.,* (2012) QTL had been identified on chromosome 2 with consistency. The markers used were SNP markers despite the SSR markers in the previous study. Sekhar babu *et al.,* (2014) and Giriraj *et al.,* (2012) found the similar result for days to flowering (DF) on linkage group 5 in different mapping populations. Days to maturity (DM) QTLs were also reported by the same researches on the chromosome 5. The compact erect canopy with early maturing will have high harvest index and yield with low biomass. The QTLs identified for days to flowering (DF) and days to maturity (DM) are having negative additive effect indicating that they are from male parent which is early maturing. Hence it will be very useful in further marker assisted selection to improve the Pigeonpea genotypes. The identified consistent QTLs for days to flowering and days to maturity are co-localized hence selecting for those markers will assist in development of short duration and early maturing varieties. So, these are the beneficial alleles useful for transforming the crop productivity on desired lines. The QTLs for plant height were observed on chromosome 3 and 5 were with negative additive effect which is to be further validated but the alleles from the female parent can also be considered in MAS. Finding the beneficial alleles in an inferior parent is not a surprising thing but mostly unanticipated as similar kind of reports have been given by Ballvora *et al.,* 201, Wang *et al.,* 2012 and Gutiérrez *et al.,* 2013 alleles for resistance to diseases in susceptible parents. Undeniably homogenous results had been found in barley by Boudiar *et al.,* (2016) where alleles for high productivity were traced out in low productivity parent. QTLs present as a cluster govern more than one trait may give an expression that they are

interrelated (Verma *et al.*, 2015). The QTL cluster may contain few to many genes that predominantly exhibit pleiotropy which may be due to co-existing of certain genes together in the cluster. This shows up that those traits are phenotypically correlated Aastveit and Aastveit (1993). To promote the application of the consistent QTLs found in Pigeonpea, validation and also development of physical maps with a greater number of markers and genomic assisted breeding are to be practiced. There by expanding the genetic maps of Pigeonpea. Transcriptome profiling may help in identifying the putative genes governing the trait of interest and candidate SNPs that will cover more genome which provides information about the entire region of the chromosomes. Due to the lack of proper tools for accurately dissecting the polymorphism in Pigeonpea there is a lack in progress of development of genomic resources. Study on synteny among the related species of Pigeonpea and model legume *Medicago trancatula* assists in generation and anchoring different genetic maps with high level of saturation.

High yielding stable varieties of a particular crop species will allow the farmer to incorporate the crop in his cropping system which is being followed by him. Ultimately plant type, seed yield components and resistance to biotic and abiotic stress are the main factor that are contributing to high returns to farmers. Substantial approach has been made in the area of abiotic and biotic stress but in case of plant type and seed yield components there is less understanding. The experiment was performed to identify the regions associated with traits related to plant type and seed yield components. RIL population developed by crossing two contrasting parents for plant type and seed yield components for identification of QTLs related to plant type and seed yield components. Study assisted in identification of three consistent QTLs for three traits. The other QTLs identified different traits cannot be crossed out and are to be stringently validated under different seasons in different environments to confirm their consistency. Significance of the correlations is in agreement with the identified QTLs in case of plant height, days to maturity and days to flowering. QTL clusters, co-localization indicates that the genes may be linked or exhibiting pleiotropic effect. Synteny based markers assist in identifying the orthologous genes in the regions nearer to the traits of interest. This will help in narrow downing the confidence interval where by identifying candidate regions. They may boost the genomic resources for marker assisted breeding.

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