

PRIL_A, PRIL_B and PRIL_C: Pigeonpea Recombinant Inbred Line Mapping Populations Segregating for Resistance to Fusarium Wilt and Sterility Mosaic Disease

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Abstract

Pigeonpea [*Cajanus cajan* (L) Millsp] bi-parental populations segregating for various traits of interest are being developed. The three most advanced populations, named PRIL_A, PRIL_B and PRIL_C (Pigeonpea Recombinant Inbred Line, population A, B and C) have reached F₆ generation. PRIL_A: derived from the cross ICPB 2049 x ICPL 99050 segregates for fusarium wilt (FW), 329 lines. PRIL_B: derived from the cross ICPL 20096 x ICPL 332 segregates for FW and sterility mosaic disease (SMD), 342 lines. PRIL_C: derived from the cross ICPL 20097 x ICP 8863 segregates for SMD, 366 lines.

Marker genotyping of the parental lines, however, showed low level of genetic variation. After screening over 4,616 (3,000 simple sequence repeats (SSRs) and 1,616 single nucleotide polymorphism (SNPs)) markers on parental genotypes of each mapping population, a total of 159 (104 SSRs and 55 SNPs), 80 (52 SSRs and 28 SNPs) and 157 (143 SSRs and 14 SNPs) markers were found polymorphic for ICPB 2049 vs ICPL 99050, ICPL 20096 vs ICPL 332 and ICPL 20097 vs ICP 8863, respectively. The polymorphic markers will be used for constructing genetic linkage maps. The populations will be screened for FW and SMD in 2012-13, while marker-trait association analysis will also be conducted to understand the genetic basis of resistance to these diseases. Further selection from the above indicated mapping populations during 2011-12, on an effort initiated in 2010, resulted in 28 lines with high yield (up to 2.4 t/ha) and disease resistance.

Summary of mapping populations.

Population	Cross name	Gen	Lines	Segregates for
PRIL_A	(ICPB 2049 x ICPL 99050)	F ₆	329	Fusarium wilt disease
PRIL_B	(ICPL 20096 x ICPL 332)	F ₆	342	Fusarium wilt and sterility mosaic disease
PRIL_C	(ICPL 20097 x ICP 8863)	F ₆	366	Sterility mosaic disease



Sick plot nursery at ICRISAT, Patancheru, AP, India.



Fusarium wilt disease.



Sterility mosaic disease.

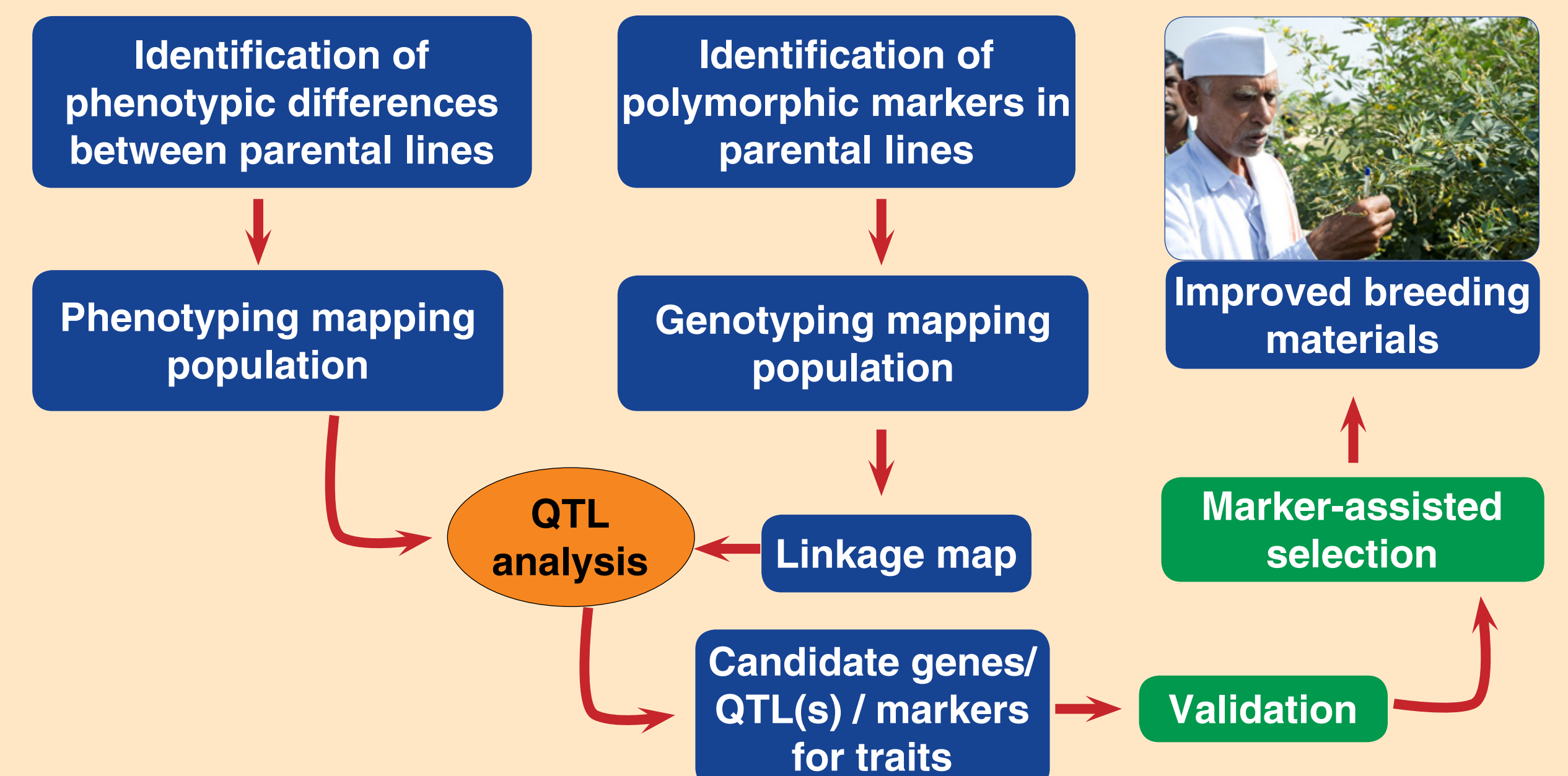
Summary of agronomic traits recorded during the rainy 2011 cropping season and mean disease nursery data for years 2009-2011 at ICRISAT, Patancheru, AP, India.

Population	Flowering days	Maturity days	Plant height (cm)	Seeds per pod (No.)	Weight of 100 seeds (g)	Pods per plant (No.)	FW (%)	SMD (%)
PRIL_A								
ICPB 2049	150	190	145	3.8	8.6	128	72	0
ICPL 99050	145	175	155	3.8	7.1	428	0	0
329 lines (mean)	133	171	141	3.5	10.7	202	-	-
Range	105-158	145-190	100-185	1.7-5.3	6.7-17.9	12-560	-	-
PRIL_B								
ICPL 20096	138	183	180	3.5	15.42	110	4	0
ICPL 332	138	185	195	3.0	14.72	310	62	41
342 lines (mean)	132	171	161	3.4	10.30	185	-	-
Range	105-149	135-185	110-200	2.0-5	5.8-14.3	28-440	-	-
PRIL_C								
ICPL 20097	140	180	190	3.4	9.20	477	10	0
ICP 8863	120	155	170	3.5	9.30	276	11	100
366 lines (mean)	129	165	164	3.4	9.20	205	-	-
Range	105-148	130-185	120-205	2.0-4.5	4.5-14.5	25-545	-	-

Promising lines selected from the mapping populations for breeding purposes.

Pedigree	Yield (kg/ha)	FW (%)	SMD (%)
(ICPB 2049 x ICPL 99050)-64-1-1-2	2289.6	10.7	0.0
ICPB 2049 (Parent 1)	1425.7	50.0	0.0
ICPL 99050 (Parent 2)	1844.8	0.0	0.0
(ICPL 20096 x ICPL 332)-140-1-1-2	2151.5	6.3	0.0
(ICPL 20096 x ICPL 332)-289-1-1-2	2075.3	0.0	0.0
(ICPL 20096 x ICPL 332)-368-1-1-2	2454.3	0.0	10.0
ICPL 20096 (Parent 1)	1322.9	0.0	0.0
ICPL 332 (Parent 2)	1901.9	45.0	38.0
(ICPL 20097 x ICP 8863)-253-1-1-2	1739.1	0.0	0.0
ICPL 20097 (Parent 1)	949.6	4.6	0.0
ICP 8863 (Parent 2)	1498.1	8.1	72.2
LSD (0.05)	785.9	-	-

Trait mapping scheme



Remarks

- Three pigeonpea RIL mapping populations have been developed and shared with partners for FW and SMD phenotypic evaluations.
- Breeders have taken advantage of the developed mapping populations to directly select new lines that combine high agronomic potential and disease resistance.
- Several lines selected from the mapping populations produced more than 2.0 t/ha and had FW and SMD resistance.

Future outlook

- The polymorphic markers observed between the parental lines will be used to genotype the pigeonpea RIL populations and linkage maps will be prepared.
- The three RIL populations will be screened for FW and SMD resistance during the current season (2012-13) at multiple locations.
- Marker-trait association analysis will be conducted to identify genes or QTLs associated with FW and SMD resistance.
- Selected lines from the mapping populations will be tested in multi-location trials and promoted as new varieties.

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