Improving pod borer complex tolerance in cultivated pigeonpea (*Cajanus cajan*) by using wild *Cajanus* species

Shivali Sharma*, Jagdish Jaba, Suraj Prashad, Ekram Hussain, Pronob J Paul, Tripura Nammi and HC Sharma
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru-502324, Telangana, India
*Corresponding author's email: shivali.sharma@cgiar.org

Background

Pod borer (*Helicoverpa armigera* Hübner) is the single largest yield reducing factor in food legumes. Worldwide, pod borer causes an estimated loss of over $2 billion annually, despite over $1 billion value of insecticides used to control this devastating pest. In pigeonpea (*Cajanus cajan* (L.) Millsp.), an important food grain legume crop of the semi-arid tropics, *Helicoverpa armigera* causes maximum yield losses (25-70%) followed by pod fly, *Melanagromyza obtusa* (10-50%), *Maruca vitrata* (5-25%) and pod bug, *Clavigralla gibbosa* (10-30%). High levels of resistance to pod borer is not available in the cultivated genepool, which necessitates the exploitation of new and diverse sources of variations.

Crop Wild Relatives (CWR) as source of pod borer resistance

Crop wild relatives of pigeonpea are highly resistant to *H. armigera*. Oviposition non preference, antibiosis, and tolerance are the major components of resistance. Wild *Cajanus* species with different mechanisms have been identified and can be used as the potential sources for introgressing resistance genes into the cultigen (Table 1).

Table 1: Wild *Cajanus* species exhibiting different mechanisms of pod borer resistance

Genepool	Species	Identity	Criteria
Secondary genepool	*C. acutifolius, C. albicans, C. sericeus, C. scarabaeoides*	ICPW # 1, 13, 14, 159, 160, 83, 90, 94, 125, 137, 141 and 280	High levels of antixenosis for oviposition and expression of antibiosis
	C. scarabaeoides, C. albicans, C. sericeus	ICPW # 281, 94, 116, 137, 13, 14 and 159	High density of non-glandular (C- & D-type) trichomes
Tertiary genepool	*C. platycarpus, Rhynchosia aurea,*	ICPW # 68 and 210	High levels of antixenosis for oviposition and expression of antibiosis

Pre-breeding for improving pod borer tolerance in pigeonpea

-Evaluation of CWR to identify promising donors and selection of recipients

- *C. scarabaeoides* and *C. acutifolius* selected as donors and popular pigeonpea varieties, Asha (ICPL 87119) and Maruti (ICP 8863) as recipients.

-Development of pre-breeding populations

Generating interspecific crosses using cultivated and wild *Cajanus* species

- Simple cross approach (Fig.1)
- Complex cross approach

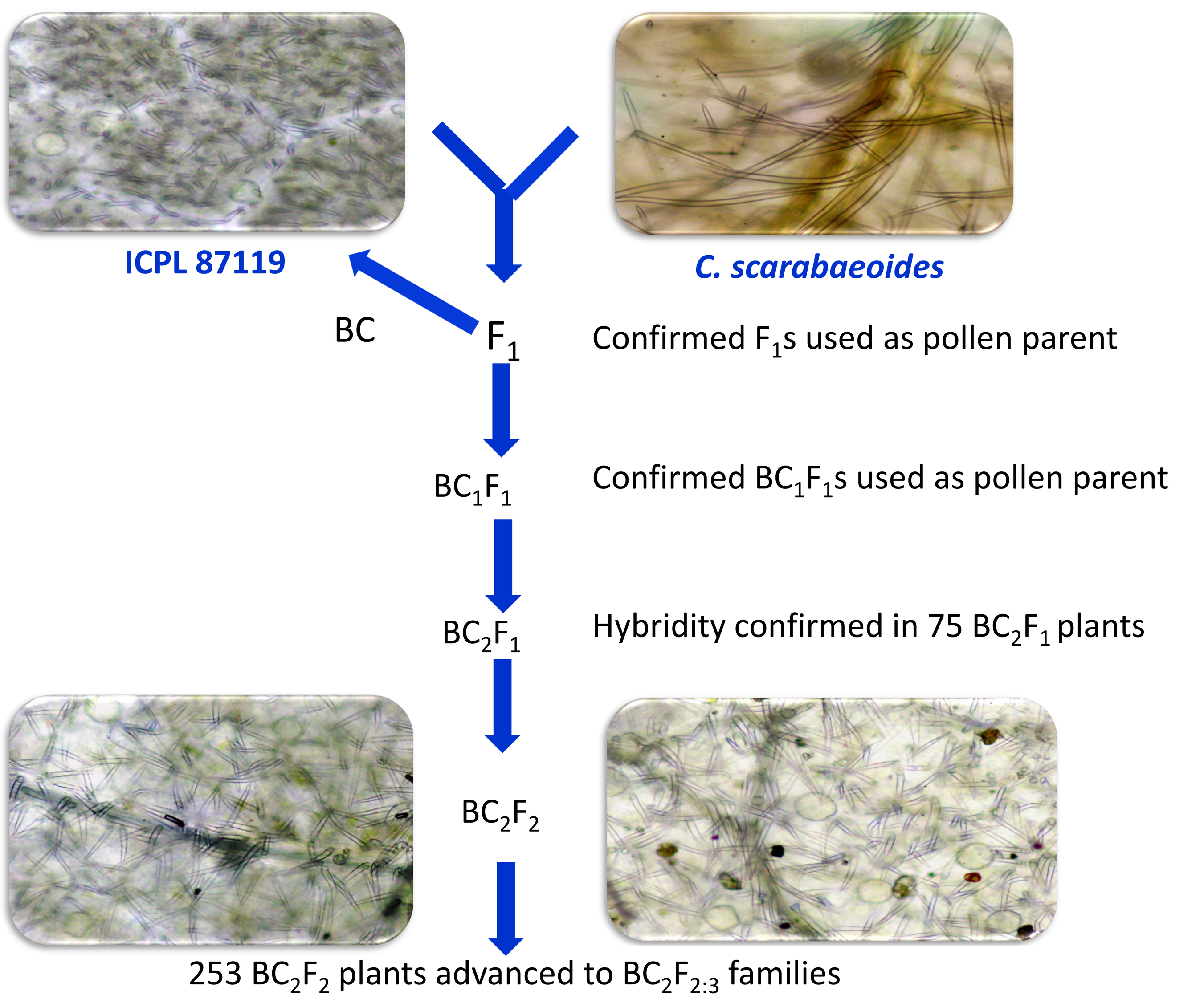

Fig. 1. Population development using *C. scarabaeoides* as donor (Simple cross approach) and introgression lines with high density of 'C' and 'D' type trichomes in BC_2F_2 generation

Table 2: Pre-breeding populations developed using wild *Cajanus* species

Population	Wild species used	Material	Generation	No. of lines
Simple cross approach				
PP 1501	*C. acutifolius*	ICP 8863 × [ICP 8863 × (ICP 8863 × ICPW 1)]	BC_2F_3	1108
PP1505	*C. scarabaeoides*	ICPL 87119 × [ICPL 87119 × (ICPL 87119 × ICPW 281)]	BC_2F_3	288
Complex cross approach				
PP 1503	*C. acutifolius and C. scarabaeoides*	ICPL 87119 × [(ICPL 87119 × ICPW 1)× (ICPL 87119 × ICPW 281)]	4-BC_1F_3	533
PP 1504	*C. acutifolius and C. scarabaeoides*	ICP 8863 × [(ICP 8863 × ICPW 1)× (ICP 8863 × ICPW 281)]	4-BC_1F_3	392

Evaluation of pre-breeding populations and identification of pod borer tolerant introgression lines

- Four backcross populations were evaluated under un-sprayed field conditions during 2018 rainy season (Table 2).
- Identified 156 introgression lines (ILs) with low visual damaging rating score (5.0-6.0) at harvesting time and low total pod borer complex damage (<50%) (Table 3).
- Introgression line: PP1505-34-3-6 exhibited lowest pod damage (5%) followed by PP1501-14-4-3 (7%), PP1501-16-7-2 (7%), PP1501-16-7-6 (7%) and PP 1505-11-2-4 (8%) compared to tolerant check ICPL 332 WR (13%).

Table 3. Screening of pre-breeding populations for pod borer tolerance

Population	Total no. of ILs screened	No. of pod borer tolerant ILs identified
PP 1501	1,108	79
PP1505	288	28
PP1503	533	41
PP1504	392	8
Total	**2,321**	**156**

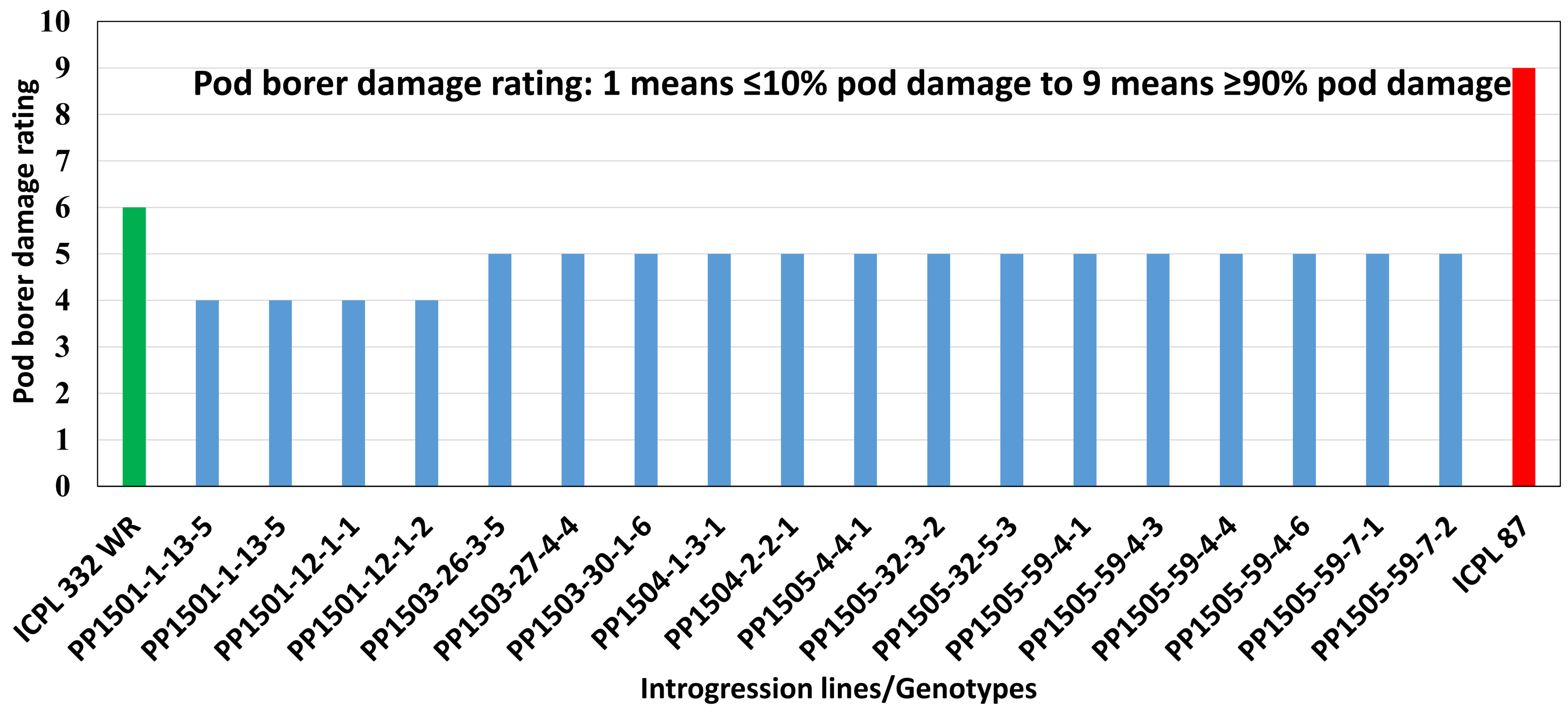

Fig. 2. Pod borer damage in pre-breeding populations

C. acutifolius

C. scarabaeoides

Future strategy

- Pod borer tolerant introgression lines identified in this study are being re-screened under field conditions by artificial infestation of *H. armigera* larvae as well as leaf and pod bioassay under laboratory conditions to study the mechanism of resistance.
- Finally, pod borer tolerant lines will be shared with different researchers globally for use in breeding programs to develop pod borer tolerant lines.

Conclusion

The study so far exhibited the large genetic variation and tolerance among the introgression lines derived from CWR. Utilization of confirmed tolerance sources in breeding programs will pave the way to develop new pigeonpea cultivars with improved pod borer tolerance and broad genetic base.

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