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# Genetic Enhancement in Major Food Legumes

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# Chapter 7

## Identification, Evaluation and Utilization of Resistance to Insect Pests in Grain Legumes: Advancement and Restrictions



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### 7.1 Introduction

India is the largest producer and consumer of pulses in the world. Pulse crops are the mainstay of Indian agriculture and principal source of dietary proteins especially among the vegetarians in India and are known to lower the risks of several non-communicable diseases such as colon cancer and cardiovascular diseases (Jukanti et al. 2012). Protein content in pulses is about 22–24 per cent, which is almost twice the protein content in wheat and thrice that of rice. Pulses can be grown on range of soil and climatic conditions and included in crop rotation, mixed cropping and intercropping, thus maintaining soil fertility through nitrogen fixation and release of soil-bound phosphorus contributing significantly to sustainability of the farming systems. Major pulses chickpea or bengal gram (*Cicer arietinum*), pigeonpea or red gram or tur dal (*Cajanus cajan*), lentil (*Lens culinaris*), urdbean or black gram (*Vigna mungo*), mung bean or green gram (*Vigna radiata*), lablab bean (*Lablab purpureus*), moth bean (*Vigna aconitifolia*), horse gram (*Dolichos uniflorus*), pea (*Pisum sativum*), grass pea or khesari (*Lathyrus sativus*), cowpea (*Vigna*

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*unguiculata*) and broad bean or faba bean (*Vicia faba*) constitute some of the most important pulses used as food worldwide. Of these, chickpea, pigeonpea, mung bean, urdbean and lentil are the major pulses grown in India. Food legumes are cultivated globally on an area of 70 million hectares with a production over 78 million tonnes and an average productivity of 846 kg ha<sup>-1</sup> (FAO 2017). It is estimated that globally about 190 million hectares under pulses contributes about five to seven million tonnes of nitrogen in soils (Anonymous, 2016a). During 2017–2018, pulses were cultivated on more than 29 million ha (Mha) and recorded the highest ever production of 25.23 million tonnes (Mt) with average productivity of 841 kg ha<sup>-1</sup> (Department of Agriculture, Cooperation & Farmers Welfare-DAC, 2018).

Chickpea and pigeonpea are the two important pulse crops in India contributing to about 62 per cent of total pulse production followed by mung bean (11%), urdbean (10–12%), lentil (8–9%) and other legumes (20%) (Anonymous, 2011). The stability in yield and production is affected by number of biotic and abiotic factors reducing the production and productivity of grain legumes worldwide, of which insect pests are the predominant ones. Over the past five decades, significant progress has been made in developing improved cultivars and crop management practices, but there has been very little success in increasing the productivity.

Grain legumes are damaged by more than 150 species of insect pests, under unprotected conditions and in storage (Clement et al. 2000, Sharma et al. 2016a). Amid the numerous insect pests damaging food/grain legumes, *Helicoverpa armigera* (Hubner) is the most economically important pest of grain legumes in Asia, Africa and Australia (Sharma 2001). The spotted pod borer, *Maruca vitrata* (Geyer), is another major pest of cowpea and pigeonpea (Jackai and Adalla 1997, Sharma 1998), but it also damages other food/grain legumes, except chickpea and lentil (Sharma et al. 1999). The pod fly (*Melanagromyza obtusa* Malloch) and pod wasp (*Tanaostigmodes cajaninae* La Salle) both cause an extensive damage to pigeonpea in India. The leaf miner (*Liriomyza cicerina* Rondani) is a significant pest of chickpea in West Asia and North Africa (Weigand et al. 1994). While pea pod borer (*Etiella zinckenella* Triet.) is an important pest of pigeonpea, field pea and lentil, the aphid (*Aphis craccivora* Koch) infests all the food legumes and is a major pest of cowpea, field pea, faba bean and *Phaseolus* beans. *Aphis fabae* (Scop.) is a major pest of faba bean and *Phaseolus* beans, and *Acyrtosiphon pisum* Harris is an important pest of field pea worldwide.

The whitefly (*Bemisia tabaci* Genn.) infests all the crops, except chickpea, but is an important pest of *Phaseolus* spp. like black gram and green gram. The defoliators, *Spodoptera litura* (Fab.) in Asia and *S. exigua* (Hubner) in Asia and North America, are occasional pests. Bihar hairy caterpillar, *Spilosoma obliqua* (Walk.), is an important pest of green gram and black gram in North India, while the red hairy caterpillars, *Amsacta* spp., damage the rainy season pulses in south central India. Sap-sucking pests, like leafhoppers, *Empoasca* spp., infest most of the food/grain legumes and cause maximum economic damage in black gram, green gram and *Phaseolus* beans. The pod-sucking bugs, *Clavigralla tomentosicollis* (Stal.), *Clavigralla gibbosa* (Spin.), *Nezara viridula* (L.) and *Bagrada hilaris* (Burm.), are occasional pests, but extensive damage has been recorded by *C. tomentosicollis* in

cowpea in Africa and by *C. gibbosa* in pigeonpea in India. Under storage conditions, bruchids (*Callosobruchus chinensis* L.) and *C. maculatus* (Fab.) cause extensive losses in stored food legumes worldwide, and stink bug (*Nezara viridula* L.) is the major damaging pest in soybean in Brazil (Borges et al. 2011). The pea weevil (*Bruchus pisorum* L.) is an important pest of field pea in major production areas (Clement and Quisenberry 1999; Mendesil et al. 2016).

## 7.2 Extent of Losses Due to Insect Pests in Grain Legumes

Biotic factors are the major constraints in achieving the potential yield in pulses. Among the biotic stresses, diseases and insect pests are the major yield-limiting factors causing a yield loss of about 30 per cent (Dhar and Ahmad 2004). In India, insect pests lead to an approximate economic loss of 15 per cent in terms of yield worth \$2285.29 million (Dhaliwal et al. 2015). Pod borer, *H. armigera*, the single largest yield-reducing factor in food legumes, causes an estimated loss of US\$ 317 million in pigeonpea and \$328 million in chickpea (ICRISAT 1992). Worldwide, it causes an estimated loss of over \$2 billion annually, despite over \$1 billion value of insecticides used to control *H. armigera* (Sharma 2005). Another pod borer, *M. vitrata* causes an estimated loss of US \$ 30 million annually (Saxena et al. 2002). In pigeonpea, maximum yield losses are reported due to pod borer (25–70%) followed by pod fly (10–50%) which is a major pest in northern and central parts of India and by *Maruca* (5–25%) and pod bug (10–30%) (Sharma et al. 2010). Besides these, soybean aphid (*A. glycines*) can induce up to 58% yield losses in soybean (Wang et al. 1994) costing around \$2.4 billion annually (Song et al. 2006, Tilmon et al. 2011). Similarly, legume flower thrips (*M. sjostedti*) have been reported to cause yield losses ranging from 20 to 100% in cowpea (*V. unguiculata*) in tropical Africa (Karungi et al. 2000) (Plate 7.1).

## 7.3 Screening Techniques

The most crucial and perhaps the most difficult task in breeding for insect resistance is the identification of insect-resistant plants/lines from the segregating generations. This requires uniform initial infestation of all the plants in the population to ensure that the plants scored as resistant should not escape the insect infestation. The screening for insect resistance may be done either (1) in the field or (2) in the glasshouse.

**Field screening:** Screening for insect resistance, particularly in breeding programmes, is usually done in the field since a much larger number of plants can be screened in the fields than in a glasshouse. In addition, under field conditions, the plants are exposed to other insect pests prevalent in the area; this reduces the possibility of unintended selection for susceptibility to them. However, field tests



Leaf roller (*G.crtica*)



Pod borer (*H.armigera*)



Spotted Pod borer (*M.virata*)



Plume moth (*E. atomosa*)



Pod fly (*M.obtusa*) infested pod and and damage symptom



Gram pod borer (*H.armigera*)



Beet armyworm(*S.exigua*)

**Plate 7.1** Pest complex damaging major legumes

Aphid, *Aphis craccivora*Bruchid, *Callosobruchus chinensis***Plate 7.1** (continued)

are carried out under uncontrolled conditions, and in many cases, it may not be possible to ensure uniform initial infestation of all the plants in the screening material. As a result, the magnitude of experimental error of the field tests is much larger than that of laboratory tests (Jaba et al. 2017a).

**Glasshouse screening:** A much smaller number of plants can be screened in a glasshouse than in the field. But the results from glasshouse tests are much more reliable than those from field tests since both the environment and the initial level of infestation can be kept more or less uniform for all the test material.

It may be noted that field and glasshouse screenings are complementary to each other. The resistant plants/lines identified through glasshouse screening should be evaluated for their resistance in the field under natural infestation, and vice versa.

## 7.4 Identification and Utilization of Resistance to Insect Pests

Identification and utilization of genetic sources of resistance is one of the economic and eco-friendly approaches for management of insect pests and increasing the availability of pulses. Significant effort has been made in recognition of sources of resistance to insect pests, but the landraces from the centre of origins have not been utilized extensively in the crop breeding programmes (Clement et al. 1994; Sharma and Ortiz 2002). Varieties with improved yield are more prone to insect pests than the landraces (Lale and Kolo 1998), and lack of strategies for positive selection for resistance against insect pests results in increased susceptibility in elite cultivars as compared to the landraces (Shaheen et al. 2006). A few cultivars with resistance/tolerance to insect pests have been identified in pigeonpea, chickpea, cowpea, black gram, green gram and field pea (Table 7.1). However, the levels of resistance/tolerance to pod borers are low to moderate but are quite more effective when deployed in combination with novel synthetic insecticides or natural plant products like neem seed kernel extract (NSKE) (Sharma and Pampapathy 2004).

**Table 7.1** Identification and utilization of host plant resistance to insect pests in grain legumes in India

Crop	Genotypes	Reference
Pigeonpea	<p><b>Pod borer, <i>Helicoverpa armigera</i></b> ICPL 332 WR<sup>a</sup>, PPE 45–2, ICPL 84060, BDN 2, ICPL 4, Bori, T 21, ICP 7035 and ICPL 88039, ICC 12475, ICC 12477, ICCL 87317, ICCV 95992, ICPL 98003, ICPL 187–1, LRG 41, ICPL 269, ICP 7203–1, ICPL 84060 and ICPL 87119</p> <p><b>Legume pod borer, <i>Maruca vitrata</i></b> ICPL 88034 and MPG 679</p> <p><b>Pod fly, <i>Melanagromyza obtusa</i></b> ICP 10531-E1, ICP 7941-E1, ICP 7946-E1 and ICP 7176–5. GP 75, GP 118, GP 233 and GP 253</p>	<p>Lateef and Pimbert (1990), Kalariya et al. (1998), Parsai (1996, 2005), Sunitha et al. (2008), Sharma et al. (2009), Srivastava and Joshi (2011), Kumari et al. (2010a) Saxena et al. (1996)</p> <p>Lateef and Pimbert (1990). Moudgal et al. (2008)</p>
Chickpea	<p><b>Pod borer, <i>Helicoverpa armigera</i></b> ICC 506, ICC 09314, ICC 738008, ICC 09104, 09116, ICCL 86105, ICC 14364, ICCV 7<sup>a</sup>, ICCV 10<sup>a</sup>, Dulia<sup>a</sup>, C 235<sup>a</sup>, JG 79<sup>a</sup>, BJ 256<sup>a</sup>, JG11, ICCL 86111, Vijay and Vishal, ICC 10667, ICC 10619, ICC 4935, ICC 10243, ICCV 95992, BGD 237 and ICC 10817</p> <p><b>Leaf miner, <i>Liriomyza cicerina</i></b> ILC 380, ILC 5901 and ILC 7738</p> <p><b>Beet armyworm, <i>Spodoptera exigua</i></b> ICC 12475</p> <p><b>Bruchid</b> DCP 923, JG 315, BG 1003, BG 372</p> <p><b>Root-knot nematode</b> <i>Meloidogyne incognita</i> and <i>M. javanica</i> Sir Please include genotypes for nematodes</p>	<p>Dixit (2015), Lateef and Sachan (1990), Bhagwat et al. (1995), Das and Kataria (1999), Deshmukh and Patil (1995). Shankar et al. (2012), Siddegowda et al. (2005) Singh and Weigand (1994), Girija et al. (2008)</p> <p>Shankar et al. (2012)</p> <p>Indian Institute of Pulses Research (2015)</p> <p>Indian Institute of Pulses Research (2015)</p>
Black gram	<p><b>Pod borer, <i>Helicoverpa armigera</i></b> Kalai<sup>a</sup>, 338–3, Krishna<sup>a</sup> and Co 3<sup>a</sup>, 4<sup>a</sup> and 5<sup>a</sup> CBG 08–011 and PLU 54; UH 82–5, IC 8219 and SPS 143</p> <p><b>Jassid, <i>Empoasca kerri</i></b> Sinkheda 1<sup>a</sup>, Krishna<sup>a</sup>, H 70–3 and UPB 1<sup>a</sup></p> <p><b>Stem fly, <i>Ophiomyia phaseoli</i></b> Killikullam<sup>a</sup>, 338/3, P 58, Co 4<sup>a</sup> and Co 5<sup>a</sup></p> <p><b>Pink pod borer, <i>Cydia ptychora</i></b> SKNU-03-03</p>	<p>Lal (1987)</p> <p>Soundararajan et al. (2010), Ponnusamy et al. (2014)</p> <p>Dawoodi et al. (2010)</p>
Green gram	<p><b>Pod borer, <i>Maruca testulalis</i></b> J1, LM 11, P 526 and P 336 ML 337, ML 5, MH 85–61 and ML 325 CGG 08–007 and CGG 08–028</p> <p><b>Stem fly, <i>Ophiomyia centrosematis</i></b> Co 3</p>	<p>Lakshminarayan and Misra et al. (2008)</p> <p>Soundararajan et al. (2010)</p> <p>Devasthali and Joshi (1994)</p> <p>Somta et al. (2008)</p>

(continued)

**Table 7.1** (continued)

Crop	Genotypes	Reference
	TAM-20, PDM-84-143 and Pusa-105 against <i>A. craccivora</i> , <i>A. kerri</i> ( <i>Empoasca kerri</i> ) and <i>M. undecimpustulatus</i> <b>Bruchids</b> V1128, V2817	
Field pea	<b>Pod borer, <i>Etiella zinckenella</i></b> EC 33860, Bonville <sup>a</sup> , T 6113 <sup>a</sup> , PS 410, 2S 21 and 172 M 32,454, 235,002 <b>Leaf miner, <i>Chromatomyia horticola</i></b> P 402, PS 41–6, T 6113, PS 40, KMPR 9, P 402 and P 200	Lal (1987) Teshome et al. (2015)
Cowpea	<b>Pod borer, <i>Maruca vitrata</i></b> TVu 946, VITA 4, VITA 5, Ife Brown and Banswara <sup>a</sup> EC 394828, ET 116932, TVNu 946, Kashi Shyamal, Arka Suman and Arka Sumurudhi <b>Jassid, <i>Empoasca kerri</i></b> TVu 123, TVu 662, JG 10–72, C 152 and 3–779 (1159) <b>Aphid, <i>Aphis craccivora</i></b> P 1473, P 1476, IT82E-16 and MS 9369 <b>Bruchids, <i>Callosobruchus maculatus</i></b> IT89KD- 288, IT99K-429–2 and IT97K-356-1	Singh (1978), Lal (1987) Chanchal and Singh (2014) Jackai (1981) Benchasri et al. (2007) Obadofin (2014)

<sup>a</sup>Released for cultivation in India. Source: Sharma et al. 2017

### 7.4.1 Pigeonpea

High levels of resistance to *H. armigera* have been identified in wild relatives of pigeonpea such as *Cajanus scarabaeoides*, *Cajanus sericeus* and *Cajanus acutifolius* (Leguminosae: Papilionoideae), which can be utilized as sources of resistance in breeding programmes (Sharma et al. 2003). On the basis of per cent pod damage and pest susceptibility rating (PSR), Kooner and Cheema (2006) identified the genotypes AL 1498, AL 1502 and AL 1340 as resistant donors to develop pod borer-resistant/pod borer-tolerant cultivars of pigeonpea. Kumari et al. (2006) studied the antixenosis mechanism of resistance to *H. armigera* and identified the promising genotypes like ICP 7203–1, ICPL 187–1, T 21, ICPL 332 and ICPL 84060 which can be used in pigeonpea breeding programme. Accessions belonging to *Cajanus scarabaeoides*, *C. sericeus*, *C. acutifolius*, *C. lineatus*, *C. albicans* and *Rhynchosia bracteata* have shown resistance to pod fly damage, while those from *C. platycarpus*, *C. cajanifolius* and *R. aurea* were found to be susceptible (Sharma et al. 2003).



On the basis of pod damage and relative resistance rating, PDA 88-2E, PDA 89-2E, PDA 92-1E, PDA 92-2E, PDA 92-3E, PDA 93-1E, SL 21-1-3, SL 21-6-2, SL 21-9-2 and SL 22-2-3 were identified as resistant donors against pod fly (Lal and Rathore 1999). Among these, the long-duration genotypes such as PDA 88-2E, PDA 87-3E, PDA 85-5E and MA 3 suffered lesser pod and grain damage and exhibited oviposition non-preference to pod fly, whereas MAL 13, MA 6 and MAL 20 supported higher maggot population and had higher grain yield indicating (the mechanism of) tolerance to pod fly (Pandey and Srivastava 2006). Similar results were observed among six long-duration genotypes (MAL-20, MAL-13, MAL-27, PDA 85-5E, KAWR 92-2, NDA-5-25) evaluated for pod fly population buildup, where KAWR 92-2 supported least maggot population per ten pods (Keval et al. 2010). When assessed on the basis of pod damage, the genotypes ICP 2514 and ICP 2454 were categorized as resistant, while ICP 2459 and ICP 2155 were identified as resistant on the basis of seed damage (Mishra et al. 2012).

### 7.4.2 Chickpea

A large number of chickpea germplasm accessions (12,000) were screened under field condition at ICRISAT, and some accessions exhibited reduced susceptibility to *H. armigera* (Lateef 1985). Cowgill and Lateef (1996) reported variability in resistance to *H. armigera* in *desi* chickpeas. Moderate level of resistance to *Helicoverpa armigera* in chickpea was found to be associated with increased acid exudates on the leaves, which served as an oviposition deterrent to moths and reduced larval damage (Lateef 1985). Oxalic acid plays an important role in antibiosis mechanism by significantly inhibiting the growth of *H. armigera* larvae (Yoshida et al. 1995), whereas malic acid has no effect on larval growth, and it stimulates the oviposition of *Helicoverpa* moths (Yoshida et al. 1997). Sharma et al. (2005) have also reported resistance to *H. armigera* in wild *Cicer* spp. such as *C. pinnatifidum* and *C. judaicum* and in some perennial *Cicer* spp., due to high level of antibiosis.

Germplasm accessions like ICC 506 EB, ICC 10667, ICC 10619, ICC 4935, ICC 10243, ICCV 95992 and ICC 10817 have been identified with resistance to *H. armigera* at ICRISAT and varieties such as ICCV 7, ICCV 10 and ICCL 86103 with moderate levels of resistance (Gowda et al. 1983; Lateef and Pimbert 1990; Jaba et al. 2017b). Several accessions belonging to *C. bijugum*, *C. judaicum*, *C. pinnatifidum* and *C. reticulatum* were found resistant to *H. armigera* based on leaf feeding, larval survival and larval weight parameters (Sharma et al. 2005).

Out of 24 genotypes screened against *H. armigera*, Phule G-92028, P-1772 B and BG-1039 emerged as resistant based on egg load, larval population, pod damage and yield under field conditions (Ramegowda et al. 2007). BG-372, HC-1, SAKI-9516, Vijay and Avrodhi were found to be relatively less susceptible among the 15 genotypes/cultivars of chickpea screened against *H. armigera* based on larval population, pod damage and yield under field screening (Deshmukh et al. 2010). Siddegowda

et al. (2005) reported that the BGD 237 cultivar recorded significantly lower pod damage of 11.35%. JAKI 5226 16.56% and BK 36 (16.68%) recorded significantly higher per cent pod damage. Brar and Singh (2015) observed moderate level of resistance in genotypes 5282, RSG 963, GL 25016 and ICCL 86111 against *H. armigera* both under field and laboratory screening which could serve as valuable insect tolerance sources in crop improvement programme.

Lateef et al. (1981) reported least pod borer damage on ICC 506 as compared to Annigeri-1, while the cultivars BDN-9-3 and Phule G-4 yielded higher than the check, Annigeri-1. A negative correlation was observed between days to flowering and yield indicating higher yield returns from early flowering cultivars. Of the 119 chickpea genotypes from NBPGR screened against *H. armigera*, IC 269317, IC 268855, IC 269218 and IC 269347 were promising based on pest resistance rating (PRR) under field conditions (Cheema et al. 2010). The genotypes ICC 12478, ICC 12479 and ICC 506 EB showed tolerance to *H. armigera* damage (Lakshmi Narayanamma et al. 2007a).

Maurya et al. (2007) identified the chickpea genotypes ICC 1964, ICC 143, ICC 729 and ICC 515 as least susceptible to pod borer. Among 11 genotypes tested at Pantnagar, ICCV 10, ICCV 97115, ICCV 97119 and ICC 16381 were found tolerant to pod borer and produced greater seed yield (Rai and Ramujagir, 2005).

Limited work has been done on insect resistance in lentil. Chhabra (1981) reported seven lines showing resistance to pea pod borer (*E. zinckenella*). Genotypic differences for susceptibility to aphids (*A. craccivora*), pod borer and seed weevil were reported, but very little efforts have been made to breed for resistance to these insect pests (Erskine et al. 1994).

### 7.4.3 Cowpea

The cowpea cultivar TVNu 946 showed high levels of resistance to *Maruca* across seasons and locations (Jackai 1981). IT82E-16 exhibited high level of resistance to cowpea aphid *A. craccivora* (Benchasri et al. 2007), and the genotypes IT89KD-288 (V4) and IT89KD-391 (V2) also exhibited outstanding performance against major insect pests of cowpea in south eastern agroecology of Nigeria (Onyishi et al. 2013). The green gram (*V. radiata*) cultivars PDM-84-139 and ML-382 were very promising against *Caliothrips indicus*, BM-112 for *Raphidopalpa* sp. (*Aulacophora* sp.) and PDM-84-143, TAM-20 and Pusa-105 against *A. craccivora*, *A. kerri* (*Empoasca kerri*) and *M. undecimpustulatus* (Devasthali and Joshi 1994) and MV 1-6 for grasshopper and cotton grey weevil. The cultivar MI-67-9 was found to be resistant against bean aphid but with increased susceptibility to blue beetle. The sap-sucking jassid infestation was relatively low in varieties MI-67-3 and MI-29-22 (Devasthali and Saran 1998). The relative susceptibility or resistance in various legumes to the pulse beetle mainly depends on the morphological and physical characteristics of the seed (Venugopal et al. 2000). Also, the chemical components comprising proteinase inhibitors, lectins and  $\alpha$ -amylase inhibitors have been reported to be important

factors forming an array of constitutive defences in legumes against attack by pulse beetle (Ignacimuthu et al. 2000). Talekar and Lin (1992) ascertained that accessions V 2709 and V 2802 were highly resistant to both *C. chinensis* and *C. maculatus*, while the cultivated accessions (V 1128 and V 2817) were resistant (Somta et al. 2008) and PLM 156 and V1123 were moderately resistant to both the bruchid species (Dixit 2015). Lower pod borer complex damage was observed in CGG 08–007 and CGG 08–028 (Soundararajan et al. 2010), and the resistant response for the borer complex in TC1966, V2709, V2802, V1128 and V 2817 was attributed to the presence of biochemical compounds in the seeds (Talekar and Lin 1992; Somta et al. 2008). Sarkar and Bhattacharyya (2015) identified wild green gram *Vigna radiata* var. *sublobata* as a source of resistance to pulse beetle. Wild *Lens* species, *L. ervoides*, was identified as highly resistant, while *L. culinaris* was highly preferred for egg laying and found to be most susceptible (Gore et al. 2016). Soumia et al. (2000) found the green gram accessions KM-12-5 and P-S-16 with lesser susceptibility index than Ganga-8. In green gram the morphological trait pod diameter showed highly significant negative correlation with pod damage as well as seed damage (Sharanabasappa and Goud, 2004). Four green gram accessions, viz. LM 131, V 1123, LM 371 and STY 2633, and three black gram accessions, viz. UH 82–5, IC 8219 and SPS 143, were identified as moderately resistant to pulse beetle (Duraimurugan et al. 2014). In cowpea, the cultivar IT89KD-288, IT99K-429–2 and IT97K-356-1 were resistant to *C. maculatus* (Obadofin 2014).

#### 7.4.4 Black Gram

Lately, the pink pod borer, *Cydia ptychora* (Meyrick), was noticed on urdbean/black gram in some regions of Gujarat (Dawoodi et al. 2009), and the variety SKNU-03-03 showed least susceptibility to pink pod borer (Dawoodi et al. 2010). Low pod borer complex damage was observed in CBG 08–011 and PLU 54 (Soundararajan et al. 2010). The field pea (*P. sativum*) accessions 32,454 (17%) and 235,002 (33%) had consistently shown lower per cent seed damage, and such promising accessions can be incorporated into pea breeding programmes, thereby exploiting enhanced resistance sources against pea weevil, *B. pisorum* L., in the affected areas (Teshome et al. 2015).

However, lack of precise evaluation strategies for resistance screening against the target insect pests probably has resulted in omitting many potentially good sources of resistance. Therefore, high-throughput phenotyping has been used lately for large-scale evaluation of germplasm or breeding lines for resistance to sap-sucking insects.

## 7.5 Wild Relatives as Sources of Resistance to Insect Pests

The traits and underlying genes governing resistance to insect pests can be found in the wild accessions of the crops unlike the cultivated species with some exceptions where high levels of resistance were reported in the cultivated germplasm of haricot bean, field pea (Clement et al. 2002), cowpea (Redden et al. 1983) and black gram (Dongre et al. 1996). The wild relatives/accessions of pigeonpea and chickpea are authoritative sources of genes for resistance to insect pests. Over the past two decades, a paradigm shift has been observed in identification and deployment of genes for resistance from wild species of pigeonpea (Dhillon and Sharma 2012). In pigeonpea, the accessions ICPW 214 (*C. bracteata*); ICPW 141, ICPW 278 and ICPW 280 (*C. scarabaeoides*); and ICPW 14 and ICPW 202 (*F. stricta*) have been reported to show resistance against pod fly (*M. obtusa* and *T. cajaninae*) (Sharma et al. 2003a). The *C. scarabaeoides* (L.) Thouars, *C. sericeus* (Benth. ex Baker) Maesen and *C. acutifolius* (F. Muell.) Maesen were found to be highly resistant to *H. armigera* (Green et al. 2006) while, ICPW 1 (*Cajanus acutifolius*), ICPW 68 (*C. platycarpus*), ICPW 13 and 14 (*C. albicans*), ICPW 159 and 160 (*C. sericeus*), ICPW 83, 90, 94, 125, 137, 141 and 280 (*C. scarabaeoides*), ICPW 207 (*Paracalyx scariosa*) and ICPW 210 (*Rhynchosia aurea*) showed higher levels of antixenosis for oviposition under no-choice, dual-choice and multi-choice conditions against pod borer, *H. armigera* (Sujana et al. 2008). High levels of antibiosis were found, when the *H. armigera* larvae were reared on leaves and/or pods of *C. acutifolius* (ICPW 1), *C. sericeus* (ICPW 160), *P. scariosa* (ICPW 207), *C. cajanifolius* (ICPW 29), *C. scarabaeoides* and *C. albicans*.

The lyophilized leaf or pod powder was incorporated into the artificial diet, which was used to assess antibiosis to *H. armigera*, and high levels of antibiosis was observed in diets having leaf and/or pod powder of some of the accessions of *C. acutifolius*, *C. lineatus*, *C. scarabaeoides*, *C. sericeus*, *C. platycarpus*, *P. scariosa* and *R. aurea*. The post-embryonic development period was prolonged, when insects were reared on leaves and pods of wild relatives of pigeonpea. Wild relatives expressing high levels of antixenosis/non-preference and antibiosis can be used to increase the levels and diversify the bases of resistance to *H. armigera* in pigeonpea (Sujana et al. 2008). Efforts have also been made for transferring pod borer resistance from the wild relatives into the cultigens (Jadhav et al. 2012; Mallikarjuna et al. 2011). Accessions MA7, TT10 and H845 and accessions of wild relatives ICWP 016 (*Cajanus albicans*), ICWP 062 (*C. platycarpus*), ICWP 086 and ICWP 097 (*C. scarabaeoides*) were identified as resistant to *Meloidogyne javanica* (Dixit 2015).

The wild relatives/accessions of chickpea species, such as *Cicer bijugum* and *C. reticulatum*, showed high levels of resistance to *H. armigera* (Sharma et al. 2005c, 2005d), and accessions *C. pinnatifidum*, *C. bijugum* and *C. echinospermum* (Davis) showed resistance to the bruchid, *C. chinensis* L. (Singh et al. 1998). Chickpea lines derived from *C. reticulatum* and *C. echinospermum* showed resistance to root lesion nematodes and *Phytophthora* root rot disease, but these lines are

still undergoing backcrossing programmes to recover the phenotype of elite lines (T. Knights, personal communication). The recent studies (Sandhu et al. 2005; Kaur et al. 2013) showed that *C. pinnatifidum*, a valuable source for major biotic and abiotic stresses, can be crossed successfully with cultivated chickpea for the deployment of high level of resistance to *Botrytis* grey mould and *Ascochyta* blight (Kaur et al. 2013).

In lentil, for the first time, the source of resistance to *Sitona* weevil (*Sitona crinitus* Herbst) was transferred from a wild accession ILWL 245 belonging to *L. culinaris* Medikus subsp. *orientalis* (Boiss.). A total of 32 accessions including cultivated landraces, *c. sp. L. orientalis*, *L. nigricans* and *L. lamottei*, which showed lower infestation rates than the susceptible check were selected as potential sources of resistance to seed weevil (*Bruchus* spp.) (Bouhssini et al. 2008). Also, 571 accessions from 27 countries including wild species (*L. culinaris* Medikus subsp. *culinaris*, *L. nigricans* (M. Bieb.) Godr., *L. culinaris* Medikus subsp. *orientalis* (Boiss.) Ponert and *L. lamottei* Cezfr.) were screened for susceptibility to seed bruchids under unprotected conditions in Central Spain and showed lower infestation rates of seed bruchids (*Bruchus* spp.) as compared to the local check 'Lyda' (Ruiz et al. 2012). In India, an extensive research on bruchid species infesting lentil has been carried out in the last decade at the National Bureau of Plant Genetic Resources, New Delhi (Bhalla et al. 2004).

Recently, a draft genome sequence of mung bean was released (Kang et al. 2014) facilitating gene identification and development of DNA markers for specific trait (s) of interest in breeding programme. To date, various sources of resistance against bruchids have been identified in mung bean crop from wild relatives (*V. radiata* var. *sublobata*) of mung bean (Fujii and Miyazaki 1987). The accessions TC1966, ACC23 and ACC41 (Lambrides and Imrie 2000) and Sub2 in *Vigna radiata* var. *sublobata* were found to be resistant to both bruchid species (Sarkar and Bhattacharyya 2015). The *Phaseolus* wild relatives are as of now by and by being screened for resistance to bruchids and other seed storage insect pests (Singh 2001; J. Beaver, individual correspondence; S. Beebe, individual correspondence; D. Debouck, individual correspondence). In case of wild relatives of pea, *Pisum fulvum* (Sibth. & Sm.) is resistant to the bruchid, *Bruchus pisorum* L. (Clement et al. 2002), while the wild relative of cowpea, *Vigna vexillata* (L.) Benth, is resistant to pod-sucking bug, *Clavigralla tomentosicollis* Stal, and spotted pod borer, *M. vitrata* (Jackai and Oghiakhe 1989).

## 7.6 Resistance Mechanisms of Pod Borers

The host plant resistance constitutes one of the most important resistance mechanisms in plants which comprises complex principles or mechanisms that are majorly classified into three main categories: antibiosis, antixenosis (non-preference) and tolerance (Painter 1951; Farrar Jr. and Kennedy 1991). Antibiosis is the property of the host plant to affect the life of an insect when it uses the plant as food (Painter

1951; Kogan 1994). Antixenosis is the property of the host plant in which insect perceives the undesirability to use it for food, oviposition or shelter (Painter 1958), while plant's physical and biochemical factors making the plant a refractory "guest" (xenos in Greek) for the insect are the main cause of non-preference (Kogan 1994). The repellence and disruption of insect behaviour are the main effects of this mechanism. The ovipositional non-preference was observed in pigeonpea varieties ICPL 187-1, ICP 7203-1, ICPL 84060, ICPL 88039, T 21 and ICPL 332 under no-choice, dual-choice and multi-choice conditions (Kumari et al. 2006). Bean cultivars IAC-Harmonia, IAPAR-81, IPR-Eldorado and IPR-Siriri were less preferred for ovipositioning; and the IAC-Harmonia stretched the whitefly *B. tabaci* life cycle, expressing non-preference for feeding and/or antibiosis-type resistance (Silva et al. 2014). Cowpea variety TVNu 946 exhibits non-preference to *M. testulalis* for oviposition/egg laying when compared to Ife Brown and VITA 1 cultivars (Macfoy et al. 1983). The pea varieties having yellow-green colour are less preferred to the pea aphids than the blue-green ones (Painter 1951), and varieties deficient in certain amino acids also show resistance to the pea aphid *A. pisum* (Harris). In soybean, the varieties lacking pubescence were extensively damaged by the potato hopper, while those with pubescence remained unaffected (Fehr 1987), and non-preference for oviposition is one of the major components in *H. zea* resistance in soybean accession PI 2227687 (Horber 1978).

Antibiosis is essentially due to plant biochemical compounds where plant showing antibiosis can kill insect or disrupts its functional biology. Some antibiosis characteristics were detected with resistance to different biotype of cowpea aphid conferred by single dominant gene (Ombakho et al. 1987; Bata et al. 1987; Pathak 1988). Antibiosis is a major component of resistance to *H. armigera* in pigeonpea and chickpea evident from reduced larval survival, fecundity and weight gain and prolonged larval development (Kumari et al. 2010b). Wild *Cajanus* accessions (*C. acutifolius* (Benth. ex Baker) Maesen) also show high manifestations of antibiosis against pod borer (Sharma et al. 2009). Larval survival and larval weights were relatively lower on ICC 506 EB, ICC 12476, ICC 12477 and ICC 12478 as compared to ICC 37. The bean genotype IAC Una and Raz 49 were classified as highly susceptible and highly resistant, respectively, by Costa et al. (2013). The cowpea cultivar MNC 99-541 F21 showed antibiosis against the whitefly *B. tabaci* biotype B, extending the life cycle of the insect, and genotypes Canapu, BRS-Urubuquara and TE97-304 G-4 also showed antibiosis, causing high nymphal mortality (Cruz et al. 2014).

Tolerance is the ability of host plant to withstand the pests' infestation or recover from insects' attack. Plant-insect friendly coexistence is the main rule of this mechanism. The chickpea genotypes (ICC 506 EB, ICC 12476 and ICC 12479) exhibiting tolerance have better recuperation from *H. armigera* damage as compared to the susceptible genotype ICC 37 (Lakshmi Narayanamma et al. 2007b). Similarly, the pigeonpea genotypes ICPL 187-1, ICPL 84060, ICP 7203-1, ICPL 87119 and ICPL 332 have shown significantly lower damage in terms of grain yield than the susceptible checks ICPL 87 and ICPL 87091 under unprotected conditions exhibiting tolerance to the insect pest (Kumari et al. 2010b).

## 7.7 Morphological and Biochemical Traits Associated with Insect Resistance

### 7.7.1 Phenological and Morphological Traits

Pigeonpea genotypes with determinate growth habit, clustered pods and dense plant canopy are more prone to attack from pod borers *H. armigera* and *M. vitrata* than genotypes with non-clustered pods (Sharma et al. 1997). The variable plant growth types and maturity also influence genotypic susceptibility to pod fly, *M. obtusa*, but pod wall thickness, trichome density and crude fibre content are associated with resistance to *H. armigera* in pigeonpea (Moudgal et al. 2008). Pubescence on the leaf tip is linked with reduced defoliation by *H. zea* (Boddie), *S. exigua* (Hubner) and *Pseudoplusia includens* (Walker) in soybean (Hulburt et al. 2004). The length of the peduncle and angle of pods also affect the expression of resistance to *M. vitrata* in cowpea (Soundararajan et al. 2013). Pubescence on the pods also shows significant effects on the oviposition, mobility and food consumption of the insects. In wild and cultivated cowpea (*V. vexillata* and *V. unguiculata*), the damage caused by the legume pod borer was found to be lower in TVNu 729 (wild, highly resistant and highly pubescent), TVNu 946 (semi-wild, moderately resistant) and IT 82D-716 (cultivated, highly susceptible and pubescent) (Oghiakhe 1995).

The seed texture and colour also play a role in imparting resistance against the insect pests, for example, in green gram, fewer number of bruchid eggs were recorded on small and shiny seeds as compared to large and dull seeds, while in black gram, small and black seeds recorded lesser number of eggs as compared to large and green seeds (Ponnusamy et al. 2014). In *Dolichus* bean, the foliage colour, days to 50% flowering, flower colour, pod colour, pod texture and fragrance influenced genotypic susceptibility to *M. vitrata* (Mallikarjuna et al. 2009).

Leaf hairs (that do not produce glandular secretions) and trichomes (hair-like outgrowths on the epidermis of plants that produce glandular secretions) also play a pivotal role in host plant resistance to insects. The wild relatives of pigeonpea such as *Cajanus scarabaeoides* and *C. acutifolius*, having non-glandular trichomes are not preferred by *H. armigera* females for egg laying (Sharma et al. 2001a, Sujana et al. 2012). Similarly, the hooked trichomes in beans disrupts the movement of the aphid, *A. craccivora* (Johnson 1953), and potato leafhopper, *E. fabae* (Pillemer and Tingey 1978), whereas the glandular trichomes in pigeonpea are linked to *H. armigera* susceptibility (Peter et al. 1995, Sharma et al. 2001a, Green et al. 2003, Sujana et al. 2012). The pod wall thickness and trichome density of type C and D in pigeonpea hybrids ICPH 3461 and ICPH 3762 and cultigens BSMR 853 offered resistance against pod borer complex (Ambidi et al. unpublished ICRISAT)

Trichomes and their organic exudates in chickpea also influence the movement and feeding behaviour of neonate larvae of *H. armigera* (Stevenson et al. 2005) and influence the feeding of spotted pod borer larvae, *M. vitrata*, in cowpea (Jackai and Oghiakhe 1989), and cabbage looper, *Trichoplusia ni* (Hubner), in soybean (Khan et al. 1986). Trichomes on the pods in a wild relative of cowpea (*Vigna vexillata*) are

partly responsible for resistance to the pod-sucking bug, *Clavigralla tomentosicollis* Stal (Chiang and Singh 1988).

Potential effects of trichomes on whiteflies may vary depending on trichome angle to the leaf surface, length and type, potentially affecting adult oviposition and immature attachment and feeding in black gram (Channarayappa et al. 1992), and the genotypes having shorter trichomes are resistant to *B. tabaci*. The black gram genotypes possessing erect trichomes were resistant to *B. tabaci*, and thus greater erectness of foliar trichomes seemed to disturb and retard the settling and probing (for oviposition and feeding) behaviour of the whitefly in resistant genotypes of black gram (Lakshminarayan et al. 2008, Taggar and Gill 2012).

## 7.8 Biochemical Traits for Resistance

### 7.8.1 Nutritional Factors

Nutritional parameters, viz. sugars, phenols, proteins, fats, sterols, essential amino acids and vitamins, also influence the host plant suitability to insect pests. Total soluble sugars and proteins are associated with susceptibility in pigeonpea, while total sugars are associated with resistance to *M. obtusa* in pigeonpea (Moudgal et al. 2008). Pea varieties are deficient in certain amino acids, which influence the resistance to the pea aphid, *A. pisum* (Auclair 1963). Higher amounts of non-reducing sugars and lower amounts of starch in chickpea variety GL 645 attributes for its low susceptibility to *H. armigera* (Chhabra et al. 1990). Mung bean varieties with high sugar and amino acid content in leaves are resistant to whitefly, *B. tabaci*, and the jassid, *Empoasca kerri* (Ruth) (Chhabra et al. 1988). Soybean-resistant genotypes possess higher amount of fats, proteins and anti-nutritional factors (phenol and trypsin inhibitors) than cowpea and chickpea (kabuli > desi) genotypes which contain higher amount of carbohydrates and lower amount of anti-nutritional factors, and were susceptible to *Callosobruchus* species (Sharma and Thakur 2014).

Non-protein or unusual amino acids confer protection against herbivores in several plant species. Among these, L-canavanine, 2,4-diaminobutyric acid, L-azetidine-2-carboxylic acid, mimosine and 3-hydroxyproline have substantial growth inhibition effects on insects (Parmar and Walia 2001). L-Canavanine is a structural homologue of L-arginine and is known to occur in over 1500 leguminous plant species. Some of the non-protein amino acids also act as enzyme inhibitors; canaline, a hydrolytic product of canavanine, inhibits pyridoxal phosphate-dependant enzymes by forming a covalent bond (Ishaaya et al. 1991). Black gram cultivars NDU 5–7 and KU 99–20 registered higher peroxidase and catalase activities at 30 and 50 DAS under whitefly-stressed plants as compared to non-stressed plants (Taggar and Gill 2012).



### 7.8.2 Secondary Metabolites

Plants also produce various defensive secondary metabolites in response to biotic stresses. The secondary metabolites affect the palatability of the plant tissues to the herbivores (Boerjan et al. 2003) and also influence the host finding, oviposition, feeding and survival and growth and development of insects and plays a major role in host plant resistance to insects in grain legumes. The plant phenols constitute one of the most common and widespread groups of defensive compounds, which plays a pivotal role in host plant resistance against herbivores, including insects (Sharma et al. 2009; Usha Rani and Jyothsna 2010; Ballhorn et al. 2011). Quercetin and quercetin-3-methyl ether in the pod surface exudates of pigeonpea also play a major role in host plant selection by *H. armigera* larvae in pigeonpea (Green et al. 2002, 2003). Total phenols and tannins present in the pod wall of pigeonpea are negatively associated with pod fly damage (Moudgal et al. 2008).

Protease inhibitors are another major class of anti-nutritional factors in chickpea and pigeonpea, which have shown *H. armigera* microbial gut protease inhibitory activity in developing seeds of wild and cultivated chickpea (Parade et al. 2012, Akbar et al., 2018). Amylase and protease inhibitors in pigeonpea showed to have an adverse effect on growth and development of *H. armigera* (Giri and Kachole 1998; Akbar et al. 2018 and Jaba unpublished). There is appreciable variation in *H. armigera* gut protease inhibitory activity in developing seeds of chickpea (Patankar et al. 1999) and proteinase inhibitors from the non-host plants (groundnut, winged bean and potato) which are more efficient in inhibiting the gut proteinases of *H. armigera* larvae than those from its favoured host plants such as chickpea, pigeonpea and cotton (Harsulkar et al. 1999). The wild relatives of pigeonpea belonging to *C. albicans*, *C. cajanifolius*, *C. sericeus*, *Flemingia bracteata* and *Rhynchosia bracteata* showed high level of resistance to *H. armigera* and exhibited high levels of protease inhibitor (PI) activity in vivo and in vitro against *H. armigera* gut proteinases (HaGPs) (Parde et al., 2012). Sterols and soybean leaf extract in combination with sucrose act as phagostimulant to the larvae of the cabbage looper, *Trichoplusia ni* (Hub.) (Sharma and Norris 1994a). Higher acidity in the leaf exudates of chickpea is linked with resistance to *H. armigera* (Srivastava and Srivastava 1989). The polar solvent extractable of the soybean genotype PI 227687, resistant to the cabbage looper, *T. ni*, contains diadzien, coumestrol, sojagol and glyceollins. These compounds reduce feeding, survival, growth and development of the cabbage looper, *T. ni* (Sharma and Norris 1991, 1994b). In soybean, pinitol confers resistance to *H. zea* (Boddie) (Dougherty 1976).

Malic acid in chickpea leaf organic acid exudates acts as an antifeedant and is less palatable to the *H. armigera* larvae (Bhagwat et al. 1995). Oxalic acid exudates inhibit the growth and development of *H. armigera* larvae when incorporated into synthetic diet, while malic acid has no such growth inhibition on *H. armigera* (Yoshida et al. 1995, 1997). The chickpea having flavonoids judaicin 7-O-glucoside, 2 methoxy judaicin, judaicin and maackiain present in wild relatives of chickpea (*Cicer bijugum* and *C. judaicum*) have shown an antifeedant activity

against *H. armigera* larvae (Simmonds and Stevenson 2001). In common bean genotypes, arcelin protein and trypsin inhibitors are the major secondary metabolites imparting resistance to bean weevil *Zabrotes subfasciatus* (Blair et al. 2010).

## 7.9 Marker-Assisted Selection

The pod borer (*H. armigera*) is perhaps the most significant threat to chickpea and pigeonpea in terms of production and productivity. In the recent past, only a few resistance sources have been identified in cultivated gene pool, but they showed either inconsistency or low levels of resistance leading to their little utilization in the breeding programmes (Lateef 1992). Therefore, there is an urgency to identify stable sources of genetic resistance in the crossable/compatible gene pool for pod borers to facilitate conventional genetic crop improvement programmes. This will facilitate the efficient utilization of undiscovered genes in existing gene pools and wild relatives which constitutes a rich reservoir for resistance genes against both abiotic and biotic stresses, thereby broadening the genetic base of breeding pool (Clement et al. 2009). In recent days, the development of newer molecular markers and other genomic sources have been accelerated in chickpea, pigeonpea and some other pulse crops, and marker-assisted trait associations have been established for a number of important agronomic traits (Kumar et al. 2011). The wide pertinency of marker-assisted selection (MAS) has already been demonstrated in crops like cowpea and pea, while in the case of lentil and faba bean, it is still in infancy stage. The recent approaches for the development of resistance mechanisms for major legume crops by deploying genomics-assisted breeding (GAB) hold promise in enhancing the genetic gains and discovery of genome-wide genetic markers; high-throughput genotyping, phenotyping and sequencing platforms, high-density genetic linkage/QTL maps and, most importantly, the availability of whole-genome sequence helps in speeding up the progress of genetic improvement of major pulses, which has led to the rapid development of cultivars with higher yield, enhanced stress tolerance and wider adaptability (Bhora et al. 2014).

Mapping the complex traits like resistance to pod borer, *H. armigera*, in chickpea has only just started (Lawlor et al. 1998). An interspecific population derived from ICC 4958 (*C. arietinum*) x PI 489777 (*C. reticulatum*) has been evaluated for opting resistance to beet armyworm, *S. exigua* (Hub.) (Clements et al. 2008), and pod borer, *H. armigera* (Sharma, H.C., Unpublished), and this population is being genotyped for identification of markers for resistance to these insects. Similarly, another mapping population (Vijay x ICC 506 EB) has also been developed and evaluated for resistance to *H. armigera*, and in pigeonpea, also a mapping population between *C. cajan* x *C. scarabaeoides* is under development at ICRISAT (Upadhyaya HD, personal communication).

However, genetic improvement programme has always been impeded with limited genetic variability under primary gene pool of pigeonpea, and its wild species present in the secondary and tertiary gene pools have been reported to carry forward

resistance against major insect pests. However, deployment of resistance genes through conventional backcrossing has not been much successful. So, there is a need for gene introgression through marker-assisted backcrossing (MABC) or advanced backcross breeding (AB breeding) for the development of improved insect pest-resistant cultivars (Choudhary et al. 2013). A cross among an aphid (*A. craccivora*)-resistant cultivated cowpea (IT 84S-2246-4) and susceptible wild cowpea (NI 963) has also been evaluated for aphid screening resistance and RFLP (restriction fragment length polymorphism) marker segregation (Myers et al. 1996). The RFLP marker bg4D9b was found linked to the aphid resistance gene (Rac1), and furthermore, a few flanking markers in a similar linkage gathering (linkage bunch 1) have additionally been described. Taran et al. (2002) identified the genetic linkage map of common bean. In green gram, TC1966, bruchid resistance gene, has been mapped using RFLP markers (Young et al. 1992). There have been no definitive efforts to identify QTLs associated with insect resistance in pigeonpea (Sharma 2009), but mapping population from the cross *C. cajan* x *C. scarabaeoides* has been developed and is under evaluation stage for resistance to *H. armigera* to identify QTLs linked to resistance against pod borer in pigeonpea.

To date, the sources of cowpea aphid resistance (CPA) and major quantitative trait loci (QTL) have been reported only for peanut crop (Herselman et al. 2004) and *M. truncatula* (Kamphuis et al. 2012). Genetic mapping for CPA resistance in cowpea would facilitate identification of syntenic areas in other legumes, as they may confer similar physiological responses against CPA infestation (Kamphuis et al. 2013). The development of molecular markers flanking the genomic regions conferring resistance to aphids can pave a way to introgress resistance genes from resistant breeding lines into susceptible varieties by backcross breeding programmes (Huynh et al. 2015). Muchero et al. (2010), while working on the cross from the foliar thrips susceptible variety IT93K503-1 and the resistant black-eyed cowpea cultivar 'California Blackeye No. 46' (CB46), identified three QTLs on the linkage groups 5 and 7. These QTLs' (*Thr-1*, *Thr-2* and *Thr-3*) peaks were collocated with the AFLP markers ACC-CAT7, ACG-CTC5 and AGG-CAT1 and were linked with foliar damage caused by *T. tabaci* and *F. schultzei*. These urging research paved the way forward for genetic characterization of major insect pest resistance in cowpea. In addition, other putative candidate markers associated with the regions governing insect or disease resistance in cowpea have also been reported (Timko and Singh 2008).

Resistance to bruchid has been reported in few mung bean cultivars (Somta et al. 2006, 2008); however, some mung bean breeders are keen to identify new sources of resistance for this important pest in other Asian *Vigna* species such as *V. umbellata* and *V. nepalensis* (Pandiyan et al. 2010; Somta et al. 2008). It has been reported that the bruchid and mung bean bug resistance is governed by a single dominant gene validated in the F<sub>1</sub> and F<sub>2</sub> populations where two QTLs were mapped for bruchid resistance and a single QTL for bean bug resistance was mapped. These new markers can be used for cloning the resistance genes to bruchid and bean bug (Hong et al. 2015). There are several reports analysing resistance to mung bean yellow mosaic virus (MYMV) in diverse germplasm, and both recessive and dominant genes have been

implicated governing the resistance against the virus like the resistant variety SML-668 which has two recessive genes for resistance. Similarly, the resistance in mung bean variety 'KMG189' is governed by a single recessive gene (Sudha et al. 2013). Also, a major QTL (variously named MYMIV'9\_25, qMYMIV1, qMYMIV4) associated with resistance against mung bean yellow mosaic Indian virus (MYMIV) has been reported and identified over the years in different locations from the wild mung bean accessions (*V. radiata* var. *sublobata*) and some of the breeding lines from Pakistan (Chen et al. 2013; Kitsanachandee et al. 2013). Specific markers flanking the locus can be used in marker-assisted selection for insect resistance in breeding programmes.

Similarly, in mung bean, a wild accession *V. nakashimae* has been used to develop an interspecific linkage map with *V. umbellata* (Somta et al. 2006). Lately, some accessions of mung bean *V. minima* and *V. nakashimae* showing a high level of resistance to all races of soybean cyst nematodes have been used in azuki breeding, to tackle the upsurging problem of soybean cyst nematode in Hokkaido, Japan (Kushida et al. 2013).

## 7.10 Transgenic Resistance to Insects

The first successful genetic transformation of chickpea with *CryIAc* gene, which inhibits the growth and development of *H. armigera*, was reported by Kar et al. (1997). Genetic transformation of chickpea using *CryIAc* gene has been reported by many workers subsequently (Indurker et al. 2007; Mehrotra et al. 2011). A second gene, *Cry2Aa*, was also incorporated for pyramiding with existing *CryIAc* in chickpea lines (Acharjee et al. 2010). Mehrotra et al. (2011) generated chickpea with pyramided genes *CryIAc* and *CryIAb*; pyramiding of two or more combination of genes with different modes of action is preferred for effective management of the insect pest. Ganguly et al. (2014) reported chickpea expressing fused *cryIAb/Ac* constitutively for resistance to *H. armigera* using pod-specific *msg* promoter from soybean. Homologous ubiquitin and RuBisCO small subunit (*rbcS*) promoters have also been used to transcribe *cryIAc* in transgenic chickpea both constitutively and in a tissue-specific manner through *Agrobacterium*-mediated transformation of chickpea var. ICCV 89314 (Chakraborty et al. 2016). The toxicity of commercial Bt formulation and *CryIAb* and *CryIAc* to *H. armigera* larvae was reduced significantly when the *H. armigera* larvae were fed on diets amended with antibiotics, suggesting that gut microbes may be one of the factors conferring resistance/susceptibility to insects in Bt transgenic crops (Paramasiva et al. 2014).

In recent years, cowpea aphid, *A. craccivora*, has been reported to cause significant yield losses in chickpea, in the Indian sub-continent, and the transgenic chickpeas expressing the *Allium sativum* leaf agglutinin (ASAL) gene exhibit a significant reduction in survival and fecundity of cowpea aphid (Chakraborti et al. 2009). Novel management strategies such as upregulating secondary metabolites, which are toxic to insect pests (Gatehouse 2002), or introducing RNAi technology

by silencing endogenous genes of insects can constitute the future management strategies to develop genetically modified chickpea cultivars (Gordon and Waterhouse 2007).

Transgenic pigeonpea plants with *cryIAb* and soybean trypsin inhibitor (*SBTI*) genes have been reported (Sharma et al. 2006), but have not been found to be effective for controlling *H. armigera* (Gopalaswamy et al. 2008). Transgenic chickpea expressing cowpea trypsin inhibitor (Thu et al. 2003) and  $\alpha$ -amylase inhibitor (Shade et al. 1994; Schroeder et al. 1995; Sarmah et al. 2004) have been found to show resistance against various bruchid species. Also, the transgenic pea expressing  $\alpha$ -amylase inhibitor has been developed for resistance against pea weevil (Morton et al. 2000).

Ikea et al. (2003) detailed the fruitful hereditary change of cowpea using the molecule particle gun bombardment of shoot meristem system. A productive and stable cowpea change/recovery framework has been created as of late (Popelka et al. 2006), so that transgenic cowpea is currently a reality. By and by, there is no distinguished cowpea assortment indicating solid imperviousness to bruchids. Interestingly, high resistance has been depicted in the wild relative *Vigna vexillata*, but the crossing with elite lines yields non-viable seeds rendering this approach unsuccessful for introgressing resistance in cultivated lines (Fatokun 2002). Be that as it may, fake eating regimen bioassay performed on cowpea weevils recommended that  $\alpha$ -amylase inhibitor 1 ( $\alpha$ AI-1) confined from regular bean (*Phaseolus vulgaris*) can be utilized against these vermin assaults (Ishimoto et al. 1999).

Currently, huge advances have been made in cowpea hereditary change which may turn out to be without further ado accessible for the African ranchers. The qualities utilized are the *Cry1Ab* communicating the delta endotoxin of *Bacillus thuringiensis* (Bt) ssp. *kurstaki* and the  $\alpha$ -amylase inhibitor 1 ( $\alpha$ AI-1) to target, individually, the unit borer (*M. vitrata*), *C. maculatus* and *C. chinensis* (Abrol 1999; Popelka et al. 2006; Tarver et al. 2007; Adesoye et al. 2008; Huesing et al. 2011). All these reviews permitted Solleti et al. (2008) to present the  $\alpha$ AI-1 quality under bean phytohemagglutinin promoter, in 'Pusa Komal' a financially imperative Indian cultivar, and to create fruitful transgenic plants which unequivocally restrained the improvement of *C. maculatus* and *C. chinensis* in insect bioassay. Due to the outcrossing observed among crops and crop to wild, the introduction of transgenic cowpea harbouring insect-resistant gene in African agriculture would be a threat for the non-GM crop and their wild relatives (Williams and Chambliss 1980; Asiwe 2009). Lüthia et al. (2013) who preceded  $\alpha$ AI-1 gene in a cotyledon-specific promoter into the breeding line IT86D-1010 and the Japanese cultivar 'Sasaque' both showed 100% grubs (*C. chinensis* and *C. maculatus*) mortality in the seeds of transgenic lines. Currently, several genes of interest such as herbicide imazapyr,  $\alpha$ -amylase inhibitor 1 (against bruchids), *Cry1Ab* and *Cry1Ac* (against *Maruca*) have been brought successfully into commercially important cultivars of cowpea, and the genes are transmitted in Mendelian fashion (Abaye et al. 2014). Investigations executed by Jackai and Adalla (1997) showed that the insect pests of cowpea are controlled by several other different forms of Bt crystal toxins, and this basic information was further used by Adesoye et al. (2008) and Bakshi et al. (2011) to

introduce *CryIAb* in cultivars ‘TVu 201’, ‘Ife Brown’, ‘IT90K-277-2’, ‘IT90K-288’ and ‘IT90K-391’ and *CryIAc* genes in cultivar ‘Pusa Komal’ in various cowpea genotypes, and their experiment results showed that the transgenes followed Mendelian inheritance in the progenies which showed significant reduction of larvae survival and weight. These findings were confirmed by several other authors as the introduction of this gene in pea (Shade et al. 1994; Schroeder et al. 1995; Morton et al. 2000; Sousamajer et al. 2007), adzuki bean (Ishimoto et al. 1996) and chickpea (Sarmah et al. 2004; Ignacimuthu and Prakash 2006) conferred resistance against bruchid beetles.

## **7.11 Potential and Limitations of HPR to Chemical Control in Grain Legumes**

Crop protection includes application of synthetic pesticides, weedicides, etc. for protecting crops against pests and diseases and has largely been helpful in curbing the losses; however, their haphazard application is having adverse effects on environment and posing serious health problems in human beings apart from increased cost of cultivation and diminishing returns. The utilization of the chemical control measures in combination with the eco-friendly measures such as host plant resistance, use of biopesticides and other cultural management practices is the most economic and effective way to tackle such problems.

### ***7.11.1 Advantages of HPR to Insects***

Host plant resistance is an important component of integrated pest management (IPM). The resistant plants offer the following advantages in the management of insect pests:

1. Insect-resistant crop varieties provide an inherent/in-built means of insect control.
2. It is an eco-friendly pest management approach.
3. It is, generally, compatible with other methods of pest control.
4. Its effectiveness is not ordinarily affected by the environment.
5. Resistant varieties can be easily adopted by the farmers.

### ***7.11.2 Problems in Breeding for HPR to Insects***

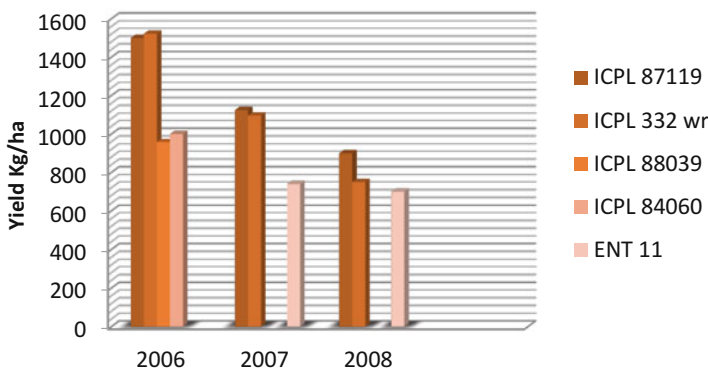
1. In some cases, breeding for resistance to one insect may lead to susceptibility to another pest. This may be because the features of host plant associated with resistance to one insect are associated with susceptibility to another insect.
2. Breeding for insect resistance may sometimes reduce the quality of produce.

3. Interspecific gene transfer poses many problems, and quite often there is some linkage drag conferring some undesirable traits along with the desired ones.
4. Breeding for insect resistance is a long-term programme; therefore, it requires adequate time and funding.
5. The high level of resistance is likely to encourage evolution of new virulent biotypes by imposing strong selection pressure. Therefore, evolution of new biotype has to be closely monitored.
6. Low heritability of resistance genes.
7. Effect of environment changes, rainfall, temperature, etc., may not give consistent results.
8. Screening technology to identify reliable sources.

## 7.12 Success of Tolerant Cultivars for Insect Pests

There are many tolerant cultivars developed for both pest and diseases. Some of the prominent cultivars are highlighted below:

Pigeonpea: To identify cultivars with resistance to pod borer, *H. armigera*, we evaluated five pigeonpea cultivars [ICPL 332WR, moderately resistant to *H. armigera*; ICPL 84060, a medium maturity variety with moderate resistance to pod borer; ICPL 88039, a short-duration cultivar with low levels of resistance to pod borer; ENT 11, a white-seeded variety, with a narrow flowering and pod maturity period; and ICPL 87119 (Asha), a medium-duration cultivar] in Tandur region of Telangana (Fig. 7.1 & Plate 7.2). Each farmer was provided with 3 kg seeds of each test variety along with their agronomic attributes and crop protection requirements between 2006 and 2008 rainy seasons.



**Fig. 7.1** Performance of pigeonpea varieties in on-farm trials in Tandur region, Telangana



**Plate 7.2** On-farm evaluation of pod borer (*Helicoverpa armigera*)-resistant cultivar, ICPL 332WR, on farmers' fields. A and B, ICPL 332WR at the flowering and maturity stages, respectively. C, Farmer demonstration field, in Tandur; interaction with the farmers about performance and grain quality of ICPL 332WR

The pod borer (*H. armigera*)-resistant cultivar, ICPL 332WR, suffered significantly lower damage and yielded significantly greater than the susceptible check, ICPL 87. ICPL 332WR, with moderate levels of resistance to *H. armigera*, yielded 750 to 1522 kg ha<sup>-1</sup> compared to 900 to 1500 kg ha<sup>-1</sup> of Asha – the commercial variety. It required 1–2 less sprays of insecticides and matured 10 to 15 days earlier than Asha. Farmers in general were appreciative of ICPL 332WR, and there will be more demand for this variety once the farmers realize the low insecticide use on this variety.

The Abhaya (ICPL 332) is the first *Helicoverpa* pod borer-tolerant variety released for cultivation in Andhra Pradesh in 1989 followed by improved version ICPL 332WR – a pod borer- and wilt-resistant variety released in both Telangana and Andhra Pradesh in 2017. It is indeterminate, medium duration (170–200 days) and has yielded up to 2.7 t ha<sup>-1</sup>. The other cultivars, viz. Amol (BDN 708), BSMR 736, Asha and Maruti, are also most widely adopted by the farmers, and these are tolerant to pod borer.

**Chickpea:** The ICCV 7 (ICCX 730008–8-1-1P-BP-8 EB) is identified as a donor parent resistant to pod borer, *Helicoverpa* for use in plant breeding programs. It was selected from a cross of H 208 (ICC 4954) and BEG 482 (ICC 4923). It is a semi-spreading variety with moderate plant height (30–40 cm) and predominantly apical branching. In multilocal trials over a period of 5 years, this variety yielded 0.90 t ha<sup>-1</sup> compared to 0.95 t ha<sup>-1</sup> from Annigeri. The pod borer damage was 5.6% in ICCV 7 and 11.2% in Annigeri. It is early maturing and takes 45 days to flower



and 90–100 days to mature in peninsular India. It is, however, like most other *Helicoverpa*-resistant lines, susceptible to wilt.

ICCC 32 (ICCV 6) was identified for release in central India in 1984 and in the North-West Plain Zone in 1985 and released in Nepal in 1990 as “Kosheli”. It is the first kabuli chickpea resistant to two races of fusarium wilt and has shown tolerance to dry root rot, pod borer attack and salinity. The cultivar is medium maturing (about 150 days). Grain yield in farmers’ fields in Madhya Pradesh in 1984/1985 was 1.6 t ha<sup>-1</sup> (as compared with 1.2 t ha<sup>-1</sup> from L550). From 1981/1982 to 1984/1985, it yielded 2.1 t ha<sup>-1</sup> in the North-West Plain Zone, compared with 1.7 t ha<sup>-1</sup> of L550. The Vishal (Phule G-87207), JG 6, Haryana Chana-1 and JG 14 are also most widely adopted cultivars which showed tolerance to pod borer.

With moderate levels of resistance in some of prominent lines to *H. armigera*, and yield potential comparable to the commercial cultivars in both chickpea and pigeonpea, it should be popularized among the farmers to reduce the need to apply insecticides for pest management. The large-scale cultivation of pod borer-resistant cultivars will not only reduce the amount of pesticides applied in the crops but will also lead to sustainable pigeonpea production.

### 7.13 Conclusions

Conventional methods of protecting the legume crops from insect pests are inadequate to meet the growing demand for pulses in future. The research efforts should be focussed on overcoming the crossing barriers between the wild and cultivated major grain legumes so as to take advantage of genes present in some wild relatives. Accuracy and preciseness of phenotyping for resistance to insect pests remains a major challenge. Improved higher-version phenotyping systems will have a substantial impact on both MAS and conventional breeding in order to develop resistant cultivars against insect pests; in addition, there is a need for focused and strategic research that feeds into these endeavours. A combination of morphological, biochemical and molecular markers is needed to introgress insect resistance genes from both cultigens’ germplasm and wild relatives of grain legumes to accelerate the process of developing genotypes with insect resistance for enhancing the crop productivity and improving the livelihoods of the farming community.

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