# Distinguishing Proof and Utilization of Resistance of Insect Pests in Grain Legumes: Progress and Limitations

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#### Abstract

Major food legumes including chickpea, pigeon pea, cowpea, field pea, lentil, faba bean, black gram, green gram, and Phaseolus beans play a vital role in food, nutritional security, and sustainable crop production. Several insect pests damage grain legumes, of which Helicoverpa armigera; Maruca vitrata; Etiella zinckenella; Spodoptera litura and S. exigua; Melanagromyza obtusa; Ophiomyia phaseoli; Aphis craccivora and Bemisia tabaci; Empoasca spp., Megalurothrips dorsalis, and Caliothrips indicus; Mylabris spp.; and Callosobruchus chinensis crusade extensive losses. Appreciable progress has been made in formulating techniques to evaluate germplasm, mapping populations, and genetically modified crops for resistance to insect pests under field and greenhouse conditions. No-choice and dual-choice cage screening techniques, detached leaf assay, and diet incorporation assays have been standardized to screen for resistance to major insect pests in grain legumes. However, some of these techniques cannot be used to screen against stem flies, pod fly, leafhoppers, thrips, and aphids. There is a need to develop methods for mass multiplication of aforesaid insects to undertake precise phenotyping for resistance to these insects. There is a necessity to identify lines with different resistance mechanisms/components of resistance for gene pyramiding to explicate cultivars with the stable source of resistance to insect pests. Prominent levels of resistance to the pod borers have been found in the wild accessions of chickpea,

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pigeon pea, and cowpea, which can be exploited to introgress genes to heighten the levels and diversify the basis of resistance to insect pests to build host plant resistance a viable component of pest management in grain legumes for sustainable crop production.

#### Keywords

Grain legumes • Host plant resistance • Pod borers • Wide hybridization • Pest management • Wild relatives

## 5.1 Introduction

India is the highest producer and consumer of pulses in the world. Chickpea or Bengal gram (Cicer arietinum), pigeon pea 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 unguiculata), and broad bean or faba bean (Vicia *faba*) are some of the most important pulses used as food worldwide. Of these, chickpea, pigeon pea, 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 which is over 78 million tons and an average productivity of 846 kg ha-1 (FAO 2012). In India, the overall pulse production for the year 2015–2016 was 17.33mt on an area of 24.89 million ha, with an average productivity of 758 kg ha<sup>-1</sup>(Anonymous 2016). Chickpea is the most predominant pulse crop in India, accounting for 40% contribution of the total pulse production, followed by pigeon pea (18-20%), mung bean (11%), urdbean (10-12%), lentil (8-9%), and other legumes (20%) (Anonymous 2011). Madhya Pradesh (20.3%), Maharashtra (13.8%), Rajasthan (16.4), Uttar Pradesh (9.5%), Karnataka (9.3%), Andhra Pradesh (7.9%), Chhattisgarh (3.8%), Bihar (2.6%), and Tamil Nadu (2.9%) are the major pulse-producing states in India (Anonymous 2009). Food/grain legumes are the primary source of dietary protein and are an integral part of daily diet in several forms worldwide. Pulses supply significant nutritional and health benefits and are known to reduce several noncommunicable diseases such as colon cancer and cardiovascular diseases (Jukanti et al. 2012).

Several biotic and abiotic factors dissemble the production and productivity of grain legumes worldwide, of which insect pests are the predominant. Over the past five decades, significant progress has been made in developing improved cultivars and crop management practices, but there has been little increase in productivity. Grains are damaged by more than 150 species of insect pests, under unprotected conditions and in storage (Clement et al. 2000, Sharma and Upadhyaya 2016). Amid the many insect pests damaging food/grain legumes, the pod borers, *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 pigeon pea (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 pigeon pea in India. The leaf miner, *Liriomyza cicerina* (Rondani), is a significant pest of chickpea in West Asia and North Africa (Weigand et al. 1994). Pea pod borer, *Etiella zinckenella* Triet, is an important pest of pigeon pea, field pea, and lentil, while the aphid, *Aphis craccivora* Koch, infests all the food legumes, but it 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 *Acyrthosiphon pisum* Harris is an important pest of field pea worldwide.

The whitefly, Bemisia tabaci Genn, infests all the crops, except chickpea crop, but is an important pest of *Phaseolus* spp. like black gram, and green gram and the defoliators, Spodoptera litura (Fab.) in Asia and S. exigua Hubner in Asia and North America, are occasional pests. Bihar hairy caterpillar, Spilosoma obliqua Walker, is a 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. Among sapsucking pests, leafhoppers, Empoasca spp., infest most of the food/grain legumes but cause the most economic damage in black gram, green gram, and Phaseolus beans, and in the case of pod-sucking bugs, Clavigralla tomentosicollis Stal., C. gibbosa Spin., Nezara viridula L., and Bagrada hilaris Burm. are occasional pests, but extensive damage has been recorded in cowpea in Africa caused by C. tomentosicollis and in pigeon pea in India caused by C. gibbosa. Under storage conditions, bruchids, Callosobruchus chinensis L. and C. maculatus Fab, crusade extensive losses in storage in all the food legumes worldwide, and stink bugs (Nezara viridula (L.)) are 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 and most vulnerable to attack major production areas (Clement and Ouisenberry 1999; Mendesil et al. 2016).

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

In India, insect pests lead to an approximate economic loss in yield of 15.00% of worth \$2285.29 million (Dhaliwal et al. 2015). Pod borer, *H. armigera* – the single largest yield shrinking factor in food legumes – causes an estimated loss of US\$ 317 million in pigeon pea 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). In general, the estimates of yield losses vary from 50 to 100% in the tropics and 5–10% in the temperate regions (van Emden et al. 1988). Another pod borer, *M. vitrata*, causes loss to be US\$ 30 million annually (Saxena et al. 2002). In pigeon pea, yield losses due to pod borer 25–70%, pod fly 10–50%, *Maruca* 5–25%, and pod bug 10–30% have been reported (Sharma et al. 2010). Soybean aphid (*A. glycines*) can induce up to 58% yield losses in soybean crop (Wang et al. 1994) and annually \$2.4 billion estimated

losses in yield (Song et al. 2006; Tilmon et al. 2011). Legume flower thrips (LFT), *M. sjostedti* Trybom, and cowpea *V. unguiculata* in tropical Africa cause yield losses ranging from 20% to 100% (Karungi et al. 2000). The avoidable losses in grain/food legumes at current production levels of 60.45 million tonnes would be nearly 18.14 million tonnes (at an average loss of 30%), worth at nearly US\$ 10 billion (Sharma et al. 2008).

## 5.3 Resistance Screening Techniques

There are difficulties in screening and choosing for resistance to some important key pests, because of the lack of uniform insect infestations across locations and seasons, and it's also difficult to rear and multiply some of the insect species on artificial diets for artificial infestation. In pigeon pea and chickpea, the screening done by infesting crop plants with ten first-instar larvae and covering with a cloth bag placed all around a wire-framed cage (40 cm in diameter, 45 cm long) can be used to screen for resistance to the pod borer (Sharma 1998), using no-choice, dualchoice, or multi-choice assays, and plants may be evaluated for insect damage after 15 days of infestation, and this technique used to confirm the resistance under field conditions and find out resistance levels in various cultivars. Most of legume crops under laboratory condition may be screened by using detached leaf bioassay techniques (Sharma et al. 2001b, Sharma 2016) and by adjusting planting date, augmenting insect populations under field conditions, caging the crop plants with insects in the field, grouping of test material according to maturity and height, and tagging the inflorescences at flowering stage (Sharma et al. 2005a). In cowpea manifestation of tolerance to *Maruca* is affected by different phenology stages of crop (Dabrowski et al. 1983). Plants with five to seven shoots are most desirable to screening for resistance prior to flowering. Taking five eggs per plant, it was easy to differentiate among the resistant and susceptible lines and can be used as selection criteria (Jackai 1982, Oghiakhe et al. 1992a, b). For free and no-choice techniques need to be affirmed under field conditions for screening against major insect pest of legume crops (Echendu and Akingbohungbe 1989). The screening technique for whitefly, B. tabaci, in black gram genotypes may be based on whitefly resistance index (WRI) scores, symptoms, kind, and intensity of leaf injury categorized grades (I–V) for developing tolerant cultivars (Taggar et al. 2012).

## 5.4 Identification and Utilization of Resistance to Insects Pests

Significant effort has been made in recognition of sources of resistance to insect pests, but the orgins of resistance have not been utilized extensively in the crop breeding programs (Clement et al. 1994; Sharma and Ortiz 2002). Varieties with having improved yield factor are more prone to be susceptible to insect pests than the landraces (Lale and Kolo 1998). Lack of strategies for positive selection for

resistance to insect pests may result in more susceptibility in elite cultivars as compared to the landraces (Shaheen et al. 2006). Some of legume cultivars with resistance/tolerance to insect pests have been identified in pigeon pea, chickpea, cowpea, black gram, green gram, and field pea (Table 5.1). However, the levels of resistance/ tolerance to pod borers are low to moderate but are quite more effective when deployed in combination with newer synthetic insecticides or natural plant products like neem seed kernel extract (NSKE) (Sharma and Pampapathy 2004). Cultivars with multiple resistance to insect pests and diseases will be in greater call for in future because of the needy concerns assorted with chemical control and environmental pollution and the changes in relative importance and severity of damage due to climate change. There is require to break the linkage amid insect pest resistance and susceptibility to diseases; e.g., in case of chickpea and pigeon pea, *H. armigera*resistant cultivars are susceptible to wilt diseases (Sharma et al. 2005a).

Screening of various germplasms of chickpea and pigeon pea at ICRISAT (over 15,000 accessions for each crop) has led for identification of a few accessions which shows moderate levels of resistance to *H. armigera* (Lateef 1985; Lateef and Pimbert 1990). Based on wide testing of pigeon pea lines, such as PPE 45-2, BDN 2, ICPL 4, Bori, and T 21, ICPL 269 and ICPL 88039, early maturity; ICPL 332, ICPL 84060, LRG 41, and ICPL 187-1, medium maturity; and ICP 7035, medium-long maturity and vegetable type were ascertained to be resistant/tolerant to *H. armigera* (Sharma 2009; Srivastava and Joshi 2011). Of these, ICPL 88039 has been widely tested in the Indo-Gangetic Plains in North India, and it found to be suited for rice-wheat cropping system. ICPL 332WR was found to be promising in Andhra Pradesh, while ICP 7035 is opted by the farmers as a vegetable type. The cultivars GP 75, GP 118, GP 233, and GP 253 were confounded to be resistant to *M. obtusa*, evoking that resistance/tolerance to pod fly is not linked to maturity period and growth type of the genotype/cultivar (Moudgal et al. 2008). The cultivar ICPL 88034 and MPG 679 were showing low *Maruca* damage (10–25%) (Saxena et al. 1996).

The breeding efforts in chickpea have developed many Helicoverpa-resistant varieties such as C 235, Anupam, Pant G 114, ICCV 10, JG 74, Dulia, Pusa 261, Vijay, Vishal, ICCV 7, ICCV 10, and ICCL 86103 and were released for cultivation in India (Sharma et al. 2005b). The accessions (ICC 506 EB, ICC 10619, ICC 10667, ICC 4935, ICC 10243, ICCV 95992, and ICC 10817) have been confounded for resistance to H. armigera. The cultivar ICC 12475 chickpea showed resistance to S. exigua (Shankar et al. 2012). However, progenies of interspecific cultivated chickpea and a wild relative (C. reticulatum) showed high levels of resistance to S. exigua. Two accessions of C. cuneatum (ILWC 40 and ILWC 187) and 10 accessions of C. judaicum with high grades of resistance while 18 lines of C. judaicum and 4 lines of C. reticulatum and C. pinnatifidum have been identified with resistance to leaf miner in chickpea (Singh and Weigand 1994) and germplasm lines, viz., ILC 3800, ILC 5901, and ILC 7738, were identified and registered as sources of resistance to Liriomyza cicerina. Accessions DCP 923, JG 315, BG 1003, and BG 372 showed promise against bruchids, and genotypes GL 88341, BG 360, and RSG 524 were identified as resistant sources against root-knot nematodes (Meloidogyne incognita and *M. javanica*) (Indian Institute of Pulses Research 2015).

Crop	Genotypes	References	
Pigeon pea	Pod borer, <i>Helicoverpa armigera</i> ICPL 332 <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 41ICPL 269, ICP 7203-1, ICPL 84060, ICPL 87119, ICPL 332	Lateef and Pimbert (1990), Kalariya et al. (1998), Parsai (1996, 2005), Sunitha et al. (2008a, b), Sharma (2009), Srivastava and Joshi (2011) Kumari et al. (2010a)	
	Legume pod borer, Maruca vitrata	Saxena et al. (1996)	
	ICPL 88034 and MPG 679		
	Pod fly Melanagromyza obtusa	Lateef and Pimbert (1990) Moudga	
	ICP 10531-E1, ICP 7941E1, ICP 7946-E1, and ICP 7176-5. GP 75, GP 118, GP 233, and GP 253	et al. (2008)	
Chickpea	Pod borer, Helicoverpa armigera	Dixit (2015), Lateef and Sachan	
	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, ICCL86111, Vijay, and Vishal. ICC 10667, ICC 10619, ICC 4935, ICC 10243, ICCV 95992, and ICC 10817	(1990), Bhagwat et al. (1995), Das and Kataria (1999), Deshmukh and Patil (1995), Shankar et al. (2012)	
	Leaf miner, Liriomyza cicerina	Singh and Weigand (1994), Girija	
	ILC 380, ILC 5901, and ILC 7738	et al. (2008)	
		Shankar et al. (2012)	
	Beet armyworm Spodoptera exigua	Indian Institute of Pulses Research	
	ICC 12475	(2015)	
	Bruchid DCP 923, JG 315, BG 1003, BG 372		
	Root-knot nematode		
	Meloidogyne incognita and M. javanica	Indian Institute of Pulses Research (2015)	
Black gram	Pod borer, <i>Helicoverpa armigera</i>	Lal (1987)	
Direct grain	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>	Soundararajan et al. (2010),	
	CBG 08-011 and PLU 54; UH 82-5, IC 8219 and SPS 143	Ponnusamy et al. (2014)	
	Jassid, Empoasca kerri		
	Sinkheda 1 <sup>a</sup> , Krishna <sup>a</sup> , H 70-3, and UPB 1 <sup>a</sup>	Dawoodi et al. (2010)	
	Stem fly, Ophiomyia phaseoli		
	Killikullam <sup>a</sup> , 338/3, P 58, Co 4 <sup>a</sup> , and Co 5 <sup>a</sup>		
	Pink Pod borer Cydia ptychora		
	SKNU-03-03		

 Table 5.1
 Identification and utilization of host plant resistance to insect pests in grain legumes in India

(continued)

Crop	Genotypes	References
Green	Pod borer, Maruca testulalis	Lakshminarayan et al. (2008)
gram	J1, LM 11, P 526, and P 336	
	ML 337, ML 5, MH 85-61, and ML 325	Soundararajan et al. (2010)
	CGG 08-007 and CGG 08-028	
	Stem fly, Ophiomyia centrosematis Co 3	Devasthali and Joshi (1994)
	TAM-20, PDM-84-143 and Pusa-105 against	-
	A. craccivora, A. kerri (Empoasca kerri) and	
	M. undecimpustulatus	
	Bruchids	Somta et al. (2008)
	V1128, V2817	
Field pea	Pod borer, Etiella zinkenella	Lal (1987)
	EC 33860, Bonville <sup>a</sup> , T 6113 <sup>a</sup> , PS 410, 2S	Teshome et al. (2015)
	21, and 172 M.	
	32,454, 235,002	
	Leaf miner, Chromatomyia horticola	
	P 402, PS 41-6, T 6113, PS 40, KMPR 9, P	
	402, and P 200	
Cowpea	Pod borer, Maruca vitrata	Singh (1978), Lal (1987)
	TVu 946, VITA 4, VITA 5, Ife Brown, and	Chanchal and Singh (2014)
	Banswara <sup>a</sup>	
	EC 394828, ET 116932, TVNu 946, Kashi	Jackai (1981)
	Shyamal, Arka Suman, and Arka	
	Sumurudhi	
	Jassid, Empoasca kerri	
	TVu 123, TVu 662, JG 10-72, C 152, and	
	3-779 (1159)	
	Aphid, Aphis craccivora	
	P 1473, P 1476, IT82E-16, and MS 9369	Benchasri et al. (2007)
	Bruchids Callosobruchus maculatus	
	IT89KD- 288, IT99K-429-2 and	Obadofin (2014)
	IT97K-356-1	

Table 5.1 (continued	1)
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<sup>a</sup>Released for cultivation in India

Limited work has been done on insect resistance in lentil crop. Chhabra (1981) reported seven lines showed resistance to pea pod borer *E. zinkenella*. Chopra and Rajni (1987) ascertained resistance of bruchids, while Sharma and Yadav (1993) accounted resistance to aphid *A. craccivora* in some of the lentil accessions. Genotypic differences for susceptibility to aphid (*A. craccivora*), pod borer (*E. zinkenella*), and seed weevil have been noticed, but no efforts have been made to breed for resistance to these insect pests (Erskine et al. 1994).

The TVNu 946 cultivar showed high levels of resistance to *Maruca* across seasons and locations (Jackai 1981), and Oghiakh and Odulaja (1993) used the principal component analysis to study the variation patterns in 18 cultivars, 7 developmental

parameters of the pest on floral buds, flower, and sliced pods against *Maruca* in cowpea crop. Singh et al. (1996) accounted several improved cowpea varieties with combination of the resistance to aphid, thrips, and bruchid, and Nkansah and Hodgson (1995) confirmed resistance of TVu 801 and TVu 3000 to the Nigerian aphid strain but found that the two lines were susceptible to aphids from the Philippines. IT82E-16 displayed a high level of resistance to cowpea aphid *A. craccivora* (Benchasri et al. 2007), and the genotypes IT89KD-288 (V4) and IT89KD-391 (V2) had the outstanding performance against major insect pests of cowpea in southeastern agroecology of Nigeria (Onyishi et al. 2013). IT89KD- 288, IT99K-429-2, and IT97K-356-1 were resistant to *C. maculatus* (Obadofin 2014).

In case of green gram (*V. radiata*) cultivars PDM-84-139 and ML-382 were assuring 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 gray weevil. The cultivar MI-67-9 was resistant against bean aphid but was more susceptible to blue beetle. The sap-sucking jassid infestation was comparatively less in varieties MI-67-3 and MI-29-22 (Devesthali and Saran 1998). Talekar and Lin (1992) ascertained accessions V2709 and V2802 were highly resistant to both *C. chinensis* and *C. maculatus*, while the cultivated accessions V1128 and V2817 were also resistant (Somta et al. 2008) and moderately resistant in PLM 156 and V 1123 for both bruchid species (Dixit 2015). Lower pod borer complex damage was observed in CGG 08-007 and CGG 08-028 (Soundararajan et al. 2010), and resistance in TC1966, V2709, V2802, V1128, and V2817 was attributed due to presence of the biochemical compounds in the seeds (Talekar and Lin 1992; Somta et al. 2008).

The soybean cultivar IAC-100 with having PI 229358 and PI 274454 in its genealogy was formally released in Brazil, and it acquits resistance to stink bug complex (Rosseto 1989). Recently, the pink pod borer, Cydia ptychora (Meyrick), on urdbean/black gram was noticed in some of the regions in Gujarat (Dawoodi et al. 2009), and the variety SKNU-03-03 was showed least susceptible to pink pod borer (Dawoodi et al. 2010). Genotype PLU 648 was found resistant to *M. javanica*. Low pod borer complex damage was observed in CBG 08-011 and PLU 54 (Soundararajan et al. 2010). In field pea (*P. sativum*), accessions 32,454 (17%) and 235,002 (33%) had consistently low percent seed damage; incorporation of such promising accessions into pea breeding programs may lead to the exploitation of varieties with enhanced resistance against pea weevil, B. pisorum L., in Ethiopia (Teshome et al. 2015). However, lack of precision strategies in evaluating thousands of accessions for resistance to the target insect pests probably resulted in missing many potentially good sources of resistance. Therefore, high-throughput phenotyping has been used in recent times for large-scale evaluation of germplasm or breeding lines for resistance to sap-sucking insects.

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

The genes responsible for resistance to insect pests are quite rare in nature for the cultivated species, but they are quite frequent in the wild accessions of many crops. In few cases high levels of resistance 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) have been reported. The wild relatives/accessions of pigeon pea and chickpea are authoritative sources of genes for resistance to insect pests. Over the past two decades, the authors ascertained a paradigm shift in identification and deployment of wild species of pigeon pea (Dhillon and Sharma 2012). In case of pigeon pea accessions ICPW 214 (C. bracteata), ICPW 141, ICPW 278, and ICPW 280 (C. scarabaeoides), ICPW 14 and ICPW 202 (F. stricta) have been reported to have resistance to pod fly M. obtusa and T. cajaninae (Sharma et al. 2003a). In case of C. scarabaeoides (L.) Thouars, C. sericeus (Benth. ex Baker) Maesen and C. acutifolius (F. Muell.) Maesen are highly resistant to H. armigera (Green et al. 2006), 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/non-preference 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 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 can be used to assess antibiosis to H. armigera, and high levels of antibiosis were 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 postembryonic development period was prolonged, when insects reared on leaves and pods of wild relatives of pigeon pea. 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 pigeon pea (Sujana et al. 2008). Efforts have also been made for transfering pod borer resistance from the wild relatives to the cultigens (Jadhav et al. 2012a; Mallikarjuna et al. 2011b). 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).

Wild relatives/accessions of chickpea species, such as *Cicer bijugum C. reticulatumtum.*, showed high levels of resistance to *H. armigera* (Sharma et al. 2005c, d), and accessions *C. pinnatifidum*, *C. bijugum*, and *C. echinosper* white mum (Davis) showed resistance to bruchid, *C. chinensis* L. (Singh and Ocampo 1998). Chickpea lines received from *C. reticulatum* and *C. echinospermum* were developed and showed for resistance to root lesion nematodes and *Phytophthora* root rot disease, but these lines are still undergoing backcrossing programs to retrieve the domesticated phenotype lines (T. Knights, personal communication). The recent studies (Sandhu et al. 2005; Kaur et al. 2013) showed that *C. pinnatifi dum*, a valuable source for major biotic and abiotic stresses, can be crossed successfully with cultivated chickpea for the deployment of high level of resistance sources to *Botrytis* gray mold and *Ascochyta* blight (Kaur et al. 2013).

In lentil, for the first time sources of resistance to *Sitona* weevil (*Sitona crinitus* Herbst) obtained from its wild accessions of *Lens* species, accession ILWL 245 belongs to the species *L. culinaris* Medikus subsp. *orientalis* (Boiss.), and a total of 32 accessions including cultivated landraces, *L. c.* sp. *orientalis*, *L. nigricans*, and *L. lamottei* showed lower infestation rates than the susceptible check and were selected as potential sources of resistance to seed weevil (*Bruchus* spp.) (Bouhssini et al. 2008). However, the exploration of 571 accessions from 27 countries including wild species was screened for susceptibility to seed bruchids under unprotected conditions in Central Spain, and the wild species were *L. culinaris* Medikus subsp. culinaris, *L. nigricans* (M. Bieb.) Godr., *L. culinaris* Medikus subsp. orientalis (Boiss.) Ponert, and *L. lamottei* Cezfr., which showed lower infestation rates of seed bruchids (*Bruchus* spp.) than the local check "Lyda"(Ruiz et al. 2012). In India, an extensive research on bruchid species infesting lentil was carried out over the past 10 years at National Bureau of Plant Genetic Resources, New Delhi (Bhalla et al. 2004).

In soybean, wild relative PI 171444 (MG VI) was found to be the majorly resistant and exhibited antixenosis, antibiosis, and temporal separation (Kester et al. 1984), and the lines PI 229358, PI 227687, and PI 274454 expressed antixenosistype resistance against Anticarsia gemmatalis (Hubner) (Lepidoptera: Noctuidae) (Hoffmann-Campo et al. 2006; Ortega et al. 2016) PI 227687 also provoked repellency to Trichoplusia ni caterpillars and adults of Epilachna varivestis, verified for the presence of volatile derivatives of their leaves (Liu et al. 1989). PI 567336A and PI 567598B were confirmed as the most resistant wild relatives and were characterized as having antibiosis resistance to kudzu bug (KZB), Megacopta punctatissima Montandon (Bray et al. 2016). For soybean cyst nematode, resistance source has been effectively exchanged from its wild-lasting soybean, Glycine tomentella Hayata (Riggs et al. 1998); however, its cultivars are still in an exploratory stage. Recently, a draft genome sequence of mung bean was described (Kang et al. 2014), and sequence is useful for gene identification and development of DNA markers for specific trait(s) of interest in breeding program. Till date, various sources of resistance against bruchids have been identified in mung bean crop. Fujii and Miyazaki (1987) depicted first report on wild relatives of mung bean (V. radiata var. sublobata) and the accession TC1966 and ACC23 and ACC41 (Lambrides and Imrie 2000) and recently identified accession Sub2 in Vigna radiata var. sublobata for resistance to both bruchid species (Sarkar and Bhattacharyya 2015). The Phaseolus wild relatives are as of now by and by being screened for resistances 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 relative of pea, Pisum fulvum (Sibth. & Sm.) is resistant to the bruchid, Brichus 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).

## 5.6 Mechanisms of Resistance to Insect Pests

Maxwell and Jennings (1980) defined insect resistance as "those heritable characteristics obsessed by the plant which regulate the ultimate degree of damage done by insects". Crop plants have developed various mechanisms of resistance, which have been classified as non-preference or antixenosis for oviposition and feeding; antibiosis showed in terms of reduced survival, prolonged development, and reduced fecundity; and recovery or tolerance to insect damage in terms of ability to withstand insect damage or production of additional branches, tillers of another flush of flowering, and fruiting bodies. All these mechanisms of resistance have been observed against different insects in various legume crops (Schoonhoven et al. 2005; Sharma et al. 2011).

#### 5.6.1 Oviposition Non-preference or Antixenosis

Cowgill and Lateef (1996) and Sison et al. (1996) commemorated fewer eggs on the resistant/tolerant genotype ICC 506 EB than on ICC 4918 and ICCC 37. Comparatively lower egg laying was also recorded in hybrids based on ICC 12477, ICC 12478, ICC 12479, and ICC 506 EB as compared to the hybrids based on the susceptible check, ICCC 37, indicating that egg laying on  $F_1$  hybrids is influenced by the parents and is inherited in the progeny (Narayanamma et al. 2007), and there is a positive correlation among numbers of eggs laid under laboratory and field conditions (Srivastava and Srivastava 1989). Antixenosis and antibiosis types of resistance have been ascertained against *C. chinensis* L. in chickpea and faba bean (Clement et al. 1994).

In case of pigeon pea, oviposition for non-preference was shown in ICPL 187-1, ICP 7203-1, ICPL 84060, ICPL 88039, T 21, and ICPL 332 under no-choice, dualchoice, and multi-choice conditions (Kumari et al. 2006). Wild *Cajanus* accessions (*C. acutifolius* and *C. sericeus*) were having extravagantly levels of antixenosis for oviposition of *H. armigera* (Sharma et al. 2009). Bean cultivars IAC-Harmonia, IAPAR-81, IPR-Eldorado, and IPR-Siriri were the less preferred for oviposition; and the IAC-Harmonia stretched the whitefly *B. tabaci* life cycle, expressing nonpreference 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); there is no ovipositional antixenosis in some of cowpea cultivars to the pod borer by Valdez (1989). Trichomes on the pods of *V. vaxillata*, a wild relative of cowpea, are partially responsible for resistance to *C. tomentosicollis* Stal. (Chiang and Singh 1988). Singh (2002a, b) suggested that varieties with pigmented calyx, petioles, pods, and pod tips suffered least damage from legume spotted pod borer *M. vitrata*. Durairaj et al. (2009) ascertained most of the wild relatives were found susceptible to aphids and other sucking insect pests, and both antixenosis and antibiotic type of resistance have been observed against *E. fabae*, *E. varivestis*, and *B. pisorum* L. (Clement et al. 1994). The pea varieties having yellow-green color are less preferred to the pea aphids than the blue-green ones (Painter 1951), and varieties deficient in certain amino acids are also shown to be resistant to the pea aphid *A. pisum* (Harris). In soybean varieties without pubescence were extensively damaged by the potato hopper, while those with pubescence seemed to be unaffected (Fehr 1987), and non-preference for oviposition is one of the major components in *H. zea* resistance in PI 2227687 soybean (Horber 1978).

### 5.6.2 Antibiosis

This mechanism of resistance is typically associated with plant biochemical parameters, like the presence of free amino acids, fatty acids, and fibers in the leaflets, which may have adverse effects on an insect that attempts to colonize it, affecting the biological performance of the insect (Panda and Khush 1995; Smith 2005). Antibiosis is a component of resistance to *H. armigera* in pigeon pea and chickpea, which is showed in terms of reduced larval survival, fecundity, and weight gain and prolonged larval development (Kumari et al. 2010b). Reduced larval and pupal weights and prolonged larval and pupal developmental periods were observed in insects reared on entire leaves or pods of ICPL 332, ICPL 84060, ICPL 88039, ICP 7035, and T 21. Similar effects were observed when larvae reared on artificial diet impregnated with lyophilized leaves or pods of aforesaid cultivars (Kumari et al. 2010a). Wild *Cajanus* accessions have high manifestations of antibiosis (*C. acutifolius* (Benth. ex Baker) Maesen) against pod borer (Sharma et al. 2009).

Antibiosis showed in terms of decreased larval, larval mortality, and pupal weights, extended larval and pupal periods, failure to pupate, and reduced fecundity, and egg viability contributed to antibiosis of resistance to *H. armigera* in chickpea (Srivastava and Srivastava 1989; Yoshida et al. 1995; Cowgill and Lateef 1996; Narayanamma et al. 2007). Larval survival and larval weight were lower on ICC 506 EB, ICC 12476, ICC 12477, and ICC 12478 when contrasted with that on ICCC 37. In addition, the isoflavonoids can interfere negatively with insect feeding, oviposition, and development (Harborne and Williams 2000; Simmonds 2003). 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); Koona et al. (2002) accounted that TVnu 151 exhibited antibiosis for *C.tomentosicollis*, causing high nymphal mortality, and the larval survival of *M. vitrata* was low on cowpea variety TVNu 946, and it was due to the antibiotic and nutritional factors (Macfoy et al. 1983; Saxena 1989). Valdez (1989) observed only a slight effect of the host on larval survival, and Okech and Saxena

(1990) indicated that stem and pods act as antibiosis component of resistance in TVNu 946 and VITA 5. In general, antibiosis consequences are expressed in terms of weight and size of insects, sex ratio, and proportion of insects entering diapause (Basandrai et al. 2011). Four green gram accessions LM 131, V 1123, LM 371, and STY 2633 and three black gram accessions UH 82-5, IC 8219, and SPS 143 were found to be moderately resistant to bruchid *C. chinensis* having less percentage survival and prolonged developmental period as compared to susceptible check (Ponnusamy et al. 2014).

#### 5.6.3 Tolerance

Ability to withstand insect damage that results in lower loss of grain yield indicates the ability of different genotypes to recover from insect damage. However, tolerance is more subject to variation because of environmental conditions than non-preference and antibiosis. The age or size and general vigor of the plant and size of the insectresistant population also strongly influence the degree of tolerance.

Reduction in grain yield also renders a good measure of agronomic performance and the genotypic ability to withstand *H. armigera* damage. If there should arise an occurrence of chickpea, plant recuperation from harm recuperation by *H. armigera* was better if there should be an occurrence of ICC 506 EB, ICC 12476, and ICC 12479 when contrasted with the vulnerable check, ICCC 37 (Narayanamma et al. 2007). The misfortune in grain yield was lesser in the event of ICCV 2, ICC 12478, ICC 12479, and ICC 506 EB crosswise over crop phenology stages and pervasion technique conventions when contrasted with that on the vulnerable check, ICCC 37. Pigeon pea ICPL 187-1, ICPL 98008, ICP 7203-1, T 21, ICP 7035, and ICPL 332 showed moderate levels of resistance to *H. armigera* across planting dates. ICPL 187-1, ICPL 84060, ICP 7203-1, ICPL 87119, and ICPL 332 suffered lower loss in grain yield than the susceptible checks, ICPL 87 and ICPL 87091, under unprotected conditions (Kumari et al. 2010b).

## 5.7 Morphological and Biochemical Traits Associated with Insect Resistance

#### 5.7.1 Phenological Traits

Pigeon pea genotypes having determinate growth habit, clustered pods, and dense plant canopy are more prone to be susceptible to pod borers, *H. armigera* and *M. vitrata*, than genotypes with non-clustered pods (Sharma et al. 1997), while the genotypes with smaller pods, pod wall thick and tightly fitting to the seeds, and a deep constriction between the seeds are less susceptible to *H. armigera* (Nanda et al. 1996). The varied plant growth types and maturity also influence genotypic susceptibility to pod fly, *M. obtusa*, but podwall thickness, trichome density, and amount crude fiber content are associated with resistance to *H.armigera* in pigeon

pea (Moudgal et al. 2008). Sharma et al. (2009) observed higher density of type "C" and "D" trichomes present in wild relatives of *C. scarabaeoides* and *C. sericeus*, and there are 5–6 traits that distinguish *C. cajanifolius* from pigeon pea such as flower morphology, pod color, morphology, pod constriction, seed color, and 100 seed weight (Mallikarjuna et al. 2012).

Pod wall thickness, plant growth habit, and crop duration influence pod borer *H. armigera* damage in chickpea (Ujagir and Khare 1988). 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 influence expression of resistance to *M. vitrata* in cowpea (Soundararajan et al. 2013). Oghiakhe et al. (1991) reported that defoliated cultivars suffered lower damage than the undefoliated ones, and the cultivars TVu 946 and TVu 4557 having attributes of high length of the peduncle and angle of pods (Singh 1978) erect and profuse flowering in TVu 946 (Oghiakhe et al. 1992a, b) for resistance *M. vitrata* in cowpea. The bunched pods suffered greater damage by legume pod borer (Usua and Singh 1979). Pubescence in wild and cultivated cowpea *V. vexillata* and *V. unguiculata* badly affected oviposition, mobility, and food consumption by the legume pod borer in tests conducted with TVNu 729 (wild, highly resistant and highly pubescent), TVNu 946 (semi wild, moderately), and IT 82D-716 (cultivated, highly susceptible, and pubescent) (Oghiakhe 1995).

In green gram, fewer number of bruchid eggs were recorded on small and shiny seeds as compared to large and dull seeds, and in black gram, small and black seeds recorded lesser number of eggs as compared to large and green seeds (Ponnusamy et al. 2014); and the neoplasm formation, thicknesses of podwall, and micromorphological traits attributed for a reduced oviposition rate of female pea weevil on genotype 235,899-1 (Mendesil et al. 2016). In *Dolichus* bean, the foliage color, days to 50% flowering, flower color, pod color, pod texture, and fragrance influenced genotypic susceptibility to *M. vitrata* (Mallikarjuna et al. 2009).

#### 5.7.2 Leaf Hairs and Trichomes

Leaf hairs (that do not produce glandular secretions) play a pivotal role in host plant resistance to insects. Wild relatives of pigeon pea such as *Cajanus scarabaeoides* and *C. acutifolius* with nonglandular trichomes are not preferred by *H. armigera* females for egg laying (Sharma et al. 2001a; Sujana et al. 2012). Trichomes (hair-like outgrowths on the epidermis of plants that produce glandular secretions) also play an important role in host plant resistance to insects. Hooked trichomes in bean vitiate the movement of the aphid, *A. craccivora* (Johnson 1953), and potato leaf-hopper, *E. fabae* (Pillemer and Tingey 1978). Glandular trichomes in pigeon pea are linked to *H. armigera* susceptibility (Peter et al. 1995; Sharma et al. 2001a; Green et al. 2003; Sujana et al. 2012).

Trichomes and their organic exudates in chickpea also influence the movement and feeding behavior 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 a wild relative of cowpea (*Vigna vexillata*) pods are partly responsible for resistance to the pod-sucking bug, *Clavigralla tomentosicollis* Stal. (Chiang and Singh 1988). The density and length of trichomes are linked with resistance to pod borers in short-duration pigeon pea, while trichome density on upper and lower surface parts of the leaf (390 and 452/9 mm<sup>2</sup>), trichome length (3.5 mm), and trichome density (442.9 mm<sup>2</sup>) and length (5.9 mm) on pods are positively correlated with the resistance to pod borer, *H. armigera* (Sunitha et al. 2008a).

Potential effects of trichomes on whiteflies may vary depending on trichome angle to the leaf surface, length and type, all factors potentially affecting adult oviposition, and immature attachment and feeding in black gram (Channarayappa et al. 1992), and the genotypes having shorter trichomes are inclined to resistance against *B. tabaci*. Another fact revealed that 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) behavior of the whitefly in resistant genotypes of black gram (Lakshminarayan et al. 2008; Taggar and Gill 2012).

## 5.8 Biochemical Mechanisms of Resistance

### 5.8.1 Nutritional Factors

Nutritional parameters, viz., sugars, phenols, proteins, fats, sterols, and essential amino acids and vitamins, also influence on host plant suitability to insect pests. Total soluble sugars present in pigeon pea pod wall, which influence the pod damage by *H. armigera*. Apart from sugars, the protein content of the pod wall is also associated with susceptibility, while total sugars are associated with resistance to *M. obtusa* in pigeon pea (Moudgal et al. 2008). Higher sugar content present in flower (22%) and pods (10.6%) was responsible for the susceptibility of ICPL 88034, while higher phenol concentration in flowers (6.5%) and pods (9.3%) in ICPL 98003 was responsible for resistance. Protein percent in pods was significantly higher (25.5%) in susceptible ICPL 88034 when compared with resistant ICPL 98003 (16.5%) (Sunitha et al. 2008b).

Pea varieties deficient in certain amino acids, which influence for resistant to the pea aphid, *A. pisum* (Auclair 1963). Higher amounts of nonreducing sugars and lower amounts of starch in chickpea variety GL 645 attribute 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 possessed high amount of fats, protein, and anti-nutritional factor (phenol and four to five times more trypisn inhibitors) than cowpea and chickpea (kabuli> desi) genotypes which contain high amount of carbohydrates and low amount of anti-nutrional factors and were susceptible toward *Callosobruchus* species (Sharma and Thakur 2014).

Nonprotein or unusual amino acids afford protection against herbivores in several plant species. The protective effect is elicited via their structural analogy to the most commonly occurring essential amino acids. Among these, L-canavanine, 2, 4-diamino butyric acid, azetidine-2-carboxylic acid, minosine, and 3-hydoxyproline have substantial growth inhibition effects on insects (Parmar and Walia 2001). L-canavanine is a structural homologue of L-arginine and takes place in over 1500 leguminous plant species. Some of the nonprotein amino acids also act as enzyme inhibitors; canaline – a hydrolytic product of canavanine – inhibits pyridoxal phosphate-dependent 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-stress conditions as compared with non-stressed plants (Taggar et al. 2012).

### 5.8.2 Secondary Metabolites

Plants also produce various defensive secondary metabolites in reaction to biotic and abiotic stresses. The secondary metabolites do not involve in the normal growth and development of plant but reduce its palatability of the plant tissues to the herbivores (Boerjan et al. 2003). Some of the secondary metabolites also influence in host finding, oviposition, feeding, and survival and growth and development of insects and play a major role in host plant resistance to insects in grain legumes. Among the secondary metabolites, plant phenols constitute one of the most common and widespread groups of defensive compounds, which play a pivotal role in host plant resistance against herbivores, including insects (Sharma et al. 2009; Usha Rani and Jyothsna 2010; Ballhorn et al. 2011). Qualitative and quantitative alterations in secondary metabolites and increase in activities of oxidative enzymes in plants in response to herbivore attack are a common mechanism of resistance to insects (War et al. 2013). Quercetin, quercitrin, and quercetin-3-methyl ether in the pod surface exudates of pigeon pea play a major role in host plant selection by H. armigera larvae in pigeon pea (Green et al. 2002, 2003). Stilbene, a phytoalexin, occurs at high concentrations in pigeon pea cultivars with resistance to H. armigera (Green et al. 2003). Total phenols and tannins present in the pod wall of pigeon pea are negatively associated with pod fly damage (Moudgal et al. 2008).

Protease inhibitors are another major class of anti-nutrional factors in chickpea and pigenopea, which have shown *H. armigera* microbial gut protease inhibitory activity in developing seeds of wild and cultivated chickpea (Parade et al. 2012). Amylase and protease inhibitors in pigeon pea showed to have an adverse effect on growth and development of *H. armigera* (Giri and Kachole 1998). 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 nonhost plants (groundnut, winged bean, and potato) are more efficient in inhibiting the gut proteinases of *H. armigera* larvae than those from its favored host plants such as chickpea, pigeon pea, and cotton (Harsulkar et al. 1999). Amounts of trypsin inhibitor (TI) in desi chickpea cultivars ranged between 17 and 31 mg/g of sample. The TI activity was greater in P-256 (39.47 $\pm$  1.91 TUI/mg) than in Pusa Pragati (6.19 $\pm$ 0.56 TUI/mg) (Kansal et al. 2008). The wild relatives of pigeon pea belonging to *C. albicans, C. cajanifolius, C. sericeus, Flemingia bracteata*, and *Rhynchosia bracteata* showed high levels of resistance to *H. armigera* and exhibit high levels of protease inhibitors (*PIs*) activity under in vivo and in vitro against *H. armigera* gut proteinases (HaGPs) (Parade 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 daidzein, coumestrol, sojagol, and glyceollins. These compounds reduce feeding, survival, and 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 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 shows no growth inhibition on *H. armigera* (Yoshida et al. 1995, 1997). The chickpea having flavonoids judaicin 7-O-glucoside, 2-methoxy-judaicin, judaicin, and maakiain present in wild relatives of chickpea (*Cicer bijugum* and *C. judaicum*) have shown an antifeedant activity for the larvae of *H. armigera* (Simmonds and Stevenson 2001). In common bean genotypes, arcelin protein and trypsin inhibitors are the major secondary metabolites for resistance to bean weevil *Zabrotes subfasciatus* (Blair et al. 2010).

### 5.9 Inheritance of Resistance to Insects in Grain Legumes

Greater magnitude of  $\sigma^2 A$  (17.39) than  $\sigma^2 D$  (3.93) clearly showed preponderance of  $\sigma^2 A$  in the inheritance of legume pod borer, *H. armigera* resistance (Narayanamma et al. 2013a). Gowda et al. (2005) ascertained that additive and dominance genetic variances were majorly predominant in early and medium maturity diallel trials, respectively. Additive as well as dominance components of genetic variances were equally important in the inheritance of legume pod borer H. armigera resistance in late maturity group. Such derivative nature of gene action controlling pod borer resistance in varied maturity groups has earlier been reported by Gowda et al. (1983) and Singh et al. (1991). Salimath et al. (2003) accounted in the involvement for both additive and nonadditive gene action in the inheritance of pod borer resistance, although their results were maturity non-specific. Cotter and Edwards (2006) reported that heritability of larval execution was maximum for neonates than for third-instar larvae in noctuid moth, H. armigera, on a resistant and a susceptible variety of the chickpea, C. arietinum. There was absence of genetic correlation between larval performance and oviposition preference, showing that female moths do not select the most suitable plant for their offspring.

Combining ability studies showed the preponderance of nonadditive type of gene action for resistance to *H. armigera* and *M. vitrata* in pigeon pea (Lal 1987). Verulkar et al. (1997) suggested the involvement of a single dominant gene in antixenosis mechanism of resistance in C. scarabaeoides to H. armigera and M. obtusa. Nonglandular trichomes, which are linked with resistance to H. armigera in C. scarabaeoides, are inherited as a predominant trait (Rupakala et al. 2005). The H. armigera-resistant parents, viz., ICC 506 EB, ICC 12478, ICC 12477, ICC 12479, and ICCV 2, proved to be the best general combiners for pod borer resistance with significantly negative gca effects and low pod borer damage (Narayanamma Lakshmi 2005; Sreelatha et al. 2008; Narayanamma et al. 2013b). The hybrids ICC 506 × ICC 3137, ICC 12477 × ICC 4918, ICC 12476 × ICC 3137, ICC 12479 × ICC 3137, and ICC 3137  $\times$  ICCV 2 showing significant and negative sca effects were having good specific combiners for resistance to pod borer damage done by H. armigera. Although there is a good balance between pod borer damage of crosses and their *sca* effects, the crosses (involving parents with contrasting gca effects) with significant sca effects need to be overworked for developing varieties on pod borer resistance and high grain yield parameters. Singh et al. (1997) could create pod borer-resistant chickpea line, ICCV 7, utilizing pedigree selection of the lines gotten from a combination of H 208 and BEG 482. Further, that the loci of pod borer resistant are different in different resistant sources (Dua et al. 2005), pyramiding of genes from different resistant sources will be effective in increasing the levels of pod borer resistance in chickpea. The identification and evaluation of breeding lines which have dual resistance to pod borer and Fusarium wilt, which help in IPM program (Singh et al. 1990; Lateef 1990; Lateef and Sachan 1990; Van Rheenen 1992; Chaturvedi et al. 1998; Sharma et al. 2003b), are important for increasing productivity of chickpea. Recently identified germplasm line (IPC 96-3 and FG 1235) having dual resistance to pod borer and Fusarium wilt (Harminder et al. 2005) could be used as potential donor source to develop chickpea varieties for sustainable crop production.

On the basis of specific combining ability estimates, the cross JAKI-9218×AKG-10-1 was found to be the best specific combination for seed yield, larval count, malic acid content, and percent of pod borer damage when compared to cross ICCV-2×Chandrapur Chanoli and JAKI-9218×Bushy Mutant (Jadhav and Vijaykumar 2015). The ratio of sca/gca was greater than one for seed yield per plant, larval count at vegetative and pod formation stages, and percentage of pod damage, thereby signifying the preponderance of nonadditive variance in the expression of these characters, whereas additive variance was found to be predominant in the expression of larval count at flowering stage and in malic acid content (Jadhav and Vijaykumar 2015). The identification of various breeding lines, viz., ICCL 87317, ICCL 87316, and ICCV 95992 having stable resistance to H. armigera and high grain yield potential, and germplasm lines, viz., ICC 12478, ICC 14876, and ICC 12479 having stable resistance to pod borer H. armigera and moderate yield potential (Sreelatha et al. 2003), could be used in heighten for pod borer resistance in elite agronomic traits. Similar results were reported by Singh and Singh (1990) in pigeon pea for pod fly resistance.

Since gca effects are the demonstration of additive properties of genes, parents selected based on gca effects will be useful for arising breeding lines with higher grain yield (Narayanamma et al. 2013b) and desirable levels of the trait of interest. Based on gca effects, the genotypes ICC-506 and ICCV-2 have good genetic potential for their utilization in further breeding programs for genetic improvement of pod borer *H.armigera* resistance in chickpea by using them as one of the parents in hybridization and isolating desirable segregants for resistance to pod borer. Most promisingly, the parent ICC-506 can be extensively used in the hybridization program to accelerate the pace of genetic improvement for pod borer resistance in chickpea. In lentil, ILWL 245 line is being used to transfer introgress resistance genes to cultivated and study the inheritance of Sitona weevil resistance in lentil (Bouhssini et al. 2008). Pathak (1988) studied the genetic resistance of cowpea aphid and reported a single dominant gene, designated as Rac1 and Rac2. Ombakho et al. (1987) also studied in F1 and F2 generation of cowpea (TVU 310, ICV10, and ICV 11) and reported that resistant gene in TVU 310 and ICV 10 was designated by Ac1, while resistant gene in ICV11 was Ac2.

## 5.10 Wide Hybridization

Transferring gene from wild relative species to the cultivated species to confer an adaptive resistance to *H. armigera* is one of the potential options for crop improvement. Wild Cajanus species are the reservoir of many important trait-specific genes and can be utilized to improve the crop cultivars, enrich variability and diversity, and broaden the genetic base and the pre-breeding populations involving wild Cajanus species from its secondary gene pools (C. cajanifolius (ICPW 29), C. scarabaeoides (ICPW 281), C. sericeus (ICPW 159 and 160), C. reticulatus, C. acutifolius (ICPW12 and ICPW 004), C. albicans (ICPW 14)) and tertiary gene pools (C. platycarpus (ICPW 68), Rhynchosia aurea, and R. bracteata)) as donors for traitspecific genes and pigeon pea cultivars as recipients, while these crosses are being further advanced to develop introgression lines (ILs) with high levels of resistance to pod borer (Sharma and Upadhyaya 2016). The wild Cicer species such as C. reticulatum, C. pinnatifidium, and C. echinospermum showing high levels of resistance to H. armigera can be used in wide hybridization in crop improvement program (Sharma et al. 2005a, 2006). The cross-incompatibility among cultivated chickpea and its tertiary gene pool are post-zygotic (Mallikarjuna 2001; Babb and Muehlbauer 2005), and hence, there is a need to formulate bridge cross between tertiary and secondary gene pool and then use the progeny in further crosses with the cultigen. Recently introgression studies have been done on pod borer (H. armigera), pod fly, bruchid resistance, and other agronomic traits in pigeon pea for opting improved cultivar for sustainable crop production (Mallikarjuna et al. 2011a), and also advanced generation population from the cross-utilizing C. acutifolius as the pollen parent has shown resistance for pod borer damage (Mallikarjuna et al. 2007; Jadhav et al. 2012a), for opting variation for seed color and high seed weight. Some of the lines showed high level of resistance to pod borers and pod fly under

natural field conditions and for bruchid resistance studies for cultivated pigeon pea under storage conditions (Jadhav et al. 2012b).

There is lack of an authentic information of resistance to pea weevil in cultivated P. sativum accessions led to the geographical expedition and identification of resistant sources from its secondary gene pool of Pisum, which ensured in the breakthrough of pod and seed resistance in P. fulvum accessions (Clement et al. 2002). The P. fulvum accession ATC113 (PI 595933) was successfully crossed with P. sativum accession Pennant, and it produced interspecific progenies with having resistant traits in lines (Byrne et al. 2008), and the development of introgression line for pea weevil resistance into cultivated field pea was further confirmed by using advanced backcross lines of the original population (Aryamanesh et al. 2012). Development of first QTL markers is developed by interspecific hybridization among cultivated field pea and P. fulvum (resistance source) against pea weevil and identified three QTL regions associated resistance in cotyledon (linkage groups LG2, LG4, and LG5), pod wall/seed coat (linkage groups LG2 and LG5), and pod wall (on LG7) (Aryamanesh et al. 2014). Recently, Pandiyan et al. (2010) described a number of cross-sectional and cross- subgenus hybrids; amid these hybrids, the cross between V. radiata and V. umbellata is especially shown significant as V. umbellata possesses with a high level of resistance to bruchid beetles, one of the most serious and concern pests of Vigna.

#### 5.11 Marker-Assisted Selection

As we know, pod borer (*H. armigera*) is perhaps the major threat to chickpea and pigeon pea in terms of production and productivity. Screening has been done over 5000 germplasm accessions divulged that still there is no resistant strain or source against this insect pest (Kumar et al. 2004). While few resistance sources were identified in the past in cultivated gene pool, they showed either inconsistency or low levels of resistance lending to their little development in breeding programs (Lateef 1990). Therefore, there is urgency to identify stable sources of genetic resistance in the crossable gene pool for pod borers to facilitate conventional genetic crop improvement programs. The use of undiscovered genes in existing gene pools and the utilization of wild relatives as a rich reservoir of resistance genes against both abiotic and biotic stresses should be given special attention to broaden the genetic base of breeding pool (Clement et al. 2009). In recent days, the development of newer molecular markers and other genomic sources has been quickened in major chickpea, pigeon pea, 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 cowpea and pea crop, while in the case of lentil and faba bean, it is in infancy stage. The recent approach for the development resistance trait for major legume crops by deploying genomics-assisted breeding (GAB) holds promise in enhancing the genetic gains and discovery of genome-wide genetic markers, highthroughput genotyping/high-throughput phenotyping and sequencing platforms,

and high-density genetic linkage/QTL maps, and, more importantly, the availability of whole-genome sequence helps in speeding up the progress of genetic improvement of major pulses, which lead to rapid development of cultivars with higher yield, enhanced stress tolerance, and wider adaptability (Bhora et al. 2014).

Progress in marker-aided selection for development of resistance to insect pests in grain legumes though limited extent has been discussed by Sharma et al. (2008). Mapping the complex traits like resistance to pod borer, *H. armigera*, in chickpea is the only that just started (Lawlor et al. 1998). A cross between a wilt-resistant kabuli variety (ICCV 2) and a wilt-susceptible desi variety (JG 62) has been used to develop the first intraspecific genetic linkage map of chickpea using mapping population (Cho et al. 2002). This population has been further evaluated for resistance to pod borer H. armigera, and the data analysis is under progress. 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 between Vijay and ICC 506EB has also been developed and evaluated for H. armigera, and in pigeon pea, also a mapping population between C. cajan and C. scarabaeoides is under development at ICRISAT (Upadhyaya HD, personal communication).

However, genetic improvement program has always been impeded with limited genetic variability under primary gene pool of pigeon pea, and its wild species present in the secondary and tertiary gene pools have been reported to carry forward resistance against major insect pests. However, till date deployment of resistance genes through conventional backcrossing has not been much successful. So now it especially calls for development of 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 (restricted fragment length polymorphism) marker segregation (Myers et al. 1996). The RFLP marker bg4D9b was connected to the aphid resistance gene (Rac1), and furthermore, a few flanking markers in a similar linkage gathering (linkage bunch 1) have additionally been identified and described. Taran et al. (2002) identified the genetic linkage map of common bean. The genetic loci for resistance to potato leafhopper, Empoasca fabae (Harris), were detected by Murray et al. (2004). In green gram, TC1966 bruchid resistance gene has been mapped by adopting RFLP markers (Young et al. 1992). Resistance was mapped to a single locus on linkage group VIII (approximately 3.6 cM from the nearest RFLP marker), and based on RFLP analysis, a progeny was also identified in the F<sub>2</sub> population that maintained the bruchid resistance gene among a tightly linked double crossover. This progeny would be useful for developing bruchid-resistant mung bean lines and free of linkage drag. For introgression of the bruchid resistance gene in green gram, Yang et al. (1998) used RFLP marker-assisted selection in backcross breeding, while Kaga and Ishimoto (1998) studied genetic determination of a

bruchid resistance gene and its relationship to insecticidal cyclopeptide alkaloids, the vignatic acids in green gram. Villareal et al. (1998) reported random amplified polymorphic DNA (RAPD) markers have also been used to identify markers linked to the bruchid resistance in mung bean. The Br locus confirms a bruchid resistance in mung bean, VrPGIP2 (encoding a polygalacturonase inhibitor) is a strong candidate gene for resistance, and VrPGIP2 sequence genes were varied between resistant and susceptible lines (Chotechung et al. 2016). The gene was 25 cM from pM151a. Whenever pM151a and pM151b were conceived considered as alleles of a similar locus, the bruchid resistance genes were found 11.9 cM from its closest RAPD marker Q04 sub 900 and 5.6 cM from pM151. The progress has been made for the crosses between field pea (P. sativum) and the wild species (P. fulvum) to locate molecular marker resistance gene to pea weevil in (Byrne et al. 2002). There have been no definitive efforts that has been made to identify OTLs associated with insect resistance in pigeon pea (Sharma 2009), but mapping population based on C. cajan x C. scarabaeoides has been developed and is under evaluation stage for resistance to *H. armigera* to identify QTLs linked for resistance to pod borer in pigeon pea.

To date, the sources of cowpea aphid (CPA) resistance and major quantitative trait loci (QTL) 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 for identifying syntenic areas in other legumes, as they may confabulate similar physiological responses against CPA infestation (Kamphuis et al. 2013). Development of African cowpea introgresses resistance allele genes from IT97K-556-6 into susceptible local blackeye varieties (CB27) by backcrossing with the help of recombinant inbred line (RIL) for aphid resistance (Huynh et al. 2015). Genome solution for a major QTL associated with the Rk locus in cowpea for resistance to root-knot nematodes Meloidogyne spp. has significance for plant breeding programs and characterization R gene by Huynh et al. (2016). Muchero et al. (2010), working on the cross from the foliar thrips susceptible 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 ACCCAT7, ACG-CTC5, and AGG-CAT1 and were linked with foliar damage caused by T. tabaci and F. schultzei. These urging researches paved the way forward for genetic characterization of major insect pest resistance in cowpea and disease causes > 15% yield loss in West Africa and impacts production in Asia and South America negatively. In addition, other putative candidate marker-assisted selection (MAS) for insect or disease resistance in cowpea was reported (Timko and Singh 2008).

Resistance to bruchid has been reported in few mung bean cultivars (Somta et al. 2006; Somta et al. 2008); however, some of mung bean breeders have keen interest in identifying new sources of resistance to this important pest from other Asian *Vigna* species such as *V. umbellata* and *V. nepalensis* (Pandiyan et al. 2010; Somta et al. 2008). It is reported that the bruchid and mung bean bug were controlled by a single dominant gene in the F1 and F2 seeds of mung bean and two QTLs were identified for bruchid resistance, and a QTL for bean bug resistance was detected.

These new markers will be further used for cloning of the resistance genes to bruchid and bean bug in the future (Hong et al. 2015). There are several reports analyzing resistance to mung bean yellow mosaic virus (MYMV) in different germplasms, and both recessive and dominant genes have been implicated. The resistant variety SML-668 has two recessive genes for resistance. Sudha et al. (2013) reported that the resistance of mung bean variety "KMG189" is controlled by a single recessive gene. Development of mung bean yellow mosaic Indian virus (MYMIV) resistance, either using the wild mung bean accessions (*V. radiata* var. *sublobata*) or some of the breeding line from Pakistan, has found a common major resistance QTL (variously named MYMIV'9\_25, qMYMIV1, qMYMIV4) (Chen et al. 2013; Kitsanachandee et al. 2013). This locus was detected in different locations/regions, years, sources of resistance, and scoring systems. The locus was having specific markers; therefore, these could be used in marker-assisted selection for resistance breeding program.

The mung bean yellow mosaic virus resistance (MYMIV) has been found in some accession of black gram, and this resistance gene has been further mapped using SSR markers (Gupta et al. 2013). An SSR marker nearly linked to the resistant locus was found that could be used for marker-assisted selection. Kushida et al. (Kushida et al. 2013) recently studied some accessions of *V. minima*, and *V. nakashi-mae* showed a high level of resistance to all races of soybean cyst nematodes in Japan, and these resistant sources are being used in azuki breeding, since the soybean cyst nematode is an increasingly problematic pest on legumes in Hokkaido, Japan. *V. nakashimae* has been used to develop an interspecific linkage map with *V. umbellata* (Somta et al. 2006). QTL-M and QTL-E enhance soybean resistance to major insects; pyramiding these QTLs with cry1Ac increases protection against Bt-tolerant pests, presenting an opportunity to effectively deploy Bt with host plant resistance genes (Ortega et al. 2016).

#### 5.12 Transgenic Resistance to Insects

The first successful genetic transformation of chickpea with *crylAc* gene, which inhibit the growth and development of *H. armigera*, was reported by Kar et al. (1997). Genetic transformation of chickpea using *CrylAc* 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 *CrylAc* in chickpea lines (Acharjee et al. 2010). Mehrotra et al. (2011) generated pyramided genes *CrylAc* and *CrylAb* chickpea; however, 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 *crylAb/Ac* constitutively for resistance to *H. armigera* using pod-specific *msg* promoter from soybean to different transgenic lines has also been reported. Homologous ubiquitin and RuBisCO small subunit (rbcS) promoters used to transcribe *crylAc* in transgenic chickpea var. ICCV89314 (Chakraborty et al. 2016).

The toxicity of commercial Bt formulation and Cry1Ab and Cry1Ac 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 days, Cowpea aphid, *A. cracciovra*, also causes significant yield losses in chickpea, an important pulse crop in the Indian subcontinent, where transgenic chickpeas expressing the *Allium sativum* leaf agglutinin (ASAL) gene resulted in a significant reduction in survival and fecundity of cowpea aphid (Chakraborti et al. 2009). A new management strategy such as upregulating secondary metabolites, which are toxic to insect pests (Gatehouse 2002), or introducing RNAi technology for insect control by silencing endogenous genes of insects could be new strategy to develop genetically modified chickpea (Gordon and Waterhouse 2007).

Transgenic pigeon pea plants with *cry1Ab* 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). Developed 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) showed resistance to bruchid species. Transgenic pea with expression of  $\alpha$ -amylase inhibitor has also been developed for resistance to pea weevil (Morton et al. 2000).

Ikea et al. (2003) detailed the fruitful hereditary change of cowpea utilizing 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 was depicted in the wild relative *Vigna vexillata*; however, nonviable seeds coming about because of their cross make this approach improper to exchange these qualities to the developed species (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*) would be utilized against these vermin assaults (Ishimoto et al. 1999).

Right now, huge advance has been made on 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) and *C. maculatus* and *C. chinensis* (Abrol 1999; Popelka et al. 2006; Tarver et al. 2007; Adesoye et al. 2008; Huesing et al. 2011). Every one of 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 harboring 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 is a cotyledon-specific promoter into the breeding line IT86D-1010 and the Japanese cultivar "Sasaque" that both showed 100% larval (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 in successfully into commercially important cultivars of cowpea, and the genes are transmitted in Mendelian fashion (Abaye et al. 2014). Investigations executed by Jackai et al. (1997) showed that the insect pests of cowpea 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 Cry1Ab in cultivars (TVu 201, Ife Brown, IT90K-277-2, IT90K-288, and IT90K- 391) and CrylAc genes in cultivar (Pusa Komal) in various cowpea genotypes, and their experiment results showed that the transgenes were carried in Mendelian fashion to 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.

#### 5.13 Potential and Limitations of HPR to Insects 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 leads to an adverse effect on environment and health hazards in human beings. The crop improvement efforts have been underway over a long period to develop varieties/cultivars with resistance to insect pests in grain legumes (Sharma 2005, 2016). Nevertheless, host plant resistance can be used as a primary constituent of pest control, as along with cultural, biological, and chemical control and as a check against the released susceptible cultivars, apart from the use of molecular approaches for the development of insect pests resistant cultivars of legumes. Adaptation of genetic alternatives, such as introgression/pyramiding of genes/quantitative trait loci associated, wide hybridization, and marker-assisted selections for development of insect pest-resistant cultivars, on the other hand, is much an ecological and eco-friendly approach (Khera et al. 2013). Special importance has been given on the current status and prospects of deploying newer molecular host plant resistance techniques and breeding approaches for developing improved cultivars with high resilience to major insect pests stress to achieve maximum genetic yield potential in all the legume crops. As we know, plant resistance to insects is the key factor of any pest management system because:

- It is specific to target insects or group of pests and generally has no adverse effects on the nontarget organisms in the ecosystem.
- · Plant resistance effects on insect pest population are cumulative over sequential generations for particular pest because of bringdown survival, delayed development, and lower fecundity.

- The most of insect-resistant crop cultivars carry moderate to high level of resistance across cropping season. In contrast, the insecticides must be applied frequently in order achieve satisfactory control of pest populations.
- HPR is easy to be compatible with other strategies of pest control, and it also improves the efficiency of other methods of pest management.

However, host plant resistance is not the only nostrum for solution for all the insect pest problems in agroecosystem. It needs a long time for the exploitation of plant genotypes/cultivars with resistance to insect pests. Some mechanisms of plant resistance may involve the diversion of plant morphological traits or biochemical traits for the production of defense chemicals and other physiological processes that helps in obtaining yield (Mooney et al. 1983). Although concentration of natural defense chemicals responsible for resistance is low in plant tissues, the total amount per hectare may be high (Mitra and Bhatia 1982). Some plant defense chemicals also affect the food nutrition quality. Most of genotypes with resistance to H. armigera are susceptible to Fusarium wilt in both pigeon pea and chickpea (Sharma 2005). There is a need to generate baseline information on the inheritance of resistance to insect pests in grain legumes and the host plant-insect-environment interactions to understand the genetic control of different mechanisms of resistance for the development of suitable strategies to increase the levels and diversify the basis of resistance for sustainable production of grain legumes. There is a necessity to break the linkage between the parameters conferring resistance to the target insect pests and the low-yield trait that results in susceptibility and at the same time do not have a negative effect on the quality of the product.

## 5.14 Conclusions

Conventional methods of protecting the legume crops from insect pests are inadequate to meet the growing demand for pulses in future. Accuracy and preciseness of phenotyping for resistance to insect pests remain a major critical limitation. Improved higher-version phenotyping systems will have a substantial impact on both MAS and conventional breeding in order to develop cultivars resistant to insect pests, in addition to there is a need of more strategic research that feeds into these endeavors. There are very limited reports concerning about the role of application of MAS for developing resistant cultivars in grain legumes. Be that as it may, those accessible neglects to exhibit an expansion in proficiency of MAS over conventional breeding methodologies. 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 cultigens with resistance to enhance the crop productivity and improve the livelihoods of the farming community.

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