12

Breeding for Resistance to *Heliothis*/ *Helicoverpa:* Effectiveness and Limitations

R.P. Dua[1], C.L.L. Gowda[2], Shiv Kumar[1], K.B. Saxena[2],
J.N. Govil[3], B.B. Singh[3], A.K. Singh[3], R.P. Singh[3], V.P. Singh[3]
and S. Kranthi[4]

Helicoverpa armigera (Hübner) has been identified as an important pest problem globally. Only a few insect pests cause as much loss to vegetative and reproductive plant parts in a range of tropical and subtropical crops around the world as *Helicoverpa*. Its geographical range of distribution extends to all the continents, but the damage in the semi-arid tropics is enormous. *Helicoverpa armigera* has been recorded from over 20 crops and 180 wild hosts in India. Cyclic appearance of *H. armigera* on cotton and pulses has rendered the mitigation of this pest to be quite difficult. It has become a central issue to overall sustainability of many cropping systems. The preferred host plants are pigeonpea, field bean, chickpea, tomato, cotton, chilies, mungbean and sorghum (Jayaraj 1982). Losses caused by *Helicoverpa* are astronomical in cotton ($290 to $350 million annually) (King 1994), but pigeonpea, chickpea, tomato, maize, and tobacco are equally affected. Average losses on account of crop

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[1] Indian Institute of Pulses Research, Department of Entomology, Kanpur 208 024, Uttar Pradesh, India. IIPR@email.com

[2] International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru 502 324, Andhra Pradesh, India.

[3] Division of Genetics, Indian Agricultural Research Institute, New Delhi 110 012, India.

[4] Central Institute for Cotton Research, Department of Entomology, Nagpur 440 010, Maharashtra, India.

damage by insect pests in cotton work out to be 10 to 30% (Russell et al. 1999). The annual losses in chickpea and pigeonpea exceed $300 million (Reed and Pawar 1982). The damage caused by this pest on chickpea may be upto 84.4%, with an average of 7% in different farming systems (Lateef 1992). *Helicoverpa* is estimated to cause 50 to 60% grain loss to pigeonpea (Puri 1998). During 1997-98, the pigeonpea crop was completely damaged due to outbreak of *Helicoverpa*. Surveys during 1974-81 have shown upto 44% pod damage in the northwest plain zone of India, where mean pod damage was found to be 30%.

Even though various chemical control measures have been devised to minimize the losses caused by *Helicoverpa*, this pest has developed considerable levels of resistance to insecticides due to their indiscriminate use. From the ecological and economical viewpoint, breeding cultivars having resistance to this pest is the most important component of integrated pest management. More than 750 cultivars with resistance to more than 50 insect species or biotypes have been developed in India. It has been documented that for each $1 invested in plant resistance, farmers have realized a return of $300 (Robinson 1996). Despite several sources of resistance available for *H. armigera* in cotton, chickpea and pigeonpea, there is no resistant cultivar in the truest sense. Transfer of resistance genes from these sources to agronomically superior backgrounds has been marred by a number of biological and technological factors. This chapter mainly deals with host plant resistance, progress in breeding for tolerance/resistance, and effectiveness and limitations encountered while breeding for resistance against *Helicoverpa* in chickpea, pigeonpea and cotton.

Sources of Resistance to *Helicoverpa armigera*

Progress in breeding for pod borer resistance depends on the availability of germplasm collections, and identification of resistant donors. Concerted efforts to screen chickpea germplasm have led to the identification of many accessions exhibiting an impressive level of resistance to *H. armigera* (Chhabra and Kooner 1980; Dias et al. 1983; Lateef and Reed 1985; Patnaik et al. 1985; Naik et al. 1986; Ujagir and Khare 1987, 1988; Patnaik and Rath 1989; Sahoo et al. 1989; Chhabra et al. 1990; Lateef and Sachan 1990; Srivastava and Srivastava 1990; Patnaik and Mohapatra 1995; Parvez et al. 1996; Yelshetty et al. 1996; Bhatnagar and Rao 1997; Chaturvedi et al. 1998; Das and Kataria 1999; Singh and Yadav 1999; Banchhor et al. 2000; Gumber et al. 2000). Screening of more than 14,800 germplasm accessions under natural infestation at ICRISAT has resulted in the identification of 21 donors showing antixenosis, antibiosis and/or tolerance mechanism of resistance, and these sources can be used in the breeding programs (Lateef and Pimbert 1990). Of them, ICC 506, GL 645, PDE 2-3, PDE 7-3, ICC 10613, ICC 10619 and ICCL 79048 are most promising (Table 12.1). Screening of wild relatives of *Cicer arietinum* has shown that the density of *Helicoverpa* larvae on *C. echinospermum*, *C. judaicum*, *C. pinnatifidum* and *C.*

Table 12.1. *Helicoverpa*-resistant donors for chickpea, pigeonpea and cotton.

Crop	Donors
Chickpea	ICC 10460, ICC 10619, ICC 10667, ICC 10817, ICC 10870, ICC 1381, ICC 2696, ICC 4935-2793, ICC 506, ICC 5294, ICC 6663, ICC 7559, ICC 7966, ICC 9526, ICCL 86111, ICCV 7, ICC 1477, ICC 2446, ICC 2996, ICC 3474, ICC 446, ICC 4662, ICC 4856, ICC 5634, ICC 5800, ICC 7394, ICC 6510, ICC 7553, ICC 7770, ICC 8334, ICC 8835, ICCC 10243, ICCL 78025, ICCL 79022, ICCL 79048, ICCL 86106, ICCV 93118, BG 79, Desi 3108, DHG 84-11, DHG 88-20, GL 645, IPC 94-93, IPC 94-94, LCG 3580, P 240, PDE 2-3, PDE 5, PDE 90-2E, ICCL 84509, ICCL 86101, ICCL 86102, ICCL 86103, ICCL 86104, ICCL 86105, ICCL 87211, ICCL 87220, ICCL 87314, ICCL 87315, ICCL 87316, ICCL 87317, ICCV 93122, ICCV 95992, ICCV 96752, JG 74, RWG 2, JG 315, F 378, C 235, 6219, C 727, GL 645, P 1324 II, P 1697, Sel 418, P 6292-I, Dulia 6-28, Chaffa, PDE 7-3, RSG 130, H 75-85, ICCC 18, Kanpur local, Gonda II local, Mirzapur local, IPC 94-102, L 2793 (C 235), GL 1014, ICCX 730020-11-2H, BG 256, ICCX 730041, ICC 10613, ICC 10817, ICCL 79048, DHG 84-11, P 240, BG 79, DHG 88-20, Pusa 244, BG 324, ICCX 730008-81-1P–BP, GL 645, ICC 10613, ICC 10619, ICCL 79048, RG 945, JAKI 9226, ICC 93512, ICC 93515, ICC 93212, BDN 9-3, GL 102, ICCC 31, ICCC 13, ICCC 22, ICCC 30, BG 246, BDNG 20.
Pigeonpea	T 21, Patna 15505, TT 6, Patna 102, P 855, TPT 11,TT 3/3, 7035, 72-64-2, TT 2/11, C 53, BC 819, NP 15, PPE 45, ICPL 8860, BWR 27, PDA 88-2E, PDA 92 1E, PDA 92-2E, ICPL 4, ICPL 91031, PDA 92-3E, PDA 89-2E, SL 21-9-2, PDA 93-1E, No. 148, 4725, Phule T-1, AS 71-37, Phule T 3, BDN 2, N 84, BDN 1, N 290-21, PL 8796, 7411, BC 819, C 23.
Cotton	CAMD-E, Stoneville 506, MHR lines (Fergo-bract types), Pee Dee 695, LA HG 063, LA HG 065, LA HG 660 (high gossypol), MAR types of Texas, Pima 54, LRA 5166, BN NISD 3, Reba B 50, Abadhita, Acala glandless, SB 289 E, CRH 71.

reticulatum were significantly lower than on the cultivated species (Kaur et al. 1999).

Field screening against pod borer damage has shown some indication of relative tolerance in a few pigeonpea genotypes. However, these results are not consistent over environments, and no dependable sources of resistance have been identified for incorporation into desired agronomic base. Screening of germplasm accessions of cultivated and wild relatives of *Cajanus* has resulted in the identification of lines with moderate resistance to this pest (Chaudhary et al. 1980; Bhosale and Nawale 1983; Deokar et al. 1983; Tripathi and Purohit 1985; Sanap et al. 1989; Nanda et al. 1996; Durairaj and Ganapathy 1997; Das 1998; Lal and Rathore 1999; Rao and Mohammed 1999; Venkateswarlu and Singh 1999). Lal and Rathore (1999) screened 2033 accessions of pigeonpea against pod borer for three years and found PDA 88-2E, PDA 89-2E, PDA 92-1E, PDA 93-1E, T 21, NP 15, ICPL 4, ICPL 91031, ICP 8860 and PPE 45 as promising donors. Accessions of *Cajanus scarabaeoides*, JM 4147, ICPW 89, ICPW 111, ICPW 94 and ICPW 118 have shown antixenosis mechanism of resistance to *Helicoverpa* (Saxena et al. 1990; Verulkar et al. 1997).

A primitive accession, V 64, from the Caribbean Islands, probably contributed to bollworms resistance in cotton. Two genotypes, NA 128 and NA 105, possess tolerance to *Helicoverpa* due to the red leaf color (Ansingkar et al. 1984). Rajarajeswari and Subbarao (1997) identified ORS 75-75, JK 260-2, RFS 3438, TX Lamo 21-5-1-18, NA 1325 and TX maroon 2-78 to be least susceptible to bollworms due to higher numbers of gossypol glands on the ovary. Similarly, other important donors such as JK 276-4, HGI-PS 625, FBRN 2-6-HG, PRS 44A, PRS 44B, EC 44772-20-1 and EC 44772-20-2 have been found to be resistant to *Helicoverpa*, and can be used in cotton breeding programs (Murthy et al. 1998). Germplasm stocks of *Gossypium hirsutum* (Abhadita, G-cot 100, SRT 1, DHY 286, NH 54 and MCU 7), *G. barbadense* (Sujata and Suvin), *G. arboreum* (G 27, G 46 and Lohit) and *G. herbaceum* (Jayadhar and Digvijay) have been found to be tolerant to *Helicoverpa* (Sundaramurthy 1991). Wild species such as *G. anomalum*, *G. raimondii*, *G. harkensii*, *G. palmeri*, *G. davidsoni*, *G. armorianum* and *G. stocksii* were the least preferred for oviposition under free-choice and no-choice tests. Of them, *G. raimondii*, *G. anomalum*, *G. davidsoni*, *G. armorianum* and *G. stocksii* were least preferred by the pest for feeding, and adversely affected most of the biological parameters of the insect (Mohite and Uthamasamy 1998). High concentration of terpenoid aldehydes in *G. mustelinium* makes it a good candidate for use in breeding for resistance to *Helicoverpa* (Altaf et al. 1997). Similarly, *G. somalense*, *G. thurberi*, *G. armorianum* and *G. raimondii* have also been reported to possess genes for bollworm tolerance (Sundaramurthy 1991).

Mechanisms of resistance

During the course of evolution, plants acquired several defense mechanisms against insect pests to reduce the damage. The major mechanisms are antixenosis (non-preference), antibiosis, tolerance and escape (Painter 1951). These mechanisms are operational within the plant, through different component traits. Using specific assays to monitor the effects of particular physical and chemical characteristics on insect behaviour and physiology, resistance has been differentiated in terms of antixenosis, antibiosis and tolerance (Table 12.2). To date, more antibiosis than antixenosis or tolerance has been reported in legume crops (Clement et al. 1994). Many morphological characteristics which contribute to non-preference have been used to breed for resistance to *Helicoverpa*.

Chickpea

Multiple types of resistance (tolerance, antixenosis, antibiosis and escape) are reported in chickpea (Clement et al. 1994). Several morphological and phenological traits such as pod shape, pod wall thickness, foliage color and crop duration seem to influence the *Helicoverpa* infestation in chickpea (Ujagir

Table 12.2: Characters associated with resistance to *Helicoverpa armigera* in chickpea, pigeonpea and cotton.

Crop	Mechanism	Character(s)
Cotton	Non-preference	Smooth leaf, frego-bract, okra leaf, nectariless, open canopy and naked seed.
	Antibiosis	High gossypol, high tannins, Heliocides, exo-endo microflora, CN ratio of leaf and silica content.
	Escape	Earliness, compact, smaller leaves, short plant and non-clustered bolls.
Chickpea	Non-preference	Pod shape, pod wall thickness, foliage color and glabrousness.
	Antibiosis	Malic acid, oxalic acid, crude fibre, non-reducing sugars, low starch, cellulose, hemicelluloses, lignin in the pod wall, trypsin inhibitors and HG proteinase inhibitor.
	Escape	Earliness and cold tolerance.
Pigeonpea	Non-preference	Nonglandular trichomes on the pods, pod length, basal girth of stem, brown seeds and green pods having streaks.
	Antibiosis	Total sugar percentage in pod wall.
	Escape	Earliness.
	Tolerance	Indeterminate growth habit.

and Khare 1987). Pundir and Reddy (1989) reported a monogenetically controlled glabrous mutant from Chaffa cultivar, which could be a good differential host for pod borer because of its inability to produce malic acid, and its effect on oviposition as the presence or absence of hairs on outer layers has a bearing on oviposition by *Helicoverpa*. Srivastava and Srivastava (1990) studied antibiosis, and observed large genotypic variation in larval survival, larval weight, pupal weight, egg viability, adult longevity and Howe's growth index. Larval weight contributed maximally to the variation, followed by larval period, pupal weight, and pupal period. A high percentage of crude fiber, non-reducing sugars and low percentage of starch have been found to be related with low incidence of *Helicoverpa* in cultivar GL 645, while a high percentage of cellulose, hemicelluloses and lignin in the pod wall is thought to inhibit pod damage (Chhabra et al. 1990). Lateef (1985) suggested that the amount of acid exudates on leaves as an useful criteria for distinguishing resistant genotypes from susceptible ones. Similarly, low amounts of acidity in the leaf extracts of genotype, ICC 14665, was associated with susceptibility to *Helicoverpa* (Srivastava and Srivastava 1989; Bhagwat et al. 1995). However, the resistance expressed by PDE 2-3, PDE 7-3 and ICC 506EB was attributed to factors other than acidity, while that of PDE 7-2 appeared due to high acidity (Patnaik and Senapati 1995). Recent reports on significant variation in *Helicoverpa* gut proteinase inhibitors (HGPI) among chickpea genotypes provided the biochemical basis for adaptation of *Helicoverpa* to the protein inhibitors of *Cicer* species (Patankar et al. 1999). Early maturing chickpea genotypes escape insect attack or suffer less damage as compared to other genotypes because of phenological asynchrony.

Among the factors responsible for *H. armigera* resistance in chickpea, the acid exudates (pH 1.3) with a high concentration of malic acid secreted from the glandular hairs on the leaves, stems and pods has been recommended as a marker for resistance (Rembold 1981). Chickpea exudates have malate and oxalate as the main components, and there were characteristic differences depending on the variety, diurnal cycles and growth stage. Varieties with the highest amount of malic acid had the highest resistance to *H. armigera* (Rembold et al. 1990).

Pigeonpea

All the four mechanisms—antixenosis, antibiosis, tolerance and avoidance—have been reported in pigeonpea. Trichomes have been reported to provide a potential antixenosis mechanism against insects. Romeis et al. (1999) attributed *Helicoverpa* resistance of *C. scarabaeoides* to high density of non-glandular trichomes on pods. Nanda et al. (1996) revealed the positive correlation of pod length and basal girth of stem with the intensity of pest attack. Varieties with brown colored seeds and green pods having streaks have been reported to be the least affected by the borer (Tripathi and Purohit 1983). In general, wild relatives of *C. cajan* have better resistance than the cultivated species. Dodia et al. (1996) found that larval mass, pupal mass, developmental period and pupal length were all adversely affected when fed on the flowers of wild species such as *C. cajanifolius*, *C. reticulatus* and *C. sericeus;* and only a few larvae survived to maturity. A single dominant gene involved in the antixenosis imparts resistance to *Helicoverpa* attack in *C. scarabaeoides* (Verulkar et al. 1997). Studies on the biochemical aspects of resistance have indicated that the total soluble sugars in the pod wall have a significant and negative correlation with pod damage. Shanower et al. (1997) established the biochemical basis of resistance to *Helicoverpa* in pigeonpea. Acetone extracts of *C. cajan* and *C. platycarpus* pods had a significant feeding stimulant effect on *H. armigera* larvae whereas extracts from *C. scarabaeoides* pod showed no such effects. Water extract of *C. scarabaeoides* pod had a significant antifeedant effect, while similar extracts from *C. cajan* and *C. platycarpus* pods had no such effect. The use of the pest avoidance approach, though complex, seems to be practical. Short-duration varieties (150 days) suffer lower pod borer damage than extra-early varieties (Singh 1996).

Cotton

Gossypium spp. acquired several defense mechanisms against insect pests during the course of evolution. Among the principal components of resistance, smooth leaves, okra leaves, hairiness, frego-bract, nectarilessness, open canopy and naked seeds are reported to be associated with antixenosis to *Helicoverpa*. A combination of nectariless, smooth and okra-type leaves have resulted in maximum reduction of damage (Bhat and Jayaswal 1988). A combination of frego, okra, red and nectariless (FORN) traits has shown superiority at certain locations (Wu et al. 1997). Jing et al. (1997) found that darker leaf color and higher chlorophyll content are associated with *Helicoverpa* resistance. As compared with *G. hirsutum*, oviposition in general is low on *G. arboreum* due to long trichomes on the upper leaf surface rather than the density. Red plant color shows tolerance to boll weevil and some bollworms. However, red plant color has been associated with low yield in upland cotton. But then, better yield potential coupled with bollworm resistance in *G. arboreum* cultivars such as in G 27 has also been reported (Singh and Bhat 1985; Narayanan et al. 1990).

High gossypol, high tannins, heliocides, exo- and endo-microflora, CN ratio of leaf, and silica contents have been reported to impart antibiosis type of resistance in cotton. The highest mortality and lowest weight of young larvae were observed in the genotypes with high gossypol gland density on the ovary surface. Analysis of antibiosis components of resistance showed that the gossypol, tannins, and oil glands contributed to maximum resistance, while total sugar and total protein content were of secondary importance (Tang and Wang 1996). Apart from gossypol, heliocide 1, heliocide 2, gossypolone, hemigossypolone, lactone and volatile terpenes are the other terpenoid aldehydes in cotton that confer resistance to *Helicoverpa*. Interestingly, gossypol was the principal foliar terpenoid aldehyde in most of the D genome species, while B, C, F, G and K genomic groups had very low foliar gossypol compared to the other terpenoid aldehyde groups. In the A D genome with minor exceptions, all the six terpenoid aldehydes (H1, H2, H3, H4, hemigossypolone and gossypol) were found to occur (Khan et al. 1999). Phenolics have also been found to impart bollworm tolerance. Catechin, chrysanthemin, isoquercitrin, quercetin, condensed tannins, cyanidin and delphinidin have been tested in laboratory bioassays against *Helicoverpa*, and found to exert a weight inhibition of 50% at variable concentrations. It appears that *Helicoverpa* tolerates higher concentrations of allelochemicals through different mechanisms, one of which is probably by high mixed function oxidase titres.

Earliness, compact, smaller leaves, short-plant and non-luster boll provide an escape mechanism to the plant to avoid the damage caused by this pest. Tolerance is evaluated in terms of rejuvenation potential, healthy leaf growth, flowering compensation potential, superior plant vigour, etc., which may be useful under rainfed conditions (Narayanan 1995). The role of cytoplasm in resistance has also been studied. *Gossypium harknessii*, *G. arboreum*, *G. harbaceum*, *G. anomalum*, *G. hirsutum* (races *punctatum*, *morillii*, *richmondii* and *palmeri*) and *G. tomentosum* have a comparatively higher level of resistance to bollworms than the cultivated *G. hirsutum* race *latifolium* (Meyer 1974; Narayanan et al. 1990). Zhang et al. (1999) showed that long staple lines exhibited better resistance to *H. armigera* besides other biotic stresses.

Genetics of resistance

Information on inheritance of resistance is useful to the breeders in choosing an appropriate breeding strategy. Resistance to *Helicoverpa* is imparted through the expression of various host plant characters. Their mode of inheritance and number of genes involved has been reported in cotton, but such information is lacking in pulses, particularly in chickpea and pigeonpea. Most of these characters in cotton are governed by oligogenes and can be transferred with ease. From several diallel and line × tester studies conducted at ICRISAT, it was clear that resistance to pod borer in chickpea (less susceptibility) is controlled by multiple genes. In most studies, the gene action was reported to be predominantly additive although non-additive gene action was reported in some studies. In pigeonpea, predominance of non-additive gene action is reported for resistance to borer (Lal et al. 1999). Verulkar et al. (1997) indicated the involvement of a single dominant gene in antixenosis mechanism of *C. scarabaeoides*. Genetic information on the morphological traits associated with resistance to *Helicoverpa* is presented in Table 12.3.

Breeding for resistance to *Helicoverpa armigera*

Development of *Helicoverpa*-resistant varieties provides a foundation on which we can build an integrated control system against any insect pest. The reduction in pest numbers achieved through the use of resistant plants is constant, cumulative, and without any extra cost to the farmers. Therefore, the breeding goal should be to identify, characterize and utilize genetic mechanisms that confer durable resistance to *Helicoverpa*, i.e. multiple factor resistance. Development of improved cultivars with resistance to *Helicoverpa* would be simple provided good sources of resistance are available, and an efficient and practical screening procedure exists that can provide good selection pressure. Depending on the reproductive system of the crop, standard selection procedures can be adopted. Pedigree, bulk and mass selection approaches have been successfully employed to select *Helicoverpa*-resistant cultivars in chickpea, pigeonpea and cotton. As many traits with quantitative inheritance are looked for in the breeding process, recurrent selection scheme is often recommended due to its potential for breaking up undesirable linkage blocks, and accumulating desirable alleles in a single genotype. Such schemes require the buildup of sufficiently large populations from repeated selection and intermating between the selected parents. The findings that the cytoplasmic differences are there in cotton for reaction to *Helicoverpa*, these can be utilized

Table 12.3: Inheritance of traits associated with resistance to *Helicoverpa armigera* in chickpea, pigeonpea and cotton.

Crop	Trait	Genetic control
Cotton	Hairiness	H_1 for hirsute H_2 for pilose
	Frego	A single recessive gene 'fg'
	Glandlessness	gl_2, gl_3, duplicate recessive genes
	Okra leaf	L^o2 simple okra L^s2 super okra
	Nectarilessness	ne 1 and ne 2 (duplicate recessive genes)
	Naked seed	dominance gene 'N_1' as well as recessive gene 'n_2'
	Red plant color	R_1 and / or R_2 dar
	Smooth leaf	Sm1 and / or Sm2 and D2
	Gossypol	Gl2 and Gl3
	Heliocides	Additive gene action with some epistatic interaction
	Yellow pollen	P_2
	Hairy Boll	Hb
Chickpea	Glabrousness	A single recessive gene 'gl'
	Tolerance	Predominantly additive gene action
Pigeonpea	Antixenosis	A single dominant gene
	Tolerance	Predominance of non-additive gene action

for the development of hybrids not only in cotton, but also in pigeonpea. Mutation breeding can also be employed to create new variability for the characters showing positive effect on resistance to pod borer.

Chickpea

The breeding approach to *Helicoverpa* resistance in chickpea is an integrated one involving antixenosis, antibiosis and tolerance. Given that malate-mediated resistance is most likely to be quantitatively inherited and that sources significantly superior to ICC 506EB have yet to be identified, the best prospect for increasing resistance using antixenosis and antibiosis is through recurrent selection. The antixenosis/antibiosis mechanisms can be complemented by tolerance, i.e. selecting for genotypes with capacity to recover from *Helicoverpa* damage. Large genetic variation for these traits has been reported, and the breeders can make use of these traits to minimize the damage caused by the *Helicoverpa*.

Genotypes such as ICC 506EB, ICC 10619 and ICCL 84205 with low borer damage have been found to be useful in the breeding for resistance to *Helicoverpa* (Singh et al. 1991). Pedigree selection has been found to be effective in differentiating low versus high borer damage. Progenies of plants selected with low borer damage (15.1%) showed a significantly greater tolerance compared to those selected under high borer damage (16.1%). Correlation between pod-borer damage in F_2 and F_3 progenies was low, but positive (0.26, $P<0.01$) (ICRISAT 1981). Pedigree selection for low-borer damage under pesticide-free conditions has been found to be effective for identifying borer-resistant lines. Singh et al. (1997) developed ICCV 7 from a cross between H 208 and BEG 482. Some of the released varieties such as Vishal and Vijay have displayed resistance to borer damage (Deshmukh et al. 1996ab).

Considering that the resistance to pod borer is polygenic and the loci may be different in different resistance sources, efforts were made to pyramid genes from several resistant sources. Eight resistant parents were involved in a multiple cross (4 single crosses, 2 double crosses, leading to one eight-way cross) at ICRISAT. The F_2s of the multiple crosses were screened under unsprayed conditions to select resistant plants. From these, 300 F_3-F_5 progenies were evaluated in unsprayed fields in 1994-95, and 42 F_5 lines were selected for further evaluation. The best F_5 progeny (ICCV 95992) showed less than 1% damage compared to 7% damage in the resistant control ICC 506EB. In the yield tests (under unsprayed and rainfed conditions), ICCV 95992 suffered 8% damage and produced seed yield of 0.93 t/ha. The resistant control (ICC 506EB) showed 8.5% damage and yielded 0.65 t/ha (ICRISAT 1996). Although complete resistance is not yet available, ICC 506EB has shown consistently lower pod damage over years under unsprayed conditions (Gowda et al. 1983). However, most of the *Helicoverpa*-resistant lines are highly susceptible to wilt caused by *Fusarium oxysporum* f. sp. *ciceri*. The problem of the linkage between pod borer resistance and susceptibility to *Fusarium* wilt has been overcome with the identification of ICCL 86102, ICCL 86111, ICPX 730020-1-1-1H, IPC 94-93, IPC 94-94 and IPC 94-102 (Singh et al. 1990; Rheenen 1991; Chaturvedi et al. 1998), which combine resistance to both wilt and pod borer.

Pigeonpea

Development of pigeonpea varieties with resistance to *H. armigera* appears to be a complex problem considering the polyphagous nature of this insect. Under these circumstances, incorporation of *Helicoverpa* resistance genes through conventional breeding may be difficult. A long-term approach for combining genes for resistance/tolerance with agronomic performance needs to be persued. Pigeonpea cultivar ICPL 87 (Pragati) developed from the pedigree selection from a cross (T 21 × JA 277) is known to compensate the damage caused by pod borer (Saxena et al. 1989). Abhaya (ICPL 332), having the least susceptibility to pod borer, was released for cultivation in Andhra Pradesh in 1989. Some pigeonpea varieties with reasonable tolerance to pod borer are: JA 4, GT 100 and Co 6. Varieties with high degree of resistance to pod borer are yet to be developed for commercial cultivation. The bulk progenies from Pusa 971, based on less than 25% damage, performed relatively better than the other elite lines over the years. Recurrent selection among these progenies was practiced to accumulate desirable alleles. Selection for agronomically superior varieties/populations should be carried out under insect infestation. Chintapalli et al. (1997) made an attempt to exploit somaclonal variation for resistant to pod borer, and indicated the possibility of additional genes for tolerance to *Helicoverpa*.

Cotton

The conventional breeding methods—pedigree selection, bulk, backcross, short-cycle recurrent selection by pyramiding genes for broad-based resistance—have resulted in either resistance to one or two pests (Maxwell et al. 1972; Niles 1980). The use of Bird's (1982) multi-adversity resistance (MAR) system has resulted in the realization of insect resistance, besides multiple disease resistance. Mass selection within breeding populations containing resistance characters is considered useful, while mutation breeding can be an additional tool in evolving early mutants coupled with escape, as well as real resistance (El-zik and Thaxton 1989; Narayanan et al. 1990). Disruptive mating for combining earliness and resistance to *Helicoverpa* appears to be an attractive proposition (Narayanan et al. 1985). Through ovule culture, the glanded and glandless-seed trait has been transferred from *G. sturtianum* into cultivated upland cotton (Altman et al. 1987). Development of cotton genotypes that have glanded aerial parts and glandless seed could be extremely useful for developing bollworm resistant cotton with high gossypol. Some of the cotton varieties/hybrids having tolerance to *Helicoverpa* are: Sumangala, SVPR 3, Sahana, RS 810, ICMF 20, RAMPBS 155, GAM 31, RG 18, Aravinda and PHH 316.

Narayanan (1995) suggested that the resistant ideotype of cotton should combine okra, nectariless and semi-smooth leaf chracteristics with reduced plant height (90 to 100 cm), reduced sympodial length and internodes, absence of monopodia (compact), around 4 to 5 g boll weight, less leafy, open canopy and rapid synchronized fruiting nature with a duration of 130–140 days from seed-to-seed for developing varieties resistance to *Helicoverpa*, jassids, whitefly, and spider mites. Even moderate levels of resistance, while perhaps inadequate as a prime defense, can be useful in integrated pest management. Optimization of components in an ideotype will be helpful in developing cultivars in an orderly fashion to combine the various components of resistance with improved yield.

Limitations in breeding *Helicoverpa*-resistant varieties

In spite of several resistance sources available for *H. armigera* in cotton, chickpea and pigeonpea, breeding efforts for developing resistant varieties have not met as remarkable successes as have been reported in case of insect pests in wheat, rice, maize, cowpea and tomato. Transfer of resistance genes from donors into well-adapted and agronomically superior genotypes has been limited by a number of biological and technological factors. This has further been complicated by the polyphagous and migratory nature of this pest, besides highly polymorphic pest populations and seasonal and temporal variability in occurrence of this pest. In the past, considerable attention has been given to tackle plant diseases, as insect-rearing programs are generally more expensive. Besides, pesticides were easily available and highly effective in controlling this pest. This might have led to erosion of *Helicoverpa*-resistance genes from the cultivated germplasm. Wild species are by far the largest reservoir of *Helicoverpa*-resistance genes. Unfortunately, resistance genes from wild species are linked with undesirable block of genes requiring repeated recombination and selection cycles for incorporation into agronomically acceptable genotypes.

No sources of resistance to *Helicoverpa* have been reported to date in crops under review that can be conveniently utilized in breeding programs. Moreover, a major part of germplasm pool is still waiting for effective screening against this pest because of the non-availability of reliable and practicable screening procedure. Most of the characteristics associated with resistance to *Helicoverpa* are polygenic in nature and are associated with undesirable traits such as susceptibility to major diseases, other insect pests, poor plant type and poor yield. A classical example is the susceptibility of pubescent genotypes to whiteflies in cotton (Navon et al. 1991). Similarly, *Helicoverpa*-resistant genotypes of chickpea are susceptible to *Fusarium* wilt. Expression of constitutive factors imparting resistance to *Helicoverpa* is also influenced by environmental factors leading to limited genetic advance.

Future breeding strategy

For an effective strategy to manage *Helicoverpa*, a dynamic program for identification of resistance genes is needed. Efforts should be made to search resistance genes in the wild and weedy relatives, besides creating variability through mutation. These genes should be accumulated in the desired agronomic background employing appropriate breeding methods. There is a need to improve the screening techniques. Use of micro-analytical methods such as use of gas liquid chromatography, mass spectrometry, high pressure liquid chromatography, and marker-assisted selection will open up newer opportunities for rapid screening of germplasm for resistance to this pest (Clement et al. 1994). It will also allow pyramiding of resistance genes with different characteristics into cultivars for stable resistance. Field screening, coupled with laboratory testing of selected plants, would enhance the efficiency of breeding methods employed for host plant resistance. Selection of varieties with specific morphological characteristics and biochemical composition may be used to select for resistance to *Helicoverpa*. Gene pyramiding could be a valuable strategy for resistance management, if more than one morphological trait is associated with resistance, e.g. in cotton. In place of the pedigree method, the bulk or bulk pedigree method and recurrent selection will provide a chance for pooling desired genes into agronomically desirable backgrounds.

Systematic studies on host range to throw light on chemical and physical attributes of plants that determine their attraction and acceptability as food is extremely urgent. For example, Tripathi and Singh (1989) confirmed that lentil is the least preferred crop, followed by broad bean, green gram, pea and black gram. Further studies are needed to determine the cause(s) of the least preference of these crops so that such chemical and physical attributes could be incorporated through conventional as well as biotechnological approaches in the crops under review. There is a problem to develop cultivars with multiple mechanisms of resistance, multiple factor resistance, and more specifically, multiple resistance. Dissection of resistance into its components and precise genetic information on these components should be pursued so that beneficial genes or quantitative trait loci (QTLs) are pyramided in the cultivars using marker-assisted selection.

Marker-assisted selection may be used to increase the efficiency of breeding for resistance to pod borer. Before DNA marker technology is applied to identify the location of resistance genes, a well-saturated and evenly distributed molecular map is essential. Insect resistance genes in crops such as maize, potato, rice, and tomato have been shown to be linked to several quantitative trait loci (QTLs). A natural pesticide, maysin, identified in the silk of a primitive race of maize, binds amino acids in the insect gut and effectively starves the insect. The new techniques in gene mapping and manipulation have created a real possibility of increasing resistance by enhanced production of maysin by plants. A gene has been identified that regulates more than half the amount of maysin produced, and researchers are looking to increase the expression of this gene to identify and manipulate other pathway genes. A greater understanding of the genetic basis of maysin synthesis and associated resistance should lead to improved crop plants for resistance to *Helicoverpa.*

New recombinant DNA technologies have extended the pool of resistance genes to unrelated organisms. Genes from *Bacillus thuringiensis* can be successfully transferred into the desired plant species. Investigations are required to study insect-derived protease inhibitors to discourage feeding on the plant by the pod borer. Transfer of plant protease inhibitor genes into transgenic plants has been shown to be an effective means of controlling some insects. Another approach for the control of plant pests is the use of non-pest derived genes to provide the plant with a trait, which will allow it to preferentially survive its competitor. The transgenic cottons with *Bt* gene conferring resistance to *Helicoverpa* have been deployed in the USA, Mexico, Australia, Argentina, South Africa, China and India. Transgenic cotton is the second largest genetically modified crop grown in the field, next to soybean. Development of cotton varieties with *cry1Aa* and *CpTI* (cowpea trypsin inhibitor) genes has shown the way to pyramid genes even from alien sources and could be a valuable strategy for resistance management. *PBinLK* carrying two insecticidal genes—*pea lectin* gene and *soybean kunitz trypsin inhibitor* gene—has been successfully transferred into cotton cultivars via *Agrobacterium*-

mediated transformation. Shen et al. (1999) selected *Helicoverpa*-resistant line 115, after introduction of exogenous DNA of dogbane (*Apocynum venetum*), a species with high gossypol and tannin contents, into ovaries of cotton variety Lumian 6 by the injection method. Availability of transgenic varieties with different *Bt* genes particularly in cotton has opened up the scope for integration of *Bt* genes in the second-generation varieties through the conventional breeding program. Recent success in developing a cotton variety, Lumianyan 15, from a cross between a wilt-resistant line of upland cotton as female parent and *Bt* transgenic cotton line with resistance to *Helicoverpa* as pollen parent demonstrates the possibility of this approach in other crops (Li et al. 2000). Various other classes of resistance genes need to be investigated for reducing the extent of losses from pod borer damage. Much more research is required to understand the role of resistance genes in *Helicoverpa* management. Research should also focus on comparing the resistance obtained through conventional breeding with resistance through biotechnological interventions for effective management of *Helicoverpa*.

Conclusions

Helicoverpa armigera has been identified as one of the most important pest problems worldwide. Its damage on cotton and pulses successively makes its mitigation a complex and central issue to overall sustainability of many cropping systems. Losses caused by *Helicoverpa* are astronomical in cotton, but pigeonpea and chickpea are equally affected. Several chemical control measures have been devized to minimize the losses. However, it has developed resistance to insecticides belonging to different groups due to indiscriminate use. From the ecological and economical viewpoint, breeding cultivars having resistance to this pest is the most important component in integrated pest management. Concerted efforts to screen germplasm have led to the identification of many accessions exhibiting an impressive level of resistance to *H. armigera* in the crops under review. Transfer of resistance genes from these sources to agronomically superior background has been marred by a number of biological and technological factors. For a strategy to be effective for managing this pest, a dynamic program for identification of resistance genes is needed. Efforts should also be made to search resistance genes in the wild and weedy relatives, besides creating variability through mutation. These genes should be accumulated in the desired agronomic background employing appropriate breeding methods. This chapter mainly deals with host plant resistance, progress in breeding for tolerance/resistance, and its effectiveness and limitations. There is a need to utilize molecular marker techniques to accelerate the progress for developing crop cultivars with resistance to *Helicoverpa*, and develop transgenic plants with resistance to this pest, so as to make host plant resistance to be an effective weapon for the management of *Helicoverpa*.

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