Journal of Physiology and Pathophysiology Vol. 1(3), pp. 22-38, November 2010
Available online http://www.academicjournals.org/ijmms
ISSN 2I41-260X ©2010 Academic Journals

Review

Mosquitocidal bacterial toxins (*Bacillus sphaericus* and *Bacillus thuringiensis* serovar *israelensis*): Mode of action, cytopathological effects and mechanism of resistance

Subbiah Poopathi* and S. Abidha

Unit of Microbiology and Immunology, Vector Control Research Centre (Indian Council of Medical Research), Medical complex, Indira Nagar, Puducherry - 60 5006, India.

Accepted 4 September, 2010

Bacillus sphaericus **Neide (*Bs*) and *Bacillus thuringiensis* serovar *israelensis* deBarjac (*Bti*) provide effective alternatives to broad spectrum larvicides in many situations with little or no environmental impact. Taking into account environmental benefits including safety for humans and other non-target organisms, reduction of pesticide residues in the aquatic environment, increased activity of most other natural enemies and increased biodiversity in aquatic ecosystems, their advantages are numerous. In addition to recombinant bacteria used as larvicides, research is also underway to develop transgenic algae and cyanobacteria using larvicidal endotoxins of *Bt*i and *Bs.* The advent of recombinant DNA technology is now having an enormous impact on agriculture and medicine and it is appropriate that the ability to manipulate and recombine genes with this technology be applied to improving larvicides for vector control. These new recombinant bacteria are as potent as many synthetic chemical insecticides yet are much less prone to resistance, as they typically contain a mixture of endotoxins with different modes of action. The existing recombinants also have what can be considered disadvantageous in that they do not show significantly improved activity against aedine and anopheline mosquitoes in comparison to *Bti*. But it may be possible to overcome this limitation using some of the newly discovered mosquitocidal proteins such as the Mtx proteins and peptides such as the trypsin-modulating oostatic factor which could be easily engineered for high expression in recombinant bacteria. While other microbial technologies such as recombinant algae and other bacteria are being evaluated, it has yet to be shown that these are as efficacious and environmentally friendly as *Bti* and *Bs*. By combining the genes from a variety of organisms, it should ultimately be possible to design `smart' bacteria that will seek out and kill larvae of specific vector mosquitoes. Thus, recombinant bacteria show excellent promise for development and use in operational vector control programs, hopefully within the next few years.**

Key words: *Bacillus sphaericus*, *Bacillus thuringiensis* serovar israelensis, bacterial toxins, *Culex quinquefasciatus*, *Anopheles stephensi*, *Aedes aegypti,* mode of action, resistance, management of resistance.

INTRODUCTION

Mosquito borne diseases such as malaria, filariasis, yellow fever and dengue cause extensive morbidity and mortality and are a major economic burden within disease-endemic countries (Sachs and Malaney, 2002; Boutayeb, 2006). Every year, about 300 million people are estimated to be affected by malaria, a major killer disease, which threatens 2,400 million (about 40%) of the world's population (Sharma, 1999; Snow et al., 2005). Similarly, lymphatic filariasis caused by *Wuchereria bancrofti* affects about 106 million people world wide and the closely related *Brugia malayi* and *B. timori* affect 12.5 million people in South East Asia. About 20 million people are infected every year by dengue viruses transmitted by

*Corresponding author. E-mail: Subbiahpoopathi@rediffmail.com. Tel: 91-9443957479. Fax: 91-413-2272041.

Aedes mosquitoes with about 24,000 deaths. The incidence of mosquito-borne diseases is increasing due to uncontrolled urbanization, creating mosquitogenic conditions for the vector mosquito populations. Therefore, mosquito control forms an essential component for the control of mosquito borne diseases. Malaria and dengue are effectively managed through a combination of vector control, drugs and management of clinical illness. Malaria vector control relies mostly on the use of an effective insecticide, which is commonly used through indoor residual spraying (IRS) or community-based deployment of insecticide impregnated bednets (ITN).There are numerous cases of insecticide resistance reported for *Anopheles* species. The emergence of mosquito species resistant to insecticides widely used in malaria and dengue control has the potential to impact severely on the control of these disease vectors. A limited number of resistance mechanisms, including modification of the insecticides' target site, or changes in rates of metabolism involving esterases, glutathione S-transferases or monooxygenases operate in all insects. The potential for developing resistance in vectors has been apparent since the 1950's, but the scale of the problem has been poorly documented (Coleman et al., 2006; Coleman and Hemingway, 2007). Vector control is recognized as an effective tool for controlling tropical diseases. Synthetic insecticides have been used during the past several decades to control varied dipteran pests. However, the use of chemical insecticides has been greatly impeded due to development of physiological resistance in the vectors, environmental pollution resulting in bio-amplification of food chain contamination and harmful effects on beneficial non-target animals. Therefore, the need for alternate, more effective and environment-friendly control agents became urgent.

Biological control agents

The last decade has witnessed an increased interest in biological control agents. More number of biocontrol agents was screened for their efficacy, mammalian safety and environmental impact. Many organisms have been investigated as potential agents for vector mosquito control, including viruses, fungi, bacteria, protozoa, nematodes, invertebrate predators and fish. However, most of these agents were shown to be of little operational use, largely because of the difficulty in multiplying them in large quantities. Only a few spore forming bacteria, copepods and fish have reached operational use and are undergoing extensive field trials. The discovery of a bacteria like *Bacillus sphaericus* Neide (*Bs*) and *B. thuringiensis* serovar *israelensis* deBarjac (*Bti*), which are highly toxic to dipteran larvae have opened up the possibility of its use as potential biolarvicides in mosquito eradication programs in the world over (Poopathi and Tyagi, 2002, 2004; Poopathi et al., 2002). These bacteria have some important advantages over conventional insecticides in mosquito control operations, besides being safe to non-target organisms including human beings. Also, it is innocuous to the environment. Besides these bacteria, several other types of bacteria such as *B.t. jegathesan*, *B.t. morrisoni*, *B.t.* subsp. medellin, *B.t*. subsp. *malaysiensis*, *B.t*. subsp. *canadensis*, *Asticcacaulis excentricus*, *Clostridium bifermentans* subsp. malaysia and *Synechococcus* are being examined as effective biological control agents. The *Bti* has been used operationally for the control of mosquitoes for over two decades and its formulations are highly effective against *Anopheles*, *Aedes*, and *Culex* mosquitoes (Mahmood, 1988). No evidence has been found that *Bs* and *Bti* toxins harm aquatic organisms sharing the breeding sites of these vectors or have an adverse effect on the environment. Although *Bti* is effective, specific, bio-degradable and possesses a long shelf life, it does not recycle in the environment at levels high enough to provide significant residual activity. It has a short duration of toxic action, usually 24 to 48 h and must, therefore, be applied at frequent intervals. Moreover, current spore forming *Bti* formulations sink in water and are consequently less efficient in controlling species of mosquito larvae that feed only near the water surface. The rate of killing with spores is slow compared with the chemical insecticides and the toxins have a narrower mosquito host range than the chemicals. *Bacillus sphaericus*, on the other hand, has been shown to recycle in the field conditions and exert larvicidal activity for a long period. However, the spores of *Bti* have the advantage over *Bs* in that *Bti* has a wider spectrum of activities against *Anopheles*, *Culex* and *Aedes* spp, while *Bs* has its effect mainly on *Culex*, for a lesser extent to *Anopheles*. Moreso, it is strongly species specific and act against only a few *Aedes* species. Field resistance has been only reported for *Bs,* while for *Bti*, it seems more difficult for mosquitoes to develop resistance even under intensive laboratory selection, which may be due to the multiple toxin complex of this bacterium.

About *Bacillus sphaericus*

Bacterial toxins

B. sphaericus is an aerobic, rod-shaped, endospore forming gram positive soil bacterium. First discovery of *Bs* strain toxic to mosquito larvae was reported by Kellen et al. (1965). Thereafter, more than 300 strains have been isolated and identified from all over the world (Singer, 1997; de Barjac et al. 1988; Thiery and Frachon, 1997). *Bacillus sphaericus* has been used to control *Culex pipiens pipiens* and *C. pipiens quinquefasciatus* mosquito larvae since the late 1980s, and in some areas it is also used to control *Anopheles* spp. This organism has several advantages, including low environmental

toxicity due to the high specificity of *B. sphaericus* toxins, high levels of efficacy and environmental persistence, and the ability to overcome resistance developed against conventional insecticides used worldwide. Only a few of the highly larvicidal *B. sphaericus* strains are sold commercially; strain 2362 (for example, VectoLex and Spherimos) is sold in the United States and Europe, strain 1593 (for example, Biocide-S) is sold in India and strain C3-41 is sold in the People's Republic of China. For unknown reasons, some free-living *B. sphaericus* strains have strong larvicidal activity directly related to the presence of a paraspore protein crystal produced during sporulation. This crystal contains two major polypeptides, a 42 kDa polypeptide and a 51 kDa polypeptide, which are designated by BinA and BinB, respectively. The mode of action of the toxin complex in susceptible mosquitoes involves highly specific binding to a receptor in the larval midgut. The two crystal components act synergistically, that is, the BinB part is responsible for the initial binding to the receptor and the BinA component confers toxicity (Nielsen-LeRoux et al., 2001). More than 180 *Bs* strains (belonging to six H serotypes) have been assayed on a wide variety of mosquito species and it has been found that the most potent strain was the H5a5b serotype. Sporulation of these *Bs* strains in a liquid culture medium was studied under the electron microscopy. Crystal-like inclusions first appeared (7 h after lag phase) and reached their final size in 72 h. The release of the spore-crystal inclusion complex occurred at 22 h after incubation. Careful choice of culture medium and bacterial serotype is needed for high spore yield and high larvicidal activity. There are two kinds of insecticidal toxins (crystals and Mtx toxins), which differ in composition and time of synthesis. The crystal toxins are the main toxic factors in highly larvicidal strains. It contains two polypeptides of molecular weights 51 and 42 kDa (BinB and BinA), which are located on the chromosome in the strains of *B. sphaericus* (*Bs* 2362, *Bs*1593 and *Bs* 2297). The amino acid sequence of these two polypeptides differs markedly from those of other bacterial or larvicidal toxins, including *Bti.* However, the BinB and BinA share four segments of sequence similarity. The 42 and 51 kDa protein genes of *Bs* have been sub-cloned independently in the downstream of the CytA gene promoter of the toxin gene in *Bti* and introduced into a non-mosquitocidal strain of *Bt*. Each protein was overproduced and accumulated as inclusion bodies which were purified. The 42 kDa protein inclusions were found to be toxic to *Culex* larvae in contrast to the 51 kDa protein inclusions which were not toxic on their own, but a synergistic effect between these two components was observed (Nielsen-LeRoux et al., 2001). Studies conducted with recombinant bacteria expressing these polypeptides individually have revealed that BinA could be toxic at high dosage in the absence of BinB, but this was not in the case for the BinB alone. However, presence of both BinB and BinA in equimolar amounts showed the highest toxicity in larvae, since they seem to act in synergy. In addition to the binary toxin, another mosquitocidal protein with molecular protein and weight of 100 kDa, appears to be synthesized in low-toxicity strains (Nielsen-LeRoux and Charles, 1992) as well as in some of the highly toxic strains. As a result, this polypeptide is expressed during the vegetative phase and is not homologous with the 51 and 42 kDa proteins. The efficient expression of this 100 kDa mosquitocidal toxin in protease deficient recombinant *Bs* was thoroughly studied and it was concluded that protease negative *Bs* strains expressing Mtx and other toxins may form the basis of an alternative to the natural highly toxic strains for mosquito control. The location of the binary toxin (btx) and mosquitocidal toxin (mtx) genes in *Bs* strains was determined by hybridization of specific gene probes to chromosomal DNA in southern blots. The introduction into *Bs* of the *Bt* subsp. medellin Cyt1 Abt gene results in higher susceptibility of which, they are otherwise resistant mosquito larval populations to *Bs*. Apart from *Bs* and *Bti*, the cloning and expression of other mosquitocidal strains such as *Bt* subsp. medellin, *Bt* subsp. *jegathesan* and *Clostridium bifermentans* have been reported (Delecluse et al., 1995).

The binary toxin of *Bs* strains is generally very toxic to *Anopheles* and *Culex* species, but poorly or non-toxic to most *Aedes* species. However, susceptibility appears to depend on the stability of bacterial strains, appropriate methodology, etc. Since these bacteria are safe for animals, the environment and cause no health risk to humans, several formulations in the form of wettable powder (WP), water dispersable concentrate (WDC), emulsifiable concentrate (EC), flowable concentrate (FC), granules (G) and dust (D) have been produced to control many species of mosquitoes. These products have been tested extensively in USA, France, Brazil, Zaire, India and Bangladesh.

Mode of action

Crystal toxins from *Bs* are ingested by mosquito larvae, and after solubilization and proteolytic cleavage, the activated toxin interacts with the midgut epithelium leading to the death of larvae. In mosquito larvae, the sequence of events follows in the manner given below; (i) ingestion of spore/crystal toxin (ii) toxin solobilization in the midgut (iii) activation of the protoxin by protease into active toxin, that is, 42 and 52 kDa of *Bs* to 39 and 43 kDa proteins (iv) binding of active toxin to specific receptors present in the midgut brush border membrane and (v) putative internalization of toxin and cell lysis. However, the eventual intracellular action of binary toxin in the cells is not completely clarified except for a few reports on cytopathological effects caused by the action of the toxin (Singh and Gill, 1988; Poopathi et al., 1999d, e). In *C. pipiens* larvae, it was shown that BinB was mainly

responsible for the binding to the receptor, while BinA had very low affinity for the receptor (Charles et al., 1997). Recently, the receptor was identified as a 60 kDa protein attached to the cell membrane by a glycosyl-phosphatidylinositol (GPI) anchor. Moreover, micro sequencing indicated that this molecule had a string homology with insect maltases and enzymatic activity suggested that it could be an alpha glucosidase (Silva-Filha et al., 1999). In the course of sporulation, *B. sphaericus* produces an inclusion body which is toxic to a variety of mosquito larvae. The larvicide of *B. sphaericus* is unique in that it consists of two proteins of 51 and 42 kDa, both of which are required for toxicity to mosquito larvae. There is a low level of sequence similarity between these two proteins, which differ in their sequences from all the other known insecticidal proteins of *B. thuringiensis*. Within the midgut, the 51 and 42 kDa proteins are processed to proteins of 43 and 39 kDa, respectively. The conversion of the 42 kDa protein to a 39 kDa protein results in a major increase in toxicity, in that the significance of processing the 51 kDa protein is not known. In contrast to the mosquito larvae' results, the 39-kDa protein is, alone, toxic for mosquito-derived tissue culture-grown cells, and this toxicity is not affected by the 51 kDa protein or its derivative, which is the 43 kDa protein. Comparisons of larvae from species which differ in their susceptibility to the *B. sphaericus* toxin indicate that the probable difference resides in the nature of the target sites of the epithelial midgut cells and not in the uptake or processing of the toxin (Baumann et al., 1991).

Binding kinetics

From studies of binding kinetics (direct binding and homologous competition assays) of *Bs* binary toxin to the midgut brush border membrane fractions (BBMFs) of larvae, it was reported that the radio-labelled toxin was bound specifically to a single class of receptors. Toxin dissociation was fast and almost complete in BBMF of all species studied. Studies showed that resistance is correlated with a reduction or absence of affinity of the toxin for the membrane receptor. The resistant strain lost the functional receptor for the *Bs* toxin (Nielsen-LeRoux et al., 1995). The resistance is encoded by a recessive gene linked to the sex locus on chromosomal and it is not associated with any loss of binding affinity between BBMF and *Bs* radiolabelled toxin. Binding affinity of the *Bs* binary toxin to a specific receptor on the midgut brush border membrane from geographically different mosquito species of *Cx. quinquefasciatus* (Indian strain) of resistant, susceptible, F1 progeny and back-crosses to susceptible and resistant strains have been studied recently (Poopathi et al., 2004). Toxicity assays in the larvae of these strains confirmed that the resistance was inherited by partially recessive gene. The similarities in susceptibilities of *Bs* susceptible and the progeny from back-crosses strain with F5 may be expected, which may reflect lack of any susceptibility variations between these two strains, whereas, the susceptibility of F1 offspring was higher than that of the susceptible parent but lower than that of the resistant parent, indicating that resistance was been controlled by partially recessive gene. SDS-PAGE studies confirmed the presence of a new polypeptide (MW: 80 kDa) in *Bs* resistant strains. Nielsen-LeRoux et al. (1995) have found that the *Bs* resistance was due to a single recessive gene in mosquitoes. However, Chaufaux et al. (1997) and Huang et al. (1999) have reported a partially recessive inheritance of resistance gene to *Bt cry1C* and phosphine along with *Bt* toxins in *Spodoptera littoralis, Tribolium castaneum* and *Ostrinia nubilalis.* Results of Poopathi and co-workers also complied with the above studies (Table 1). Validation tests for four consecutive generations of *Cx. quinquefasciatus* (F_{49} to F_{52}) regarding toxicity of *B. sphaericus* against susceptible (MS) and resistant (GR) larvae were conducted. Their F_1 progeny derived from reciprocal parental crosses (MS♂ x GR♀; MS♀ x GR♂) also concurred with the report of partially recessive inheritance of resistance (Table 2). The LC_{50} and LC_{95} in *Bs* susceptible parental strain (MS) was very low, whereas it was high for *Bs* resistant parental strain (GR). SDS-PAGE profile of the GR strain showed an additional protein band (M.wt: 80 kDa) that was possibly linked to resistance development. A similar protein band was also visualized in back- cross offsprings from resistant parents (F_3♂ x GR♀). Although back- cross offsprings lacked protein, it was developed from susceptible parent (F_3♂ x MS♀). The studies indicated that the levels of resistance were found to be high in *C. quinquefasciatus* larvae maintained by selection pressure with *Bs* toxin. Table 3 presents *in-vitro* binding competition experiments by using ^{125}I labeled *Bs* binary toxin with brush border membrane fractions (BBMFs) from *C. quinquefasciatus* larval midgut. In *Bs* susceptible (MS) strain, clear specific binding of radiolabeled toxin of *Bs* to receptors of BBMF was found. The binding capacity was 1.74 pmole / mg BBMF protein at 150 nM concentration level, whereas, in *Bs* resistant strain, it was significantly low due to limited specific binding of radiolabeled toxin to receptors.

Cytopathological effects by bacterial toxins

Transmission electron microscopic (TEM) studies showed that the midgut epithelial cells of *Bs* susceptible and resistant strains of *C. quinquefasciatus* had well defined microvilli in a parallel line on the outer boundary. Each microvillus contained a microfibrillar core and it extended below the plasma membrane to form a terminal web. It has been reported that *Bs* and *Bti* treatments bring about some changes in the midgut structure of the mosquitoes (Poopathi et al., 1999a, b, 2000c). Before *Bs*

treatment, the nuclei of midgut epithelial cells were packed with nucleolar granules inside the nucleoplasm. The nucleolemma was well defined on the outer boundary. The mitochondria, rough endoplasmic reticulum, lysosome and golgi body were also visible in the cytoplasm. The binary toxin from *Bs* and the multiple toxins from *Bti*, after being absorbed into the gut cells, exert their effects on the midgut epithelium by causing disruption, separation and ploughing of columnar epithelial cells into the gut lumen. It has been argued that disruption and swelling of the midgut causes the death of the insect following *Bs* or *Bti* poisoning. *B. sphaericus* toxin is a slow acting larvicide that does not paralyze mosquito larvae until 24 to 48 h treatment. However, pathological lesions in the midgut of toxin treated larvae are also observed as early as 7 to 10 h after treatment. This caused a delayed paralysis and the death of *Bs* exposed larvae was a certainty (Poopathi et al., 2000c). *B. thuringiensis* subsp. *israelensis* toxin destroys the structure of the cells in the midgut epithelium, whereas *Bs* toxin does not and takes a longer time to disintegrate (Singh and Gill, 1988; Poopathi et al., 1999d). The difference in the toxin effect is probably due to variation in the size of active toxins from the two bacteria. Ultrastructural variations were also found to be similar in both *Bs* resistant and susceptible larval strains (Poopathi et al., 1999e).

Resistance to bacterial toxins

Mosquito control using the entomopathogenic bacteria *Bacillus sphaericus* and *B. thuringiensis* subsp. *israelensis* has gained importance due to the rising trend in the development of resistance of mosquitoes to chemical pesticides, as well as due to their deleterious effects to man and the environment, worldwide. *B. sphaericus* is advantageous to *B. thuringiensis* subsp. *israelensis* due to the increased duration of larvicidal activity against certain mosquito species, especially in organically enriched larval habitats. There is also evidence of spore recycling in dead mosquito larvae in certain environments. *B. sphaericus* (*Bs*) has been recognized as an effective mosquito larvicide since its discovery 20 years ago. Various strains of this agent, such as 2362, 2297, 1593 and C3-41, have been developed, formulated and field-evaluated against mosquito larvae in different countries. Their high efficacy in controlling mosquitoes breeding in various habitats, especially those in polluted water, has been documented. *B. sphaericus* has therefore been considered a promising agent for mosquito control, especially for *Culex* spp. in urban environments. However, recent reports have shown that microbial larvicides based on *B. sphaericus* leads to resistance in mosquitoes in some areas of the world. This is mainly because under continuous selection pressure, mosquito populations develop resistance to *B. sphaericus* binary toxin (Bin), both in the laboratory and in the field. It has been demonstrated that *Cx. quinquefasciatus* can develop from 35 to 150,000- and from 10 to 10,000 fold resistance to *B. sphaericus* in the laboratory and in the field, respectively (Sinègre et al., 1994). Laboratory studies have shown that the resistance developed to certain strains of *B. sphaericus* confers more or less cross-resistance to other strains of the same species of toxin-producing organisms. Therefore, the resistance of mosquito populations to *B. sphaericus* toxin would seriously threaten the sustainability of current mosquito control programs using this microbial insecticide. Selection of resistance in two distinct *Cx. quinquefasciatus* populations to commercial *B. sphaericus* strains, 2362 and C3-41, is possible under laboratory conditions. However, *B. sphaericus* strain IAB59 appeared to induce a different evolution of resistance, causing much more slowly evolving and lower resistances in both the field-collected susceptible colony and the low-level-resistant colony after the same number of generations was subjected to selection approximately (Guofeng Pei et al., 2002). A laboratory investigation was undertaken to study the cyclic usage of field recommended doses of *B. thuringiensis israelensis* (*Bti*), *B. sphaericus* (*Bs*) and combination of *Bti* and *Bs* (half the recommended dose of each) with deltamethrin to attain better control of mosquito larvae. The results revealed that *Bti* excels *Bs*, as it recorded 54% mortality only on the 17th day after application. The other salient finding of this study is that LC50 of deltamethrin is sufficient to follow the biopesticides application for an effective control of *Culex* larvae (Gayathri et al., 2004). Though *B. sphaericus* spore/crystal toxins are powerful tools to control mosquito vectors, the recent development of resistance in *Culex* species has impeded progress in mosquito control operations. The magnitude of *Bs* cross-resistance to different strains of *Bs* and *Bti* in filarial vector of *Cx. quinquefasciatus* have been reported (Poopathi et al., 1999a, b, c, 2000a, b). The resistance ratio recorded between *Bs* resistant and susceptible larvae were several thousand folds at the LC50 and LC95 levels. These results indicated a need for judicious use of appropriate strains of *Bs* and *Bti* in the event of biopesticide resistance for mosquito control.

Reports of *Bs* resistance

However, resistance to *Bs* has been reported in *Culex pipiens* complex in both laboratory colonies and natural populations. During field trials on *Bs* water-dispersible granules (WDG) against natural populations of *Cx. quinquefasciatus* in a low-income community in Thailand, control failure occurred within 4 months after 5 treatments using VectoLex WDG at the dosages of 50 - 200 mg/m. The resistance ratios (RR) at LC 50, depending on reference colonies, were 21, 100 – 28 and 100 fold

against *Bs* WDG and *Bs* technical-grade material. These *Bs*-resistant mosquitoes, however, were completely susceptible to *B. thuringiensis* var. *israelensis*, (*Bti*) preparations and LC50 ranging from 0.017 ppm for technical material with 7,000 ITU/ mg to 0.052 ppm for water-dispersible granules with 3,000 ITU/mg; but addition of *Bti* to *Bs* substantially enhanced the mosquitocidal activity (synergism) against these highly *Bs*-resistant *Cx. quinquefasciatus* (Su and Mulla, 2004).

For *Bs*, the Bin toxin has to be considered as a one site-acting molecule, because of the single receptor interaction with BinB component (at least in *C. pipiens*). Resistance to *B. sphaericus* has been reported in *B. sphaericus*-treated field populations of the *C. pipiens* complex in Brazil and India and *C. pipiens pipiens* in France and China. *Bs* resistance has been recorded during the last four years in Brazil (10 fold resistance; Silva-Filha et al., 1995), India (150 fold; Rao et al., 1995) and France on *C. pipiens* (10,000 fold, Charles and Nielsen-LeRoux, 2000). Reports from China (25,000) and Tunisia (2,000 fold) confirmed that resistance to *Bs* may develop in the field when this bacteria is used intensively. Before records of field resistance to *Bs*, active laboratory selections for resistance had been done in two different laboratories in California (>100,000 fold, Georghiou et al., 1992; about 37 fold, Rodcharoen and Mulla, 1994). Studies were done to investigate the evolution of resistance to *B. sphaericus* strains, C3-41, 2362 and IAB59, in field-collected populations of *C. quinquefasciatus* from China and Brazil under laboratory conditions. Particular attention was paid to strain IAB59 for its toxicity against *B. sphaericus*-resistant mosquito larvae, with the aim of investigating whether this strain could be an alternative to the already commercialized *B. sphaericus* strains. The stability of resistance in the selected mosquito colonies and their cross-resistance to *B. sphaericus* strains, C3-41, 2362 and IAB59, and *B. thuringiensis* subsp. *israelensis* were also investigated. Two independent laboratory selections with California mosquitoes (*C. pipiens quinquefasciatus*) have also led to resistance. Levels of stable laboratory-selected resistance of between 35 fold and more than 100,000 fold have been reported, suggesting that there may be different resistance mechanisms. Investigations of the mechanisms and genetics of resistance to *B. sphaericus* have been carried out for some of the resistant populations. All of the *B. sphaericus*-resistant *C. pipiens* populations selected on strain 2362, 1593 or C3-41 belong to the same serotype and have identical genes encoding the binary toxin. However, there are small differences in the amino acid sequences of the *B. sphaericus* Bin toxins, which may be important in the structure and function of the toxin-receptor complex and therefore for larvicidal activity (Nielsen-LeRoux et al., 2001). All these studies would help to understand the inheritance of resistance and to develop approaches for resistance detection and monitoring, as well as for management strategies for resistant mosquito colonies (Guofeng Pei et al., 2002).

Mechanism of resistance to *Bs*

In vitro binding studies between the toxin and midgut BBMF (brush–border membrane fractions) from three resistant *Culex* populations gave some knowledge about the mechanisms of resistance. For the high level resistant population from France and the low-level resistant population from Brazil (both field-selected), no changes were found in binding kinetics (Nielsen-LeRoux et al., 1995) meaning that the receptor was not functional. Further, the gut proteases from this colony were able to proteolyse the protoxins to the activated forms. Then if the *Bs* crystal toxin has selected highly resistant individuals possessing a mutation influencing the initial toxin-binding in one case, in the other case, the same toxin selected highly resistant individuals expressing their resistance at another level of the intoxication process. However, the receptor molecule, in another site than the binding site, could also be involved in the resistance from France. This indicates that different genes can be involved in the resistance to *Bs*, depending on various factors like the origin of *Culex* populations, the frequency of the resistance genes and the conditions of selection (Silva-Filha, 1997). The use of *Bacillus sphaericus* (*Bs*) as a potential biolarvicide in India is limited, due to development of resistance by the target mosquito species. Observations on the biological processes of development and resistance in the *Bs* susceptible population of *Culex quinquefasciatus* have provided good insight towards developing a better control strategy for vector mosquitoes. In a laboratory evaluation, *C. quinquefasciatus* susceptible to *Bs* attained a high resistance level (70 and 90.5 fold) at LC_{50} and LC_{95} levels, with several important underlying factors involving binding of *Bs* toxic molecules to the receptor proteins at the site of action. The resistant larvae showed insignificant variation from susceptible larvae in biological features, especially pre-oviposition period, number of egg rafts laid, incubation period, hatching percentage, stadial period, adult longevity and mortality rate. However, *in vitro* binding assays showed a significant reduction in the affinity of *Bs* toxin for the membrane receptors in the resistant strain compared to the susceptible strain (Poopathi, et al., 2004).

Inheritance of resistance to *Bs*

The genetical basis of *Bs* resistance have been investigated on the two high-level resistant populations, from France and California, by crossing homozygous resistant colonies with susceptible homozygous and backcross experiments between F1 and the resistant colonies. This indicated that resistance was due to one major gene, sex linked for the colony from France but

autosomal for the colony from California, by crossing homozygous resistant colonies with susceptible homozygous and backcross experiments between F1 and the resistant colonies (Nielsen-LeRoux et al., 1995, 1997; Wirth et al., 2000). In other populations such as the low-level Brazilian one, resistance is also supposed to be recessive, because of the fast decline in resistance when *Bs* treatments were interrupted.

Although resistance is recessive in all studied cases, high-level resistance may constitute a major threat to the future use of *Bs* toxins for mosquito control. However, it seems that in some areas, even with intensively field applications (for example, in Cameroon, Tanzania, Brazil and India), decrease in susceptibility has not occurred. In southern France, *Bs* had been used for eight years from March to October with 1 - 2 treatments per month. Resistance occurred faster in closed breeding sites. This was also the case in Tunis, meaning that in such breeding sites only low migration of susceptible *Culex* individuals from non-treated areas could occur. In Recife (Brazil), the 10 fold resistant population was found in open drains and covered cesspits in a small area where all breeding sites were treated during a two year period with a total of 37 treatments (Wirth et al., 2000). In Cochin (India), resistance occurred in different kinds of open breeding sites after about two years (35 treatments) and in Doungguan (China) after eight years with about 36 treatments per year (Rao et al., 1995). This shows that the key elements for appearance of resistance are the selection pressure in time and dose and the genetic background of the populations.

Cross-resistance to *Bs*

In the above mentioned treated areas, only three different *Bs* strains were used 2362, 1593 and C3-41, all belonging to serotype H5a5b, which express the same crystal toxin (identical amino acid compositions). These strains are used in most commercial *Bs* formulations.

Investigations on the level of cross-resistance among natural *Bs* strains have been done by testing the toxicity of several highly active *Bs* strains on some of the above mentioned *Bs* resistant *Culex* colonies. For the laboratory in the selected low-level resistant colony from California, cross-resistance was found in strain 2297 (Rodcharoen and Mulla, 1996). This was also the case for the field-selected population from India (Poncet et al., 1997). There is no cross-resistance to *Bti* within the populations resistant to Bs and there is even evidence for an increased susceptibility to *Bti* (Rao et al., 1995, Silva-Filha et al., 1995). This is in agreement with the finding that the crystal toxin from *Bs* and *Bti* do not compete for the same binding sites. In all cases of binding site modification, resistance seems to be inherited as a single recessive or partially recessive major gene, and the resistance levels are high. In these cases, cross-resistance seems to be very limited and extends only to ICPs binding to the same binding site. In contrast, in those cases where resistance is due to another as yet unknown, modification, inheritance was found to follow an additive pattern. Levels of resistance were moderate and at least in one case, a more general cross-resistance was observed (Ferre et al., 1995). *B. sphaericus* IAB872 has high toxicity against susceptible *Culex* spp. and medium larvicidal activity against binary toxin-resistant *Culex* spp. Sequence analysis revealed that the sequence of the binary toxin gene from IAB872 was totally identical to that of the reference strain 2362. Mosquito larvicides based on the bacteria *B. thuringiensis* subsp. *israelensis* (*Bti*) or *B. sphaericus* (*Bs*) are effective in many habitats, but their use is limited by their high cost. Moreover, mosquito resistance evolves rapidly to *Bs* where it is used intensively (Park et al., 2005). *B sphaericus* 1593M resistant larvae of *Cx. quinquefasciatus* were reared in the laboratory since 1995, while its resistance in the larvae was monitored by subjecting selection pressure using *B. sphaericus* 1593M at every generation. Bioassays were conducted with different strains of *B. sphaericus* (*Bs* 2297, 2362 and IAB 59) and cross-resistance in the present study was confirmed. The level ranged from 27.3 to 18.2 fold in comparison with susceptible larvae.

Resistance management

Combined application of neem based biopesticides with microbial agents revealed that the neem biopesticide showed synergistic interaction with the *Bs* toxin against resistant larvae *C. quinquefasciatus* (Poopathi et al., 1997). Resistance is believed to be a complex, genetic, evolutionary and ecological phenomenon. Its management tactics are most likely to succeed if they are directed at reducing the single-factored selection pressure that occurs with conventional biocide or chemical control. During a pesticide change, 2 factors are pivotal for the dynamics of the resistance genes (Curtis et al., 1978). The effectiveness of resistance management is central for maintaining adequate pest control, while critical evolutionary factors determine the dynamics of pesticide resistance in the field. One of the factors is the fitness cost required to induce a rapid reversal in the frequency of resistance genes when the selecting pesticide is withdrawn from pest-control programs (Eritja and Chevillon, 1999). For insect species, where adaptation results from an alteration in ICP binding, resistance management strategies should consider combinations (either simultaneously or in rotation) of ICPs with different binding site specificity. Obvious counter measures include: (i) rotation or alternation of *Bs* or *Bti* toxins with other toxins, insecticides or cultural or biological control strategies (ii) reducing the frequency of biocide treatments (iii) avoiding insecticides with prolonged

environmental persistence and slow-release formulations (iv) avoiding treatments that apply selection pressure and (v) incorporating source reduction methods.

The combination of these principles is essentially a blue print for integrated pest management (IPM) which will successfully delay or prevent the development of resistance in vector population. Theoretically, integrated pest management (IPM) helps delay resistance by providing multiple sources of pest mortality.

There is evidence for development of resistance to any bacterial toxin, as soon as its mode of action implies only one toxin or toxins with identical mode of action (binding on the same receptor). However, *Bs* belongs to this category. This microbial insecticide has therefore been used in a reasonable way in the integrated control program. Monitoring the susceptibility of the treated mosquito populations before and during treatments is necessary. Other measures to be taken are to multiply the control methods and/or insecticides. *Bti* could be used as an alternative in certain conditions and formulations. In addition, other *Bs* strains or recombinant *Bs* expressing additional toxins from other mosquitocidal bacteria have to be considered. Nevertheless, there is a risk in introducing the *Bs* crystal toxin genes alone into natural mosquito larval food (for example, Cyanobacteria), because this would expose the larvae to a continuous selection pressure. Besides this, further understanding on the mode of action, on the receptor identification for other mosquito species and putative intracellular activity of the *Bs* crystal toxin, may give good tools to identify other mechanisms of resistance, in order to predict and reduce resistance (Charles and Nielsen-LeRoux, 2000). Genetic analysis revealed that *B. sphaericus* resistance was inherited as a recessive trait and controlled by a single major locus. *B. sphaericus*-resistant mosquito colonies remained highly susceptible to *B. thuringiensis israelensis,* suggesting that *Bti* would be of value in the management of *B. sphaericus*-resistant *Cx. quinquefasciatus* colonies (Yuan et al., 2003). The 2362 strain of *B. sphaericus*, which produces a binary toxin that is highly active against *Culex* mosquitoes, has been developed recently as a commercial larvicide. It is being used currently in operational mosquito control programs in several countries including Brazil, France, India and the United States. Laboratory studies have shown that mosquitoes can develop resistance to *B. sphaericus*, and low levels of resistance have already been reported in field populations in Brazil, France and India. To develop tools for resistance management, the Cyt1A protein of *B. thuringiensis* subsp*. israelensis* deBarjac was evaluated for its ability to suppress resistance to *B. sphaericus* in a highly resistant population of *Cx. quinquefasciatus*. Synergism was observed between the Cyt1A toxin and *B. sphaericus* against the resistant mosquito population and it accounted for the marked reduction in resistance. However, no synergism was observed between the toxins against a nonresistant mosquito population. These results indicate that Cyt1A could be useful for managing resistance to *B. sphaericus* 2362 in *Culex* populations and also provide additional evidence that Cyt1A may synergize toxicity by enhancing the binding to and insertion of toxins into the mosquito microvillar membrane (Wirth et al., 2000). The 2362 strain of *B. sphaericus* (*Bs*) Neide is a highly mosquitocidal bacterium used in commercial bacterial larvicides, primarily to control mosquitoes of the genus *Culex*. Unfortunately, *Bs* is at high risk for selecting resistance in mosquito populations, because its binary toxin apparently only binds to a single receptor type on midgut microvilli. A potential key strategy for delaying resistance to insecticidal proteins is to use mixtures of toxins that act at different targets within the insect, especially mixtures that interact synergistically. This hypothesis was tested for delaying the phenotypic expression of resistance by exposing *Culex quinquefasciatus*, say larvae to *Bs* alone or in combination with Cyt1A from *Bacillus thuringiensis* subsp*. israelensis*. Two laboratory lines of *Cx. quinquefasciatus* (one sensitive to *Bs* and the other containing *Bs* resistance alleles) were subjected to intensive selection pressure for 20 generations with either *Bs* 2362 or a 3:1 mixture of *Bs* 2362+Cyt1A. At the end of the study, the sensitive line had evolved >1000-fold resistance when selected with *Bs* alone, whereas the parallel line selected with *Bs*+Cyt1A exhibited only low resistance toward this mixture (RR95, 1.4). Similar results were observed in the lines containing *Bs* resistance alleles. Both lines selected with *Bs*+Cyt1A exhibited substantial resistance to *Bs* in the absence of Cyt1A. Although selection with *Bs*+Cyt1A did not prevent the underlying evolution of resistance to *Bs*, these results suggest that a mixture of *Bs* with other endotoxins, particularly one like *Bs*+Cyt1A in which the components interact synergistically, would provide longer lasting and more effective mosquito control than *Bs* alone (Wirth et al., 2005).

***Bacillus thuringiensis* serovar. *israelensis* (*Bti*)**

Bt toxins

Goldberg and Margalit (1977) isolated a bacterial mosquito pathogen that was designated by de Barjac (1978) as *B. thuringiensis* var*. israelensis* (*Bti*). Laboratory bioassays and field applications of this entomopathogen have shown biological control of several mosquito species and black flies (Ignoffo et al., 1981; Ali et al., 1984; de Barjac and Sutherland, 1990). There are 34 recognized subspecies of *B. thuringiensis*. Some of the most commonly used include subspecies *kurstaki* (against Lepidoptera), *israelensis* (against Diptera, primarily mosquitoes and blackflies) and subspecies *tenebrionis* (against *Leptinotarsa decemlineata*, the Colorado potato beetle) (Whalon and McGaughey, 1998). Two general groups of insecticidal crystal proteins made

by this wide variety of subspecies have been identified by Cyt (cytolysins) and Cry (crystal delta-endotoxins). Hofte and Whiteley (1989) define four classes of Cry genes and two classes of Cyt genes. However, CryI and CryII toxins are active against lepidopterans, CryII and CryIV against dipterans and CryIII against coleopterans. While CryIII toxins are produced by subspecies *tenebrionis* and *tolworthi* and CryIV by *israelensis*, generally, very little correlation between certain toxins and subspecies exists. *Bti* crystals are composed of four major polypeptides with molecular weights of 125, 135, 68 and 28 kDa, now referred to as Cry IVA, Cry IVB, CryIVD and CytA, respectively. Like *B. sphaericus*, *B. thuringiensis* serovar israelensis (*Bti*) is also a spore forming gram-positive soil bacterium. Since its discovery about two decades ago (Goldberg and Margalit, 1977), more than 50, 000 isolates have been screened and tested in insect control. This bacterium, during sporulation, synthesizes proteins that assemble into crystals which are toxic to mosquitoes. Crystal development during sporulation of *Bt* strains has been studied extensively. The crystals are comoposed of four polypeptides (M.wt. 125, 135. 68 and 28 kDa proteins) referred to as CryIVA, CryIVB, CryIVD and CytA. These genes, encoding this Cry toxin, are located on a 72 kDa resident plasmid and they have been cloned and expressed in various hosts. Chromosomal Cry genes have also been reported in some *Bt* strains and the role, structure and molecular organization of genes coding for the parasporal delta endotoxin of *Bt.* A review of the biochemical mechanisms of insects' resistance to *Bt* indicates that altered proteolytic processing of *Bt* crystal proteins may be involved in one case of resistance in mosquitoes. The presence of IS240 elements responsible for mosquitocidal action was investigated in sixty nine *Bt* strains. A PCR-based approach for detection of Cry genes in *Bt* has been reported. Since the toxins of this bacterium are highly potent for mosquito control, evaluation of the activity of *Bt* preparations is currently carried out by bioassay with a target insect and compared to a defined standard.

Mode of action of *Bti* and binding kinetics

Genes encoding these polypeptides are located on a 72 MDa resident plasmid and have all been cloned and expressed in various hosts. Expression of *Bti* genes either individually or in combination in crystal-negative *Bt* strains, as well as disruption of genes by *in-vivo* recombination from toxic strains, have led to the conclusion that 1) Cry IV A, CryIVB and CryIVD are to various extents, involved in the toxicity towards mosquitoes, although, displaying different specificities depending on the mosquito species tested. CytA is not a key factor for toxicity, but can potentiate the activity of the toxins and synergistic interactions that seem to account for the high toxicity of the wild strain (Delecluse et al., 1993). However, Cry toxins are bound to specific receptors on cells in the insect midgut. Cyt genes are active against dipteran and coleopteran pests, and additionally have shown an action against hemipterans (true bugs) and dictyopterans (roaches and termites) (Frutos et al., 1999; Gould and Keeton, 1996). Cyt, unlike Cry toxins, do not recognize specific binding sites. *Bt* directly causes mortality in insects, and isolates of the toxin from different strains follow similar modes of action. After the delta-endotoxin crystals are ingested, they are dissolved in the insect midgut, liberating the protoxins of which they are made. These are proteolytically processed into fragments, one of which binds to cells of the midgut epithelium. The activated protein disrupts the osmotic balance of these cells by forming pores in the cell membrane causing the cells to lyse (Van Rie et al., 1992). The gut becomes paralyzed and the insect stops feeding; and as a result, most insects will die within a few hours of ingestion (Marrone and Macintosh, 1993). The binding affinity of these toxin fragments is often directly related to the toxicity, though binding does not assure toxicity (Whalon and McGaughey, 1998).

Resistance to *Bacillus thuringiensis* (*Bt*)

While *Bt* is very unlike other insecticides in its origin, mode of action and use, it still shares some of the problems of any insecticide. One major problem with insect control via insecticides is the evolution in insects of resistance to those insecticides. The first reported cases of insecticide resistance to early synthetic insecticides occurred over 50 years ago. About thirty years later, in 1979, the United Nations Environmental Programme declared that pesticide resistance is one of the world's most serious environmental problems. Its seriousness to the environment stems from problems of human nutrition due to crop loss, spread of disease by resistant insects, addition to the environment of new and potentially dangerous insecticides after resistance has developed, and application of greater and greater amounts of chemicals to which pests have already gained resistance (Pimentel and Burgess, 1985). Insecticide resistance is a major problem, not only in agriculture, but also in health and economics. The development of resistance to *B. thuringiensis* toxins is, however, particularly unfortunate. *Bt* toxins are more pest-specific and environmentally safe than conventional pesticides, yet they are effective against problem insects (McGaughey et al., 1998).

In 1985, the first evidence of resistance developing in the field against *Bt* delta-endotoxins was published. Low levels of resistance were found in *Plodia interpunctella* (the Indian meal moth), in storage bins of *Bt*-treated grain (McGaughey, 1985). Recognition of the potential of the *Bt* resistance problem became greater when the first reports of high resistance to *Bt* toxins in the field came in 1990 from Hawaii, Florida and New York in the United States,

thirty years after its commercial debut here. The species found to be losing susceptibility to *Bt* toxin was *Plutella xylostella* (the diamondback moth), treated with spray formulations of the toxins. At about that same time, resistance was detected in *P. xylostella* after intensive use in several other countries, including Japan, China, the Philippines and Thailand (Liu and Tabashnik, 1997). Malaysia also reported *Bt* resistance in the diamondback moth in 1990, where interviews with local farmers confirmed their personal experiences with this unfortunate situation (Iqbal et al., 1996). Thus, *P. xylostella* is still the only insect species in which very considerable resistance has been found to develop outside the laboratory. In fifteen years, since *Bt* resistance was discovered in *P. interpunctella*, *Bt* resistance has been selected in laboratory populations of a total of thirteen insect species. Eleven of these species have developed resistance to various strains of *Bt* toxin in the laboratory, but not in the field: *Ostrinia nubilalis* (the European corn borer), *Heliothis virescens* (the tobacco budworm), *Pectinophora gossypiella* (the pink bollworm moth), *Cx. quinquefasciatus* (the mosquito), *Caudra cautella* (the almond moth), *Chrysomela scripta* (the cottonwood leaf beetle), *Spodoptera exigua* (the beet armyworm), *Spodoptera littoralis* (the Egyptian cotton leafworm), *Trichoplusiani* (the tiger moth), *L. decemlineata* (the Colorado potato beetle) and *Aedes aegypti* (the yellow fever mosquito) (Huang et al., 1999; Gould et al., 1997; Liu et al., 1999; Tabashnik et al., 1994; Wirth et al., 1997; Frutos et al., 1999). Many other species have been tested in the lab, but they retained susceptibility to *Bt* (Whalon and McGaughey, 1998). While none of the species listed here has yet developed resistance in the field, these laboratory studies show that the potential to develop resistance is real. No records of field resistance have been found to *Bti* because of the presence of the four different toxins with putative different modes of action; but *B. thuringiensis* var *israelensis* strains (*Bti* PG14 and *Bti* 426) did not show any cross-resistance in the larvae and it emphasized a need to study the mode of action of *B. sphaericus* toxin that induced cross-resistance in the larval strain (Poopathi et al., 1999). Wei et al. (2007) studied the toxicity and delayed effects of a mosquitocidal toxin (Mtx1) and a binary toxin (Bin) produced in *Escherchia coli* E-TH21 and *Bacillus thuringiensis* B-CW1, respectively, on *Culex quinquefasciatus* (*Diptera*: *Culicidae*). Bioassay results showed that both E-TH21 powder and B-CW1 sporulated culture were highly toxic against susceptible *Cx. quinquefasciatus*, with LC50 values of 0.65 and 1.70 mg/liter against third and fourth instars at 48 h, respectively. After initial 48 h exposure of larvae to different concentrations of Mtx1 and Bin, significant continued mortality could be observed in larval, pupal and emergence stages of *Cx. quinquefasciatus*. Importantly, the Mtx1 could induce higher cumulative larval and pre-adult mortalities than Bin toxin on the target mosquito. This finding is important for understanding the mode of action of Mtx1 and Bin toxins and for developing a new bioassay procedure for the evaluation of *B. sphaericus* Neide toxicity, in which some strains produce Mtx1 and Bin, in the laboratory and field.

How resistance develops?

Insects have developed resistance to nearly every type of insecticide. Resistance to other insecticides is, in fact, one of the many reasons why *B. thuringiensis* has come into common use today. Insecticide resistance develops due to genetic variation in large insect populations. A few individuals in the original insect population are unaffected by a given insecticide. Generally, unaffected (resistant) individuals differ from affected (susceptible) individuals either in the nature of the insecticide's target molecules in the insect, or in the method the insect uses to break down toxin molecules (Michaud, 1997). When the insecticide is applied, individuals who are unaffected by it are those who survive to pass their genes onto the following generations. Over time, a greater and greater proportion of the insect population is unaffected by the insecticide (Hoy, 1998). Insecticides based on *B. thuringiensis* subsp. *israelensis* have been used for mosquito and black fly control for more than 20 years, yet no resistance to this bacterium has been reported. Moreover, in contrast to *B. thuringiensis* subspecies that is toxic to coleopteran or lepidopteran larvae, only low levels of resistance to *B. thuringiensis* subsp. *israelensis* have been obtained in laboratory experiments, where mosquito larvae were placed under heavy selection pressure for more than 30 generations. Selection of *Culex quinquefasciatus* with mutants of *B. thuringiensis* subsp. *israelensis* that contained different combinations of its Cry proteins and Cyt1Aa suggested that the latter protein delayed resistance. These results indicated that Cyt1Aa was the principal factor responsible for delaying the evolution and expression of resistance to mosquitocidal Cry proteins (Wirth et al., 2005).

Factors affecting the development of resistance

There are several factors that increase the rate at which insecticide resistance is generally developed. Some factors related to the insect population itself are: species with higher reproductive rates, shorter generation times, greater numbers of progeny and more genetically varied local populations that develop a large resistance population more quickly (Pimentel and Burgess, 1985). Whether the genetic basis of insect resistance is dominant or recessive is also of importance (Wearing and Hokkanen, 1995). Other factors are dependent upon the insecticide. Resistance develops more rapidly to more persistent insecticides, in that their staying power in the

environment increases the chance that susceptible individuals are exposed to the toxin and die, thus not passing on their insecticide-susceptible traits to the next generation. This is selected more strongly on resistant insects because only the resistant insects thrive. By similar logic, frequent application of non-persistent insecticides has the same effect (Wood, 1981). Insect populations with little immigration into the gene pool of new, non-exposed susceptible individuals also develop resistance more readily (Comins, 1977). Populations that have in the past been exposed to an insecticide with a mode of action similar to that of a new insecticide are quick to develop resistance to the new toxin. This phenomenon is known as cross-resistance.

Mechanism of resistance

Learning how to curb the resistance of *Bti* is central to understanding the mechanism by which an insect resists the toxins. Mechanisms by which insects resist the lethal effects of *B. thuringiensis* toxins are, naturally, closely related to the mode of action of *Bt.* As stated earlier, *Bti* protoxins are activated by proteases in the insect midgut. After activation, they bind to receptors on the epithelium. Thereafter, a number of steps lead to the death of the insect. The specifics of the mode of action are complex and varied among insect and *Bt* strains. In fact, prior to 1985, it was thought that the complexity itself would prevent the evolution of resistance (Whalon and McGaughey, 1998). However, mechanisms of resistance are equally complex. Due to the fact that so many steps are involved in the full process of *Bti*'s mode of action, many ways of stopping the process and resisting the toxin are possible. Thus, far studies have most commonly shown the resistance mechanism to involve a change in the membrane receptors to which *Bti* toxins bind are activated (Tabashnik et al., 1997).

Resistance management

The goals and types of resistance management

It will be necessary to counter resistance in order to preserve the efficacy of *Bt*. There are three goals of resistance management: avoiding resistance where and if possible, delaying resistance as long as possible and making resistant populations revert to susceptibility (Croft, 1990). Several possible resistance programs have been conceived in the past 25 years, most of which could potentially be used in conserving susceptibility to *Bt*. The transgenic plant forms of *Bti*, and the use of which is on the rise, are especially prone to resistance development. Transgenic plants expose insects to toxins continually, even at times when they are not causing economic damage (Mallet and Porter, 1992).

Resistance management programs generally use one of the just three basic approaches to delay resistance. One approach seeks to minimize exposure to toxins and/or allow for mating between resistant insects and a large population of susceptible insects, in order to keep susceptible traits in the gene pool continually. These strategies include tissue-specific and time-specific expression of toxins, mixtures, mosaics, rotations, refuges and occasional release of susceptible males into the field. Another approach focuses on combining pest-control techniques and is based on the assumption that an insect is more likely to develop resistance to just one type of control than more than one type of control simultaneously. Strategies in this category include gene stacking, high doses, combinations of toxins with completely different modes of action and combinations of low toxin dose and natural enemies.

The release of susceptible insects into an exposed population

Among the oldest strategies are those involving the mating of resistant insects with susceptible ones; however, the simplest of these ideas is the periodic release of susceptible males, raised in the lab or collected elsewhere into a local *Bt*-treated population. This would theoretically make it possible to keep the frequency of resistance in a population below a predefined level (Curtis, 1981). This method is best used on populations of insects such as mosquitoes, in which insecticides generally target females (Wood, 1981). However, *Bt* is not a gender-specific pesticide, and as a result, there is a risk that many of the susceptible males released would die in the *Bt* field before mating. Additionally, the feasibility of rearing and transporting large colonies is very questionable.

Synergistic interactions among the multiple endotoxins of *Bacillus thuringiensis* subsp. *israelensis* de Barjac play an important role in its high toxicity to mosquito larvae and the absence of insecticide resistance in populations treated with this bacterium. A lack of toxin complexity and synergism are the apparent causes of resistance to *Bacillus sphaericus* Neide in particular *Culex* field populations. The proposed strategies for improving bacterial larvicides are a combination of *B. sphaericus* with *Bt* subsp. *israelensis* or by engineering recombinant bacteria that express endotoxins from both strains. These combinations increase both endotoxin complexity and synergistic interactions and thereby enhance activity and help avoid insecticide resistance (Wirth et al., 2004).

Application of genetic engineering to combat resistance

Genetic engineering techniques have been used to significantly improve mosquito larvicides based on the

bacteria *B. thuringiensis* (*Bt*) subsp. *israelensis* (*Bti*) and *B. sphaericus* (*Bs*). By cloning the genes, encoding various endotoxins from *Bt* and *Bs* species, and engineering these for high levels of synthesis, we have been able to generate recombinant bacterial strains based on *Bti* that are more than 10 times as effective as the conventional strains of *Bti* or *Bs* that serve as the active ingredients of commercial bacterial larvicides currently used for mosquito control. The best of these recombinants contain all major *Bti* endotoxins, specifically, Cry4A, Cry4B, Cry11A and Cyt1A, plus the binary (Bin) endotoxin of Bs, the principal mosquitocidal protein responsible for the activity of this species. The presence of Cyt1A in these recombinants, which synergizes Cry toxicity and delays resistance to these proteins and *Bs* Bin, should enable long term use of these recombinants with, little if any, development of resistance (Federici et al., 2007). Recently, however, recombinant DNA techniques have been used to improve bacterial insecticide efficacy by markedly increasing the synthesis of mosquitocidal proteins and enabling new endotoxin combinations from different bacteria to be produced within single strains. These new strains combine mosquitocidal Cry and Cyt proteins of *B. thuringiensis* with the binary toxin of *B. sphaericus*, improving efficacy against *Culex* species by 10 fold and greatly reducing the potential for resistance through the presence of Cyt1A. For example, the recombinant *Bti* species produce Cyt1A, Cry proteins and *Bs* Bin toxin, with each type having a different mode of action. Significantly, Cyt1A adds the important trait of making it difficult for the mosquitoes to develop resistance to these strains, that is, something not achieved with chemical insecticides. Moreover, although intensive use of *B. sphaericus* against *Culex* populations in the field can result in high levels of resistance, most of this can be suppressed by combining this bacterial species with Cyt1A. The latter enables the binary toxin of this species to enter midgut epithelial cells via the microvillar membrane in the absence of a midgut receptor. The availability of these novel strains and newly discovered mosquitocidal proteins, such as the Mtx toxins of *B. sphaericus*, offers the potential for constructing a range of recombinant bacterial insecticides for more effective control of the mosquito vectors (Federici et al., 2003). Similar to Cyt toxins from *Bti*, Mtx toxins (produced during vegetative growth) can increase the toxicity of other mosquitocidal proteins and may be useful for both increasing the activity of commercial bacterial larvicides and managing potential resistance to these substances among mosquito populations (Wirth et al., 2007). Thus, there were two obvious strategies for making improved recombinant mosquitocidal bacteria: (1) introduce *Bti* or related mosquitocidal endotoxin genes into the best *Bs* strains and (2) introduce *Bs* toxin genes into *Bti.* Both of these approaches have been to construct a variety of ^{Bt} and *Bs* recombinants that produce different combinations of *Bt* and *Bs* proteins. Integrative plasmids have been constructed by researches in genetic engineering to enable integration of foreign DNA into the chromosome of *Bacillus sphaericus* 2297 by *in vivo* recombination. This strategy was applicable with the antibiotic resistance selection. Hybridization experiments evidenced two copies of the operon encoding the binary toxin from *B. sphaericus* in the recipient strain. Synthesis of Cry11A toxin conferred toxicity to the recombinant strains against *Aedes aegypti* larvae, for which the parental strain was not toxic. Interestingly, the level of larvicidal activity of strain 2297 against *Anopheles stephensi* was as high as that of *B. thuringiensis* subsp*. israelensis* and suggested synergy between the *B. thuringiensis* and *B. sphaericus* toxins. The toxicities of parental and recombinant *B. sphaericus* strains against *Cx. quinquefasciatus* were similar, but the recombinant strains killed the larvae more rapidly. The production of the Cry11A toxin in *B. sphaericus* also partially restored toxicity for *C. quinquefasciatus* larvae from a population resistant to *B. sphaericus* 1593. *In vivo* recombination therefore appears to be a promising approach to the creation of new *B. sphaericus* strains for vector control (Poncet et al., 1997). The results suggested that the Cry27A protein is responsible for the Anopheles-preferential toxicity of the *B. thuringiensis* serovar high strain (Saitoh et al., 2000). These inclusions exhibited no larvicidal activities against three mosquito species: *Aedes aegypti*, *Anopheles stephensi* and *Cx. pipiens molestus*. Likewise, the inclusions contained no cytocidal activity against HeLa cells (Ohgushi et al., 2005). A novel mosquitocidal bacterium, *B. thuringiensis* subsp. *jegathesan*, and one of its toxins (Cry11B), in a recombinant *B. thuringiensis* strain were evaluated for cross-resistance with strains of the mosquito *Cx. quinquefasciatus* that are resistant to single and multiple toxins of *B. thuringiensis* subsp*. israelensis*. The high levels of activity of *B. thuringiensis* subsp. *jegathesan* and *B. thuringiensis* subsp. *israelensis,* both of which contain a complex mixture of Cry and Cyt proteins, against Cry4- and Cry11-resistant mosquitoes suggested that novel bacterial strains with multiple Cry and Cyt proteins may be useful in managing resistance to bacterial insecticides in mosquito populations (Wirth et al., 1998). The cross-resistance spectra of the mosquitoes were similar to the profiles for recombinant *B. thuringiensis* strains expressing *B. thuringiensis* toxin genes, but with varied toxicity levels. These results indicated that *B. thuringiensis* sp*. israelensis* genes expressed in a heterologous host, such as *E. coli*, can be effective against susceptible and *B. thuringiensis*-resistant larvae and suppress resistance (Wirth et al., 2007). The LC50 values were 2.5 and 4.8 mg/ml respectively, against 3 - 4 instar susceptible and resistant larvae for the final sporulated cultures of recombinants B-pMT9 (Mtx1), and little toxicity was detected for B-pMT4 (Mtx1) (Zhang et al., 2006).

Previous work showed that the resistance to *B. sphaericus* in a *Cx. quinquefasciatus* colony is assiociated

with the absence of the approximately 60-kDa binary toxin receptor in larvae midgut microvilli. Here, the gene encoding the *C. quinquefasciatus* toxin receptor, Cqm1, was cloned and sequenced from a susceptible colony. The deduced amino-acid sequence confirmed its identity as an alpha-glucosidase, and analysis of the corresponding gene sequence from resistant larvae implicated a 19-nucleotide deletion as the basis for resistance (Romao et al., 2006). The toxicities of Mtx1 toxin against dipteran and lepidopteran species showed that Mtx1 has little or no toxicity to the tested lepidopteran species, but has moderate-level toxicity to *Aedes albopictus* Skuse (Diptera: Culicidae) and high-level toxicity to both susceptible and binary toxin-resistant *Culex quinquefasciatus*, say (Diptera: Culicidae). This indicated that Mtx1 has a different mode of action from the binary toxin, and that it could be an alternative toxin to delay or overcome resistance development to binary toxin in *C. quinquefasciatus* (Wei and Yuan, 2006). Cry toxins from *Bacillus thuringiensis* (*Bt)* are used for insect control. Their primary action was to lyse midgut epithelial cells. In the case of mosquitocidal *Bt* strains, two different toxins (Cry and Cyt) participated. These toxins have a synergistic effect and Cyt1Aa overcomes Cry toxin-resistance. Recent findings on the identification of Cry receptors in mosquitoes and the mechanism of synergism summarizes that Cyt1Aa synergizes or suppresses resistance to Cry toxins by functioning as a Cry membrane-bound receptor (Soberon et al., 2007). The results obtained in toxicological tests showed significant differences in the larval sensitivities of the four populations for both insecticides. These differences appeared to be related to the activity of the three main families of detoxifying enzymes: Cytochrome P450 monooxygenases, glutathione-S-transferases (GSTs) and esterases. All three enzyme families were significantly over expressed in the less susceptible larval population, and after multiple regressions, it was found that GSTs and esterases were the most explicative variables of the larval sensitivity. Considering these results and the chemical history of the sites in terms of insecticide treatments, the hypothesis of cross-effects of insecticides leading to resistance acquisition to *Bti* in field organisms emerges. The mechanism of resistance to the binary toxin in a natural population of the West Nile virus vector, *Culex pipiens* showed that the insertion of a transposable element-like DNA into the coding sequence of the midgut toxin receptor induced a new mRNA splicing event, unmasking cryptic donor and acceptor sites located in the host gene. The creation of the new intron causes the expression of an altered membrane protein, which is incapable of interacting with the toxin, thus providing the host mosquito with an advantageous phenotype. As a large portion of insect genomes is composed of transposable elements or transposable elements-related sequences, this new mechanism may be of general importance to appreciate their significance as potent agents for insect resistance to the microbial insecticides (Darboux et al., 2007). These results indicate that *B. thuringiensis* ssp. *israelensis* genes expressed in a heterologous host such as *E. coli* can be effective against susceptible and *B. thuringiensis*-resistant larvae and suppress resistance (Wirth et al., 2007). Mixtures of *B. sphaericus* with either cytolytic toxin were synergistic, and *B. sphaericus* resistance in *C. quinquefasciatus* was suppressed from >17,000 to 2 fold with a 3:1 mixture of *B. sphaericus* and Cyt1Ab. This trait may prove useful for combating insecticide resistance and for improving the activity of microbial insecticides (Wirth et al., 2003). Synergistic interactions among the multiple endotoxins of *B. thuringiensis* subsp. *israelensis* de Barjac play an important role in its high toxicity to mosquito larvae and the absence of insecticide resistance in populations treated with this bacterium. A lack of toxin complexity and synergism are the apparent causes of resistance to *B. sphaericus* Neide in particular Culex field populations. To identify endotoxin combinations of the two *B.* species that might improve insecticidal activity and manage mosquito resistance to *B. sphaericus*, the toxins were tested alone and in combination. Most combinations of *B. sphaericus* and *B. t*. subsp. *israelensis* toxins were synergistic and they enhanced toxicity relative to *B. sphaericus*, particularly against *Cx. quinquefasciatus*, say larvae resistant to *B. sphaericus* and *Aedes aegypti* (L.), a species poorly susceptible to *B. sphaericus*. Toxicity also improved against susceptible *Cx. quinquefasciatus*. For example, when the CytlAa toxin from *B. t.* subsp. *israelensis* was added to Bin and Cry toxins, or when native *B. t.* subsp. *israelensis* was combined with *B. sphaericus*, synergism values as high as 883-fold were observed and their combinations were 4-59,000 fold more active than *B. sphaericus*. These data and the previous studies, using cytolytic toxins, validate the proposed strategies for improving bacterial larvicides by combining *B. sphaericus* with *B. t*. subsp. *israelensis* or by engineering recombinant bacteria that express endotoxins from both strains. These combinations increase both endotoxin complexity and synergistic interactions and thereby enhance activity and help avoid insecticide resistance (Wirth et al., 2004). The 2362 strain of *B. sphaericus*, which produces a binary toxin highly active against *Culex* mosquitoes, has been developed recently as a commercial larvicide. It is being used currently in operational mosquito control programs in several countries including Brazil, France, India and the United States. Laboratory studies have shown that mosquitoes can develop resistance to *B. sphaericus*, and low levels of resistance have already been reported in field populations in Brazil, France and India. To develop tools for resistance management, the Cyt1A protein of *B. thuringiensis* subsp. *israelensis* De Barjac was evaluated for its ability to suppress resistance to *B. sphaericus* in a highly resistant population of *Cx. quinquefasciatus*. A combination of *B. sphaericus* 2362 in a 10:1 ratio with a

strain of *B. thuringiensis* subsp. *israelensis* that only produces Cyt1A reduced resistance by >30,000-fold. Resistance was suppressed completely when *B. sphaericus* was combined with purified Cyt1A crystals in a 10:1 ratio. Synergism was observed between the Cyt1A toxin and *B. sphaericus* against the resistant mosquito population and accounted for the marked reduction in resistance. However, no synergism was observed between the toxins against a nonresistant mosquito population. These results indicate that Cyt1A could be useful for managing resistance to *B. sphaericus* 2362 in Culex populations, and also provide additional evidence that Cyt1A may synergize toxicity by enhancing the binding to and insertion of toxins into the mosquito microvillar membrane (Wirth et al., 2000). Expression of a chitinase gene, chiAC, from *B. thuringiensis* in *B. sphaericus* 2297 using the binary toxin promoter yielded a recombinant strain that was 4,297 fold more toxic than strain 2297 against resistant *Cx. quinquefasciatus*. These results show that this chitinase can synergize the toxicity of the binary toxin against mosquitoes, and thus may be useful in managing mosquito resistance to *B. sphaericus* (Cai et al., 2007). In the laboratory, three microbial mosquito larvicidal products consisting of *B. thuringiensis* ssp. *israelensis* de Barjac (*Bti*), *B. sphaericus* (Neide) (*Bs*) (strain 2362) and the University of California Riverside (UCR) recombinant (producing toxins of both *B. sphaericus* and *B. thuringiensis* ssp. *israelensis)* were bioassayed against larvae of *Cx. quinequefasciatus*, say (susceptible and resistant to *Bs* 2362), while *Aedes aegypti* (L.). *Bti* proved highly effective against *Cx. quinquefasciatus* susceptible and resistant strains. *Bti* was also highly active against *Ae. aegypti* with LC50 and LC90 values of 0.014 and 0.055 ppm, respectively. The UCR recombinant was equally active against both *Bs*-susceptible and -resistant strains of *Cx. quinquefasciatus*. *Bti* and the UCR recombinant essentially showed similar activity against *Bs*-susceptible and -resistant strains. *Bs* was highly active against susceptible strain of *Cx. quinquefasciatus* and exhibited little toxicity against *Ae. aegypti* larvae with no toxicity to *Bs* resistance. In the field, the experimental corn grit formulations of *Bti*, *Bs* and UCR recombinants VBC 60023 in simulated field (microcosms) against *Bs*-susceptible Culex mosquitoes were studied. *Bti* and low-concentrate UCR recombinant showed similar initial activity as well as persistence. Both materials provided high-to-moderate level of control for 2 - 7 d post treatment at low treatment rates.

CONCLUSION

Bti and Bs *provide* effective alternatives to broad spectrum larvicides in many situations with little or no environmental impact. Taking into account environmental benefits including safety for humans and other non-target organisms, reduction of pesticide residues in the aquatic environment, increased the activity of most other natural enemies and increased biodiversity in aquatic ecosystems. As a result, their advantages are numerous (Lacey et al., 2001). In addition to recombinant bacteria used as larvicides, research is also underway to develop transgenic algae and cyanobacteria using larvicidal endotoxins of *Bt*i and *Bs.* The advent of recombinant DNA technology is now having an enormous impact on agriculture and medicine and it is appropriate that the ability to manipulate and recombine genes with this technology should be applied to improving larvicides for vector control. These new recombinant bacteria are as potent as many synthetic chemical insecticides yet are much less prone to resistance, as they typically contain a mixture of endotoxins with different modes of action. The existing recombinants also have what can be considered disadvantageous in that they do not show significantly improved activity against aedine and anopheline mosquitoes in comparison to *Bti*; but it may be possible to overcome this limitation using some of the newly discovered mosquitocidal proteins such as the Mtx proteins (Delécluse et al., 2000) and peptides such as the trypsin-modulating oostatic factor, which could be easily engineered for high expression in recombinant bacteria. While other microbial technologies such as recombinant algae and other bacteria are being evaluated, it is yet to be shown that these are as efficacious and environmentally friendly as *Bti* and *Bs*. By combining the genes from a variety of organisms, it should ultimately be possible to design `smart' bacteria that will seek out and kill larvae of specific vector mosquitoes. Thus, recombinant bacteria show an excellent promise for the development and use in operational vector control programs, hopefully within the next few years.

ACKNOWLEDGEMENTS

The first author thanked the Department of Science and Technology (DST) and the Government of India, New Delhi for sanction of the project on “characterization of biopesticide resistance in *Culex quinquefasciatus* (Ref: DST:F.No:SR/SO/HS-02/2008 dated 30/12/2009). The authors also thank the Director of Vector Control Research Centre (ICMR), Pondicherry for permission and Smt. R. Sundarammal, Senior Library Information Officer, VCRC, Pondicherry for providing valuable information on current trend in the research.

REFERENCES

Ali A, Sauerman DM, Nayar JK (1984). Pathogenicity of an industrial formulation of *Bacillus thuringiensis* serovar *israelensis* to larvae of some culicine mosquitoes in the laboratory. Fla. Entomol., 67: 193-197.

Baumann P, Clark MA, Baumann L, Broadwell AH (1991). *Bacillus sphaericus* as a mosquito pathogen: properties of the organism and and its toxins. Microbiol. Mol. Biol. Rev., 55(3): 425-436.

Boutayeb A (2006). The double burden of communicable and non-communicable diseases in developing countries. Trans. R. Soc. Trop. Med. Hyg., 100(3): 191-199.
Cai Y, Yan J, Hu X, Han B, Yuan Z (2007). Improving the insecticidal activity against resistant *Culex quinquefasciatus* by expression of chitinase gene chiAC in *Bacillus sphaericus.* Appl. Environ. Microbiol., 12: 141–149.
Chaufaux J, Muller-Cohn J, Buisson C, Sanchis V, Lereclus D, Pasteur N (1997). Inheritance of resistance to the *Bacillus thuringiensis* CryIC toxin in *Spodoptera littoralis* (Lepidoptera: Noctuidae) J. Econ. Entomol., 90(4) 873-878.
Charles JF, Silva-Filha MH, Nielsen-LeRoux C, Humphreys M, Berry C (1997). Binding of the 51 and 42 kDa individual components from the *Bacillus sphaericus* crystal toxin on mosquito larval midgut membranes from *Culex* and *Anopheles* sp. (Diptera: Culicidae) FEMS Microbiol., 63: 3254-3260.
Charles JF, Nielsen-LeRoux C (2000). Mosquitocidal bacterial toxins: diversity, mode of action and resistance phenomena. Mem. Inst. Oswaldo Cruz.95 Suppl., 1: 201-6.
Coleman M, Sharp B, Seocharan I, Hemingway J (2006). J. Developing as evidence-based decision support system for rational insecticide choice in the control of African malaria vectors. J. Med. Entomol., 43 (4), 663-668.
Coleman M, Hemingway J (2007). Insecticide resistance monitoring and evaluation in disease transmitting mosquitoes. J. Pesticide Sci., 32(2): 69-76.
Comins HN (1977). The development of insecticide resistance in the presence of migration. J. Theor. Biol., 64: 177-197.
Croft BA (1990). Developing a philosophy and program of pesticide resistance management. In: Pesticide Resistance in Arthropods, Roush, R. T. and Tabashnik, B. E., Eds., Chapman and Hall, New York, NY, pp. 277-296.
Curtis CF, Cook LM, Wood RJ (1978). Selection for and against insecticide resistance and possible methods of inhibiting the evolution of resistance in mosquitoes. Ecol. Entomol., 3: 273-287.
Curtis CF (1981). Possible methods of inhibiting or reversing the evolution of insecticide resistance in mosquitoes. Pestic. Sci., 12: 557-564.
Darboux I, Charles J-F, Pauchet Y, Warot S, Pauron D (2007). Transposon-mediated resistance to *Bacillus sphaericus* in a field-evolved population of *Culex pipiens* (Diptera: Culicidae). Cell Microbiol., 9(8):2022-2029.
de Barjac H, Thiery I, Cosmao Dumanior V, Frachon E, Laurent PH, Ofori J, Charles J-F, Hamon S (1988). Another *Bacillus sphaericus* serotype harbouring strains very toxic to mosquito larvae: Serotype H6. Ann. Inst. Pasteur. Microbiol., 139: 363-377.
de Barjac H, Sutherland DJ (1990). Part 1, pp. 3-217. In: Bacterial control of mosquitoes and blackflies. Rutgers Univ. Press, (editors). New Brunswick, NJ.
Delecluse A, Barloy F, Thiery I (1995). Mosquitocidal toxins from various *Bacillus thuringiensis* and *Clostridium bifermentans* in *Bacillus thuringiensis.* Biotechnology and Environmental Benefits, ed by Feng T-Y *et al.,* Hua Shiang Yuan Publishing Co, Taiwan. Vol. 1 pp.125-141.
Federici BA, Park HW, Bideshi DK, Wirth MC, Johnson JJ (2003). Recombinant bacteria for mosquito control (Review Article) J. Exp. Biol., 206: 3877-3885 (2003).
Ferre J, Escriche B, Bel Y, Rie JV (1995). Biochemistry and genetics of insect resistance to *Bacillus thuringiensis* insecticidal crystal proteins FEMS Microbiol. Lett., 132: 1-7.
Frutos R, Rang C, Royer M (1999). Managing insect resistance to plants producing *Bacillus thuringiensis* toxins. Critical Rev. Biotech.. 19: 227-276.
Gayathri V, Jeyalakshmi T, Shanmugasundaram R, Murthy PB (2004). Rotational application of bioinsecticide with deltamethrin-An antilarval measure for the control of filarial vector, *Culex quinquefasciatus* (Culicidae: Diptera). J. Environ. Biol., 25(4): 419-421.
Georghiou GP, Malik JI, Wirth M, Sainato K (1992). Characterization of resistance of *Culex quinquefasciatus* to the insecticidal toxins of *Bacillus sphaericus* (strain 2362). University of California, Mosquito Control Research, Annual Report 1992. University of California, Riverside, CA.. pp. 34-35.
Goldberg LJ, Margalit J (1977). A bacterial spore demonstrating rapid larvicidal activity against *Anopheles sergentii*, *Uranotaenia unguiculata, Culex univitatus, Aedes aegypti* and *Culex pipiens*. Mosq. News, 37: 355-358.
Gould JL, Keeton WT (1996). Biological Science (6th Ed.) New York: W. W. Norton and Company. pp. 143-185.
Gould F, Anderson A, Jones A, Sumerford D, Heckel DG, Lopez J, Micinski S, Leonard R, Laster M (1997). Initial frequency of alleles for resistance to *Bacillus thuringiensis* toxins in field populations of *Heliothis virescens*. Proc. Natl. Acad. Sci. USA, 94: 3519-3523.
Guofeng P, Cláudia MF, Oliveira ZY, Christina N-L, Maria HS-F, Jianpin Y, Regis L (2002). A Strain of *Bacillus sphaericus* Causes Slower Development of Resistance in *Culex quinquefasciatus* Appl. Environ. Microbiol., 68 (6): 3003-3009.
Hofte H, Whitley HR (1989). Insecticidal crystal proteins of *Bacillus thuringiensis.* Microbiol. Rev., 53: 242-255.
Hoy MA (1998) Myths, models and mitigation of resistance to pesticides. Phil. Trans. R. Soc. Lond. B., 353: 1787-1795.
Huang F, Buschman LL, Higgins RA, McGaughey WH (1999). Inheritance of resistance to *Bacillus thuringiensis* toxin (Dipel ES) in the European corn borer. Science, 284: 965-967.
Ignoffo CM, Garacia C, Kroha MJ, Fukuda T, Couch TL (1981). Laboratory tests to evaluate the potential efficacy of *Bacillus thuringiensis* var *israelensis* for use against mosquitoes. Mosq. News. 42: 85-93.
Iqbal M, Verkerk RHJ, Furlong MJ, Ong PC, Rahman SA, Wright DJ (1996). Evidence for resistance to *Bacillus thuringiensis* (*Bt*) subsp. *kurstaki* HD-1, *Bt* subsp. *aizawa*i and abamectin in field populations of *Plutella xylostella* from Malaysia. Pestic. Sci., 48: 89-97.
Kellen W, Clark T, Windergren J, Ho B, Rogoff M (1965). *Bacillus sphaericus* Neide as a pathogen of mosquitoes. J. Invertebr. Pathol., 7: 442-448
Lacey LA, Frutos R, Kaya HK, Vail P (2001). Insect pathogens as biological control agents: Do they have a future? Biol. Control., 21: 230-248.
Liu YB, Tabashnik BE (1997). Experimental evidence that refuges delay insect adaptation to *Bacillus thuringiensis*. Proc. R. Soc. Lond. B., 264: 605-10
Liu YB, Tabashnik BE, Dennehy TJ, Patin AL, Bartlett AC (1999). Development time and resistance to *Bt* crops. Nature, 400: 519.
Mahmood F (1998). Laboratory bioassay to compare susceptibilities of *Aedes aegypti* and *Anopheles albimanus* to *Bacillus thuringiensis* var. *israelensis* as affected by their feeding rates. J. Amer. Mosq. Control Assoc., 14: 69-71.
Mallet J, Porter P (1992). Preventing insect adaptation to insect-resistant crops: are seed mixtures or refugia the best strategy? Proc. R. Soc. Lond. B., 250: 165-169.
Marrone PG, MacIntosh SC (1993). Resistance to *Bacillus thuringiensis* and Resistance Management. In: *Bacillus thuringiensis*, An Environmental Biopesticide: Theory and Practice, Entwistle, P. F., Cory, J. S., Bailey, M. J., and Higgs, S., Eds., John Wiley and Sons, Chichester, UK, 221-235.
McGaughey WH, Gould F, Gelernter W (1998). *Bt* resistance management. Nat. Biotech., 16: 144-6.
Michaud D (1997) Avoiding protease-mediated resistance in herbivorous pests. Trends Biotech., 15: 4-6.
Nielsen-LeRoux C, Charles J-F (1992). Binding of *Bacillus sphaericus* binary toxin to a specific receptor on midgut brush border membranes from mosquito larvae. Eur. J. Biochem., 210: 585-590
Nielsen-LeRoux C, Charles J-F, Thiery I, Georghiou GP (1995). Resistance in the laboratory population of *Culex quinquefasciatus* Diptera: Culicidae) to *Bacillus sphaericus* binary toxin is due to a change in the receptor on midgut-brush-border membranes. Eur. J. Biochem., 228: 206-210.
Nielsen-LeRoux C, Pasquier F, Charles J-F, Sinegre G, Gaven B, Pasteur N (1997). Resistance to *Bacillus sphaericus* involves different mechanisms in *Culex pipiens* (Diptera: Culicidae) larvae. J. Med. Entomol., 34: 321-327
Nielsen-LeRoux C, Raghunatha Rao D, Rodcharoen JM, Carron A, Mani TR, Hamon S, Mulla MS (2001). Various Levels of Cross-Resistance to *Bacillus sphaericus* Strains in *Culex pipiens* (Diptera: Culicidae) Colonies Resistant to *B. sphaericus* Strain 2362. Appl.

Environ. Microbiol., 67(11): 5049–5054.
Ohgushi A, Saitoh H, Wasano N, Uemori A, Ohba M (2005). Cloning and characterization of two novel genes, cry24B and s1orf2, from a mosquitocidal strain of *Bacillus thuringiensis* serovar *sotto*. Curr. Microbiol., 51(2): 131-136.
Park H-W, Bideshi DK, Federici BA (2005a). Synthesis of additional endotoxins in *Bacillus thuringiensis* subsp. *morrisoni* PG-14 and *Bacillus thuringiensis* subsp. *jegathesan* significantly improves their mosquitocidal efficacy. J. Med. Entomol., 42: 337-341.
Park HW, Bideshi DK, Wirth MC, Johnson JJ, Walton WE, Federici BA (2005b). Recombinant larvicidal bacteria with markedly improved efficacy against *Culex* vectors of West Nile virus. Am. J. Trop. Med. Hyg., 72: 732-738.
Pimentel D, Burgess M (1985). Effects of single versus combinations of insecticides on the development of resistance. Environ. Entomol., 14: 582-589.
Poncet S, Bernard C, Dervyn E, Cayley J, Klier A, Rapoport G (1997). Improvement of *Bacillus sphaericus* toxicity against dipteran larvae by integration, via homologous recombination, of the Cry11A toxin gene from *Bacillus thuringiensis* subsp. *israelensis*. Appl. Environ. Microbiol., 63: 4413-4420.
Poopathi S, Muthukrishnan J, Baskaran G (1997). Synergism by azadirachtin based biopesticide to *B.sphaericus* resistant field population of *Culex quinquefasciatus* larvae (Diptera: Culicidae)-An approach for management of resistance. 3rd Sym. Vectors and Vector-borne diseases, Bhubaneshwar, India., pp. 72-77.
Poopathi S, Mani TR, Rao DR, Baskaran G, Kabilan L (1999). Cross-resistance to *Bacillus sphaericus* strains in *Culex quinquefasciatus* resistant to *B. sphaericus* 1593M. Southeast Asian J. Trop. Med. Public Health., 30(3): 477-481.
Poopathi S, Mani TR, Raghunatha RD, Baskaran G, Kabilan L (1999a). Evaluation of synergistic interaction between *Bacillus sphaericus* and *Bacillus thuringiensis* var *israelensis* against *Culex quinquefasciatus* resistant and susceptible to *B.sphaericus* 1593M. J. Ecobiol., 11: 289-298.
Poopathi S, Mani TR, Raghunatha RD, Baskaran G, Kabilan L (1999b). Cross-resistance to *Bacillus sphaericus* strains in *Culex quinquefasciatus* resistance to *B.sphaericus* 1593M. South East Asian J. Trop. Med. Publ. Health, 30: 477-481.
Poopathi S, Raghunatha RD, Mani TR, Baskaran G, Kabilan L (1999c). An approach to evaluate the stability of resistance in *Culex quinquefasciatus* after a five year selection process with *Bacillus sphaericus* 1593M spore toxin. Trop. Biomed., 16: 15-23.
Poopathi S, Mani TR, Raghunatha RD, Baskaran G, Kabilan L (1999d). Effect of *Bacillus sphaericus* and *Bacillus thuringiensis* var israelensis on the ultrastructural changes in the midgut of *Culex quinquefasciatus* Say (Diptera: Culicidae). J. Ent. Res., 23: 347-357.
Poopathi S, Kabilan L, Mani TR, Raghunatha RD, Baskaran G (1999e). A comparative ultrastructural studies on the midgut of *Bacillus sphaericus* resistant and susceptible *Culex quinquefasciatus* say. Insect Environ., 5: 129-130.
Poopathi S, Raghunatha RD, Mani TR, Baskaran G, Kabilan L (2000a). Susceptibilty levels of resistance of *Culex quinquefasciatus* to the insecticidal toxin of *Bacillus sphaericus* (strain 2362). Environ. Ecol., 18(3):703-710.
Poopathi S, Kabilan L, Mani TR, Raghunatha RD, Baskaran G (2000b). Observation of low tolerance to *Bacillus thuringiensis* var *israelensis* in *Culex quinquefasciatus* resistant to *Bacillus sphaericus*. Entomology, 25(3): 201-208.
Poopathi S, Mani TR, Raghunatha RD, Baskaran G, Kabilan L (2000c). A need to study ultrastructural changes in the tissues of *Culex quinquefasciatus* resistant to *Bacillus sphaericus*. Entomology, 25(3): 201-208.
Poopathi S, Mani TR, Raghunatha RD, Baskaran G, Kabilan L (2002). Evaluation of synergistic interaction between *Bacillus sphaericus* and a neem based biopesticide against *Culex quinquefasciatus* larvae susceptible to *Bacillus sphaericus*. 1593M. Insect Sci. Appl., (Kenya), 22: 303-306.
Poopathi S, Tyagi BK (2002). Studies on *Bacillus sphaericus* toxicity-related resistance development and biology in the filariasis vector, *Culex quinquefasciatus* (Diptera: Culicidae) from South India. Appl. Entomol. Zool., 37(3): 365-371.
Poopathi S, Tyagi BK (2004). Review: Mosquitocidal toxins of spore forming bacteria: recent advancement. Afr. J. Biotechnol., 3(12): 643-650.
Rao DR, Mani TR, Rajendran R, Joseph ASJ, Gajanana A, Reuben R (1995). Development of a high level of resistance to *Bacillus sphaericus* in a field population of *Culex quinquefasciatus* from Kochi, India. J. Am. Mosq. Contr. Assoc., 11: 1-5.
Rodcharoen J, Mulla S (1994). Resistance development in *Culex quinquefasciatus* (Diptera: Culicidae) to microbial agent *Bacillus sphaericus*. J. Econ. Entomol., 87: 1133-1140.
Romão TP, de Melo, Chalegre KD, Key S, Ayres CF, Fontes de Oliveira CM, de-Melo-Neto OP, Silva-Filha MH (2006). A second independent resistance mechanism to *Bacillus sphaericus* binary toxin targets its alpha-glucosidase receptor in *Culex quinquefasciatus* FEBS J., 273(7): 1556-1568.
Sachs J, Malaney P (2002). The economic and social burden of malaria Nature, 11; 416(6881):581.
Saitoh H, Hwang SH, Park YS, Higuchi K, Mizuki E, Ohba M (2000). Cloning and characterization of a *Bacillus thuringiensis* serovar gene encoding a novel class of the delta-endotoxin protein, Cry27A, specifically active on the Anopheles mosquito. Syst. Appl. Microbiol., 23(1): 25-30.
Sharma VP (1999). Fighting malaria in India. Ind. J. Med. Res., 75: 1127-1140.
Silva-Filha M-H, Regis L, Nielsen-LeRoux C, Charles J-F (1995). Low level resistance to *Bacillus sphaericus* in a field-treated population of *Culex quinquefasciatus* (Diptera: Culicidae). J. Econ. Entomol., 88: 525-530.
Silva-Filha MH, Nielsen-LeRoux C, Charles J-F (1997). Binding kinetics of *Bacillus sphaericus* binary toxin to midgut brush-border membranes of *Anopheles* and *Culex* sp. mosquito larvae. Eur. J. Biochem., 247(3): 754-761.
Silva-Filha MH, Nielsen-LeRoux C, Charles J-F (1999). Identification of the receptor for *Bacillus sphaericus* crystal toxin in the brush border membrane of the mosquito *Culex pipiens* (Diptera: Culicidae). Insect Biochem. Mol. Biol., 29: 711-721.
Sinègre G, Babinot M, Quermei JM, Gaven B (1994). Abstr. 8th Eur. Meet. Soc. Vector Ecol., p. 17.
Singer S (1997). Isolation and development of bacterial pathogens in vectors, in Biological regulation of vectors. DHEW Publ. No. (NIH) 77-1180. Bethesda, MD:NIH. pp. 3-18.
Singh GJP, Gill SS (1988). An electron microscope study of the toxic action of *Bacillus sphaericus* in *Culex quinquefasciatus* larvae. J. Invertebr. Pathol., 52: 237-247.
Snow RW, Guerra CA, Noor AM, Myint HY, Hay SI (2005). The global distribution of episodes of *Plasmodium falciparum* malaria. Nature ,434: 214-217.
Soberón M, Fernández LE, Pérez C, Gill SS, Bravo A (2007). Mode of action of mosquitocidal *Bacillus thuringiensis* toxins. Toxicon., 49(5): 597-600.
Su T, Mulla MS (2004). Documentation of high-level *Bacillus sphaericus* 2362 resistance in field populations of *Culex quinquefasciatus* breeding in polluted water in Thailand. J. Am. Mosq. Control Assoc., 20 (4):405-11.
Tabashnik BE, Liu Y-B, Malvar T, Heckel DG, Masson L, Ballester V, Granero F, Mensua JL, Ferre J (1997). Global variation in the genetic and biochemical basis of diamondback moth resistance to *Bacillus thuringiensis*. Proc. Natl. Acad. Sci. USA, 94: 12780-12785.
Thiery I, Frachon E (1997). Identification, isolation, culture and prevention of entomopathogenic bacteria, in Manual Tech. Insect Pathol. Academic press limited, London, New York, pp. 55-57.
Van Rie J, Van Mellaert H, Peferoen M (1992). Mechanism of insect resistance to *Bacillus thuringiensis* in *Plodia interpunctella* and *Plutella xylostella*. In: Molecular mechanisms of insecticide resistance: diversity among insects, Mullin, C. A. and Scott, J. G., Eds., American Chemical Society, Washington, DC.
Wearing CH, Hokkanen HMT (1995). Pest resistance to *Bacillus thuringiensis*: ecological crop assessment for *Bt* gene incorporation and strategies of management. In: Biological control: benefits and risks, Hokkanen, H. M. T. and Lynch, J. M., Eds., Cambridge University Press, Cambridge, UK, pp. 236-252.
Wei S, Cai Q, Yuan Z (2006). Mosquitocidal toxin from *Bacillus*

sphaericus induces stronger delayed effects than binary toxin on *Culex quinquefasciatus* (Diptera: Culicidae) J. Med. Entomol., 43(4): 726-730.
Wei S, Cai Q, Cai Y, Yuan Z (2007). Lack of cross-resistance to Mtx1 from *Bacillus sphaericus* in *B. sphaericus*-resistant *Culex quinquefasciatus* (Diptera: Culicidae). Pest. Manag. Sci., 63(2):190-3.
Wirth MC, Georghiou GP, Federici BA (1997). CytA enables CryIV endotoxins of *Bacillus thuringiensis* to overcome high levels of CryIV resistance in the mosquito, *Culex quinquefasciatus*. Proc. Natl. Acad. Sci. USA 94: 10536-10540.
Wirth MC, Delécluse A, Federici BA, Walton WE (1998). Variable cross-resistance to Cry11B from *Bacillus thuringiensis* subsp. *jegathesan* in *Culex quinquefasciatus* (Diptera: Culicidae) resistant to single or multiple toxins of *Bacillus thuringiensis* subsp. *israelensis*. Appl. Environ. Microbiol., 64(11): 4174-4179.
Wirth MC, Georghiou GP, Malik JI, Abro GH (2000a). Laboratory selection for resistance to *Bacillus sphaericus* in *Culex quinquefasciatus* (Diptera: Culicidae) from California, USA. J. Med. Entomol., 37(4): 534-540.
Wirth MC, Walton WE, Federici BA (2000b). Cyt1A from *Bacillus thuringiensis* restores toxicity of *Bacillus sphaericus* against resistant *Culex quinquefasciatus* (Diptera: Culicidae) J. Med. Entomol., 37(3):401-407.
Wirth MC, Delécluse A, Walton WE (2003). Cyt1Ab1 and Cyt2Ba1 from *Bacillus thuringiensis* subsp. *medellin* and *B. thuringiensis* subsp. *israelensis* Synergize *Bacillus sphaericus* against *Aedes aegypti* and Resistant *Culex quinquefasciatus* (Diptera: Culicidae) J. Am. Mosq. Control Assoc., 9(1) 39-46
Wirth MC, Jiannino JA, Federici BA, Walton WE (2004). Synergy between toxins of *Bacillus thuringiensis* subsp. *israelensis* and *Bacillus sphaericus*. J. Med. Entomol., 41(5): 935-941.
Wirth MC, Park HW, Walton WE, Federici BA (2005). Cyt1A of *Bacillus thuringiensis* delays evolution of resistance to Cry11A in the mosquito *Culex quinquefasciatus*. Appl. Environ. Microbiol., 71(1):185-189.
Wirth MC, Jiannino JA, Federici BA Walton WE (2005). Evolution of resistance toward *Bacillus sphaericus* or a mixture of *B.sphaericus*+Cyt1A from *Bacillus thuringiensis*, in the mosquito, *Culex quinquefasciatus* (Diptera: Culicidae). J. Invertebr. Pathol., 88(2): 154-162.
Wirth MC, Zaritsky A, Ben-Dov E, Manasherob R, Khasdan V, Boussiba S, Walton WE (2007). Cross-resistance spectra of *Culex quinquefasciatus* resistant to mosquitocidal toxins of *Bacillus thuringiensis* towards recombinant *Escherichia coli* expressing genes from *B. thuringiensis* ssp. *israelensis*. Environ. Microbiol., 9(6): 1393-1401.
Whalon ME, McGaughey WH (1998). *Bacillus thuringiensis*: Use and Resistance management. In: Insecticides with novel modes of action: mechanism and application, Ishaaya, I. and Degheele, D., Eds., Springer, Berlin, pp. 106-137.
Wood RJ (1981). Strategies for conserving susceptibility to insecticides. Parasitology, 82: 69-80.
Yuan ZM, Pei GF, Regis L, Nielsen LC, Cai QX (2003). Cross-resistance between strains of *Bacillus sphaericus* but not *B. thuringiensis israelensis* in colonies of the mosquito *Culex quinquefasciatus*. Med. Vet. Entomol., 17(3): 251-256.
Zhang B, Liu M, Yang Y, Yuan Z (2006). Cytolytic toxin Cyt1Aa of *Bacillus thuringiensis* synergizes the mosquitocidal toxin Mtx1 of *Bacillus sphaericus*. Biosci. Biotechnol. Biochem., 70(9): 2199-2204.