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Vegetative Insecticidal Protein (VIP): Next Generation Pest Killers

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Bacillus thuringiensis (Bt) is an aerobic, gram-positive, entomopathogenic bacterium which is indigenous to various environments having most advantageous growth temperature. Globally, the different strains of this bacteria have been isolated from a variety of environments. Therefore, an opportunist pathogen is the best explanation for this ubiquitous bacteria with its unknown ecology. Identification of Bt is done by the presence of one or more parasporal bodies (recognized as the crystal), observable within the sporangia on a phase-contrast microscope. Biopesticides prepared from this bacterium have become a vital part of insect pest management strategies and is also utilized as a source of cry genes for plant genetic engineering to create transgenic crops with diverse harmful insect pest resistance.

It is also utilized as a nematicide. In addition to Cry and Cyt toxins, Bt strains can also produce other insecticidal proteins known as vip, during the vegetative growth phase, which are not alike with cry proteins in structure and sequence according to many researchers and as such considered these as a tremendous complement or supplement source of Cry toxins in resistance management and protection of the crops.

Commercially various Bt-crops has been developed by combining Vip3 and Cry proteins. For the effective management of resistance development in target insects, pyramiding of toxic proteins has been carried out.

To date, 15 Vip1 proteins, 20 vip 2 proteins,111 vip 3 proteins and 5 vip 4 proteins has been reported and named. Vip 1 and Vip 2 heterodimer toxins are effective against coleopteran and Hemipteran orders. Vip3 being the largest family, is effective against many species of Lepidoptera, and crops like cotton and maize. Structure and function of vip proteins:

Vip proteins are also inactive in their native form, and are activated after being secreted in the membranes of insect midgut cells through the action of enzymes just like other Bt toxins. Vip1 and Vip2 function as binary toxins with an active ADP ribosyl transferase. The genes of the Vip1 and Vip2 proteins possess different reading frames. Vip1 is produced as a 100 kDa protoxin with a 35 amino acid N terminal signal peptide sequence, according to sequence analyses. Vip2 proteins have an N-terminal signal peptide of 50 amino acids and are 52 kDa in size when they are in protoxin form. Vip1 and Vip2 are changed into mature proteins of 80 kDa and 45 kDa, respectively, after undergoing alteration at the N terminal signal peptide. Two domains, a NAD-binding (nicotinamide adenine dinucleotide) C-terminal (Ct) domain and an N-terminal (Nt) domain, have been validated by Vip2's structural analysis. Moreover, X-ray crystallography revealed similarities between the N and C terminal domains of the Vip2 protein, and both domains are formed by the perpendicular packing of

five mixed sheets, with one flanking helix and three anti parallel sheets with three flanking helices.

The most extensively researched Vip toxin to yet, Vip3A, has been shown to strongly impede insect larval growth at low concentrations, and the structural variations among Vip3 members promise a broader mechanism of action against a variety of insects.Least amount of research has been reported for vip4 toxin The original Vip4 toxin, Vip4Aa1 (now known as Vpb4Aa1), was isolated from the Bt strain Sbt009 and had any insecticidal properties.

Future Perspectives

For Bt toxins to continue to be effective in pest control, it is essential to have a thorough understanding of how they work and how insects resist them. Development of novel toxins and the use of several pest control methods are essential for the management of pest. Because of their broad spectrum of insect targets, Vip toxins are a promising new generation of insecticides to be used in spray formulation and transgenic crops. The structure and function of VIP proteins are the subject of research, and new VIP proteins are being sought after from both known and unidentified Bt strains. To combat Bt toxin resistance, one method that might be used is to find new proteins. Next generation sequencing (NGS) can accelerate the discovery of novel proteins through the complete sequencing of novel genomes and already known Bt strains.