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Advancement of Molecular and Genetic Techniques in Insect Pest Management

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Introduction

Global population expansion, resource depletion, climate change, and developing pests are just a few of the many factors that have a significant impact on agricultural productivity and output. Pests are known to reduce crop output by 25–50% or entirely due to biotic limitations, in particular. The destruction of insect pests causes significant losses in important crops. According to a recent FAO estimate from the United Nations, invasive pests cost at least $70 billion annually. One of the main factors in the decline of biodiversity is invasive pests, which also pose a risk to the biosecurity of plants. A fresh wave of interest in finding alternatives to chemical pesticides for managing agricultural pests has also been sparked by growing awareness of the environmental effects of their indiscriminate usage. One such idea that has gained a lot of attention is integrated pest management (IPM), which places an emphasis on the development of a healthy crop with the least interruption to the agroecosystems. Through the integration of the many elements of pest management strategies, it promotes natural pest control and works to reduce the usage of risky chemicals.

The advent of genomic era:

The effective application of contemporary biotechnological tools in various IPM components has become increasingly important in recent years due to advancements in science and technology. The efficiency of a pest control approach is influenced by a variety of factors. For crop pest management, a variety of plant protection strategies are being used, however it is now essential to apply the most effective current biotechnological tools. Understanding entomological issues requires knowledge of genetics and molecular biology. It is now thought that informational molecules like nucleic acids and proteins contain a high level of taxonomic information, pointing to the growing popularity of molecular approaches to systematics. The application of biotechnology in plant protection can be broadly divided into two categories namely characterization of pests and management of pests which made significant advances and has a huge influence on IPM.

Insect Genomics:

For a better understanding of biology and to identify desirable genes of pest species large numbers of insect genomes have been wholly sequenced in the last decades viz. *Henosepilachna pusillanima* (Mulsant), *Pseudonemorphus versteegi* (Ritsema), *Aristobia reticulator* (Voet), *Bactrocera zonata* (Saunders), *Samia canningi* (Hutton), etc. Such sequence information serves as a tool for development of molecular markers. The genomic analysis led to the identification of genes related to its specific behaviour. Similarly, the genome of flower thrips, Thrips hawaiiensis (Morgan) has been sequenced and characterized by using the next-generation sequencing technique. It is the common thysanopteran insect distributed widely in Asia and the Pacific with varied morphology. The complete mitochondrial genome sequence provided the information for mitochondrial genome research on Thysanoptera (Wang *et al*., 2021). Apart from nucleic acid based information, there is fast-growing information coming from proteomics and metabolomics studies too. Additionally, different molecular markers are being used to investigate the variety of pest species populations. For instance, amplified fragment length polymorphism (AFLP) markers were employed to examine the richness of rice gall midge populations throughout Asia. Sequence analysis has also been used to distinguish genetic diversity in potential pests including *Plutella xylostella* and *Pectinophora gossypiella*. The ability to identify the variables causing populations of crop pests to react differently to different selection pressures (insecticides, pheromones, parasitoids, etc.) is made possible by having a thorough grasp of the variety among their populations.

Insect taxonomy:

The most critical issue on a global scale is the accurate identification of pest species, which serves as the foundation for all research and efficient management programme implementation. In the past, taxonomy and descriptions of species were solely dependent on morphology. As a result, a number of negative effects took place, misidentification being one of them. The scarcity of taxonomists, the time-consuming nature of the work, the difficulty of taxonomically complex orders, and the need for contemporary taxonomic keys for the updated taxa are additional major issues in taxonomic study. In order to differentiate between species, a small region of the mitochondrial genome called the cytochrome c oxidase subunit or COI gene is used to identify the species of an individual organism using DNA-based identification, which has now gained widespread acceptance as a transformative technology (Hebert *et al*., 2003). In the current agricultural scenario, invasive insect pests are of enormous socioeconomic and ecological concern due to their rapid global expansion. The use of genetic methods in addition to conventional taxonomical instruments allows researchers to quickly identify a number of invasive pests and develop prompt control measures. Understanding a person's genetic makeup is made easier by the use of molecular and genomic techniques. Additionally, the increasing accessibility of genomic techniques is beneficial for the application of alternate approaches to controlling invasive insect pests and also aids in understanding the pest demography and reconstructing the invasion routes.

Development of resistant crop varieties:

The concept of the genetic manipulation technique in the field of crop protection has been completely transformed by the transgenic Bacillus thuringiensis (*Bt*). Insecticide use significantly decreased after the *Bt* technology was introduced, providing significant advantages. Later on, however, issues with additional pests and viral diseases appeared in cotton, and pest emergence (crop sensitivity to sucking bugs) increased. In order to combat pest resistance, the government promoted the development of non-*Bt* cotton in 2016 by introducing the refuge in bag (RIB) concept. In order to ensure that the management solutions for biotic stress are implemented as soon as possible, *Bt* cotton is currently under close observation by all technical stakeholders. Recently, a synthetic vip3A gene for transgenic cotton has been created and tested against eating insect pests. Successful vip3A transgenic incorporation into the plant nuclear genome was discovered using PCR amplification and southern hybridization. The synthetic vip3A gene has demonstrated excellent promise for inclusion in the list of promising genes that can be utilised to create insect-resistant transgenic plants thanks to its improved insecticidal expression. On the other hand, durability is a key restriction in the host plant resistance programme. The emergence of pathogenic biotypes of the insect frequently overcomes the single gene-based resistance. By using molecular markers to create improved crop types, this issue will be successfully solved.

Improvement in biocontrol programmes

An environmentally beneficial, technically practicable, and financially viable approach to pest management is biological control. The effectiveness of natural enemies against the pest population has been improved by the adaptation of a number of technologies. Through artificial selection and hybridization, significant progress has been made in the creation of pesticide- and temperature-resistant strains of natural enemies including *Chrysoperla zastrowi arabica* and *Trichogramma chilonis* (Ishii). However, developments in molecular science have expanded the methods that can be used to genetically modify arthropods for a range of traits of the species, including improved climatic tolerance, improved host finding ability, host preference, pesticide and disease resistance, non-diapause, high fecundity, and female-biasness. The cutting-edge strategy also makes it possible for the emergence of entomopathogenic microorganisms with hypervirulent strains. For instance, the genes that code for the neurotoxin in the *Androctonus australis* (Hector) and *Atrax robustus* have been engineered into the baculoviruses *Ac*NPV (specific for *Autographa californica* Speyer) and *Ha*NPV (specific for *Helicoverpa armigera* Hübner), respectively, to increase the effectiveness of entomopathogenic viruses.

Conclusion

The use of biotechnological methods to manage pests has enormous potential, and by using these methods successfully, pesticide use has decreased, and they are also safe for the environment. However, there is much discussion about the environmental dangers of using such technology, including threats to human health, gene pool dilution, and gene flow to closely related wild cousins. Such impacts, though, have not yet been conclusively confirmed by science. To gain the greatest benefits in pest management, it is equally crucial to communicate the advantages of biotechnology technologies and products to the general public and farming community in a balanced way.

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