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Genomic Study of Insecticide Resistance in Rice Brown Planthopper, Nilaparvata lugens (Stål) (Delphacidae: Hemiptera) in Rice

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ABSTRACT

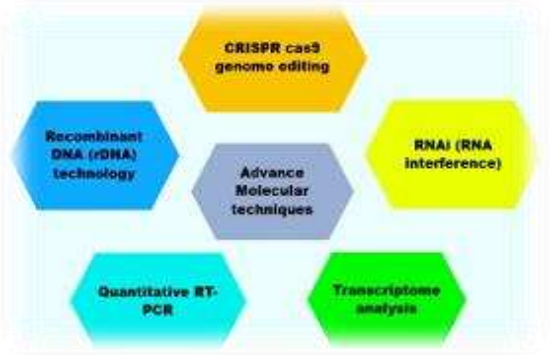
Insecticide resistance is the mechanism of detoxification of synthetic chemical insecticide through various methods that involve several detoxifying enzymes as well as metabolic pathways, which are directly controlled by the over-expression of some resistant genes expressed at specific loci at the insect chromosomes. The resistance can be broken by extraction or modification of that gene involved, which in turn changes the expression pattern of several xenobiotic compounds inside the insect body. This review article comprises several resistant genes involved in insecticide resistance in rice brown planthopper (BPH), Nilaparvata lugens (Stål), along with molecular methods involving genetic alteration of resistant genes involved in resistance.

INTRODUCTION

Metabolic resistance is the most prevalent type of pesticide resistance mechanism, although there are other features as well (Bass *et al*., 2015). The significant harm that BPH does to rice and the growing issue of pesticide resistance make the resistance mechanism to pesticides a major worry (Liao *et al*., 2018). Furthermore, resistance to a range of insecticides has also been linked to the overproduction of detoxification enzymes through the activation of resistant gene transcription (Wang *et al*., 2015). Deciphering the role of molecular mechanisms underlying

N. lugens's insecticide resistance is crucial for creating effective pest management strategies, as the fast evolution of insecticide resistance poses a serious threat to the successful and sustainable use of chemical pesticides.

Advanced technology available for genomic characterization: Many advanced molecular technologies have been developed through the passing years for detailed genomic study in several insects. Some of the recent and advanced technologies are as follows;



Steps involved in resistant gene identification:

Large complex gene families, including those involved in detoxification, are easier to investigate thanks to the quick development of genomics and post-genomic technology. The general procedures for employing mRNA isolation, cDNA synthesis, and qRT-PCR to identify resistance genes (Elzaki *et al*., 2016);

RNA isolation from insecticide-resistant BPH nymphs

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Quality and quantity measurement of RNA by using a Nano-Drop spectrophotometer

↓

Gel Electrophoresis of mRNA with EDBR after measurements

↓

Some RNA of each sample is reverse transcribed to form cDNA

↓

Quantitative RT-PCR performed with the resistant and susceptible strains

↓

Expression-confirmed detoxification unigenes are selected using qRT-PCR

Molecular characterization of insecticide resistance in BPH:

P450 mix-function Oxidases (encoded by *CYP* genes) constitute a multigenic superfamily of enzymes, known for their major ability for xenobiotic detoxification (Feyereisen, 2005). It has been identified in several studies that the insecticide resistance in BPH, *Nilaparvata lugens* (Stål), has been characterized through the identification of some resistant genes, whose over-expression is the main cause of functional and structural changes of the detoxifying enzymes in the insect body (Wen *et al*., 2009).

- Studies have demonstrated that two CarE genes are responsive to exposure to chlorpyrifos and that their up-regulated expression contributes to chlorpyrifos resistance in BPH. Resistance to malathion is commonly attained by the amplification of the CarE gene *NlEST1* (Lu *et al*., 2017).

- To study the inheritance, potential resistance mechanisms, and potential fitness costs, a dinotefuran-resistant (Din-R) strain of *N. lugens* was chosen. RNA interference (RNAi)-mediated suppression of *NlCYP6ER1*, *NlCYP6CS1*, and *NlCYP314A1* expression increased *N. lugens* susceptibility to dinotefuran (Zhang *et al*., 2023).

- Using quantitative real-time PCR and insecticide exposure, researchers found that the resistance of brown planthoppers, *Nilaparvata lugens*, was mostly linked to the cytochrome P450 gene *CYP6AY1*. This gene is known to metabolize imidacloprid, but it is unclear how it affects buprofezin (Pang *et al*., 2014).

- A comparison of the transcriptomic analysis of buprofezin-R (BPR) and the Sus strain of BPH showed that 1110

genes, including 13 cytochrome P450 genes, were upregulated in the BPR strain relative to the Sus strain. Four of the P450 genes, CYP6ER1vA, CYP6CW1, CYP4C77, and CYP439A1, were found to be significantly overexpressed in both the BRP and YC2017 strains when compared to the Sus strain (Zeng *et al*., 2023).

- 4 UGT genes—UGT386H2, UGT386J2, UGT386N2, and UGT386P1, out of the 20 discovered UGT genes were found to be highly overexpressed in the resistant strain and are efficiently triggered by chlorpyrifos. The resistant strain became much more susceptible to chlorpyrifos after UGT386H2 or UGT386P1 was knocked down using RNA interference technology (Yang *et al*., 2023).

Table: Some identified important resistant genes from *Nilaparvata lugens* (Stål) in rice

Sl. No	Resistance Genes	Molecular Technology	Insecticides	References
1	*CYP4CE3* and *CYPSF01*	RNAi	Triflumezopyrim	Gong *et al.* (2022)
2	*CarE3*, *CarE17* and *CarE19*	RNAi	Chlorpyrifos	Lu *et al.* (2022)
3	*nlgst1-1*	cDNA synthesis, and qRT-PCR	Synthetic pyrethroids	Vontas *et al.* (2002)
4	*CYP417A2* and *CYP417A2v2*	RNAi	Triflumezopyrim	Gong *et al.* (2022)
5	CYP4C71v2, CYP4C72, CYP6AY3v2 and CYP353D1v2	cDNA synthesis, and qRT-PCR	Imidacloprid	Elzaki *et al.* (2022)
6	*NlABCA1, NlABCB8, NlABCC3, NlABCG8* and *NlABCG12*	Nucleotide polymorphism and Phylogenetic analysis	Nitenpyram, clothianidin chlorpyrifos, Etofenprox, and Isoprocarb	Li *et al.* (2020)
7	*CYP6CS1*	Transcriptome analysis and RNAi	Pymetrozine	Wang *et al.* (2021)

CONCLUSION:

Insecticide-resistant genes are confirmed to exist in BPH by metabolic analysis of the insect body. These genes control the genomic expression of specific resistance features that are made available by xenobiotic detoxification via specific genes. Therefore, by using different genome editing techniques, these genes can be changed or eliminated, making the insect body more vulnerable to certain insecticides. To determine whether resistance-related genes may be selected stably early in the development of resistance, which may be crucial for resistance prediction, more research on these genes needs to be done.

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Certificate of Publication

This is to certify that ***Satyabrata Sarangi*** has published a popular article entitled ***Genomic Study of Insecticide Resistance in Rice Brown Planthopper, Nilaparvata lugens (Stål) (Delphacidae: Hemiptera) in Rice*** in Vigyan Varta: An International E-Magazine for Science Enthusiasts, Volume 5 Issue 4, Page No. 244-244, 2024.

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