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Breeding for Brown Plant Hopper Resistance in Rice

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Rice is an important staple food crop for more than half of the world's population. India ranks world's second-largest producer of rice with output reaching 150.18 million tons during the agricultural year 2024-25. However, rice production is frequently affected by various biotic and abiotic stresses, causing a huge loss in both quantity and quality (Kesh and Kaushik, 2020). Among the biotic stresses, brown plant hopper (*Nilaparvata lugens*) is the most devastating pest of rice accounting up to 80% yield loss and in terms of value around $300 million annually in Asia. The insect feeds directly on the growing plants causing a serious damage to crop by sucking sap from xylem and phloem tissues with a modified mouthpart called stylet. Both nymphs and adults infest the crop and cause heavy losses. As insect consumes plant sap, rapid yellowing and drying take place which eventually causes plant death and ultimately leads to "hopper burn". Brown plant hopper (BPH) also acts as vector for many viruses such as grassy stunt virus rice, wilted stunt virus and ragged stunt virus, which can further reduce yield. Globally four biotypes of BPH have been categorized, the biotypes 1 and 2 are more common in East and Southeast Asia, biotype 3 was originated under a laboratory condition and biotype 4 is common in South Asia, particularly in the Indian subcontinent. Apart from these, biotypes 5, 6, and 7 were reported in the Chaing Rai province of Thailand nation. In the course of time, new virulent biotypes may evolve, which can overcome the existing resistant gene. Chemical control of the pest is expensive and hazardous to humans and environment. It kills natural predators and ultimately develops insecticide resistant BPH biotypes (Tanaka et al, 2000). While resistant varieties offer durable resistance to the pest and consistent yield benefits to the farmers. Hence, host-plant resistance is the most economic, effective and eco-friendly approach to manage the BPH (Jena and Kim, 2010).

BPH resistant genes

The first BPH resistant gene was discovered in 1967 followed by identification of two genes *Bph1* in Mudgo and *bph2* in ASD7 that provide resistance to BPH (Athwal et al 1971). The rice cultivar IR 36 harbouring Bph 1 gene became susceptible, so a new recessive gene bph 2 was introgressed into it. Another line IR 36 with bph 2, a widely grown cultivar exerts tremendous pressure on the existing biotypes (Jena and Kim, 2010). As a consequence, a new biotype BPH biotype (biotype 3) evolved. Subsequently resistance loci, *Bph3* and *bph4* were identified in two Sri Lankan varieties, *i.e.* Rathu Heenati and Babawee, respectively and were introgressed into many high yielding rice cultivars including IR56, IR60, IR66, IR68, IR70, IR72 and IR74. Later a new biotype 4 was identified which could feed on all those elite rice varieties having Bph3 and bph4. Khush et al (1985) identified a single recessive gene *bph5* conveying resistance to BPH biotype 4 in rice cultivar ARC10550, which segregated independently of *Bph1, bph2, Bph3* and *bph4*. In total, around 40 BPH resistance genes have been identified in rice (Akanksha et al., 2019), of which 20 genes (Bph1-9, Bph17, Bph19, Bph25-26, Bph28, Bph30- 33 and Bph37-38) have been identified in indica varieties (Balachiranjeevi et al., 2019) and other 20 (Bph10-16, Bph18, Bph20- 24, Bph27, bph29,

Bph34-36 and bph39-40) are from wild species of rice (Zhang et al., 2020). Such a rich diversity in sources of resistance in rice may be due to a long-time interaction and co-evolution between rice and variable BPH populations (Zhao et al., 2016). Recently, varieties possessing the Bph14 and Bph15 genes have been developed through marker-assisted breeding to achieve durable and stable BPH resistance (Wang et al., 2016).

Breeding Methods

In response to damage caused by BPH, several resistant varieties were developed based on identification and incorporation of resistant genes. For example, BPH resistant varieties, IR 26 and IR 36 developed by International Rice Research Institute, Philippines during 1970s. However, resistance of these verities was quickly broken down within a few years of cultivation due to evolution of new BPH biotypes (Ye et al., 2024). Molecular breeding is considered a rapid and efficient approach for introgression of resistant genes, as traditional breeding methods are generally time- and labour- consuming especially when transferring multiple genes. Marker-assisted backcross programme is used to transfer the resistance gene BPH18 from IR65482-7-216-1-2 into Junambyeo, leads to the development of improved lines possessing higher resistance to concerned biotype and excellent grain quality (Suh et al, 2011). The introgression of BPH 31 gene into an indica rice variety Jaya, significantly improves the resistance to different BPH biotypes (Prahalada et al, 2017). However, the introduction of a single resistant gene into an elite rice genotype through marker assisted breeding generally results in resistance breakdown shortly, as the pertinent pathogen evolves and develops resistance to the gene's effects. While, the incorporation of two to three or multiple resistance genes provides comprehensive resistance against a wide array of races through cooperative and complementary gene actions. To address the problem of rapid breakdown of resistance, gene pyramiding strategy of resistance genes is recommended for the development of rice varieties. Pyramiding of major QTLs provides long lasting and broad-spectrum resistance to all accessible biotypes. Many earlier studies have demonstrated the successful introgression of multiple QTLs into a single rice cultivar to confer resistance against BPH. For example, isogenic lines harbouring two resistant genes Bph14 and Bph15 genes exhibit higher resistance as compared to introgression lines containing either of the Bph14 or Bph15 genes (Hu et al, 2012). Jiang et al. (2018) used to pyramid six dominant BPH-resistance genes, Bph3, Bph14, Bph15, Bph18, Bph20 and Bph21 into an important hybrid parent Jin 23B. The line with two gene combined Bph14 and Bph15 was more resistant than lines with the respective single genes. The strategic combination of genes originated from different origins represents the most effective method to develop varieties with broad spectrum resistance.

Table 1: BPH resistant lines developed using molecular breeding approaches.

Lines developed	Breeding approach	Resistant genes	Reference
NILs HB13002-5-30-10, HB13002-5-31-24 & HB13002-50-9-7	Marker-assisted backcross breeding	Bph14 and Bph15	Wang et al., 2016
BILs 12-35-6-3, 12-35-7-16 & 12-35-13-1	Marker assisted backcross breeding	Bph20 and Bph21	Thiyagarajan et al., 2020
DB18129-34-268-38 & DB18129-34-303-6	Marker assisted backcross breeding	Pi2, Xa23, Bph14, and Bph15	Yang et al., 2022
Huahui7713 and Huahui3006	Marker assisted selection	Pigm, Bph6, Bph9	Deng et al., 2024

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