



Genetic dissection and identification of candidate genes for brown planthopper, *Nilaparvata lugens* (Delphacidae: Hemiptera) resistance in farmers' varieties of rice in Odisha

Aashish Kumar Anant^{a,b}, Govindharaj Guru-Pirasanna-Pandi^{a,*}, Mayabini Jena^a, Gajendra Chandrakar^b, Parameshwaran Chidambaranathan^a, Raghu S^a, G Basana Gowda^a, Mahendiran Annamalai^a, Naveenkumar Patil^a, Totan Adak^a, Naveenkumar Ramasamy^a, Prakash Chandra Rath^a

^a Division of Crop Protection, ICAR-National Rice Research Institute, Cuttack, 753006, India

^b Department of Entomology, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, 492012, India

ARTICLE INFO

Keywords:

Biotic stress
Novel genes
Quantitative trait loci
Rice
Resistance

ABSTRACT

Globally, rice production is severely affected by brown planthopper (*Nilaparvata lugens*) populations. Among the four different biotypes of *N. lugens* reported worldwide, biotype 4 is the most damaging and prevalent insect pest in South East Asian countries, especially in the Indian sub-continent. Management of this pest with resistant genotypes is effective and thus it has received considerable attention worldwide. In the present work, a total of 600 farmer's varieties (FVs) were screened against *N. lugens* and subsequently 104 panel populations were selected for genotyping. Marker-trait association and genetic diversity were worked out for 87 molecular markers linked to 34 different *N. lugens* resistance genes. The average content of polymorphism information was 0.354 for 34 genes with a threshold level 0.018 to 0.750. One hundred and four FVs were categorized into three main genetic groups according to cluster analysis and population structure. Resistant and moderately resistant FVs were separately distributed according to principal co-ordinate analysis. Analysis of molecular variance displayed maximum diversity (83%) within population and minimum diversity (17%) between populations. In both generalized linear model (GLM) and multi linear model (MLM), eight markers linked to *Bph* genes were found to be common for four different phenotypic parameters like honeydew excretion, nymphal survival, percent damage, and feeding mark. Our study suggests that presently available monogenic BPH resistant lines were not withstanding BPH biotype-4 pressure. Thus, the reported resistance genes either alone or in combination could be introgressed into elite varieties with genomic approach to develop robust resistant rice varieties against *N. lugens* biotype 4. Further, the identified FVs are useful for novel R genes identification, host-insect interaction, and genomic studies.

1. Introduction

Rice (*Oryza sativa* L.) is the foremost essential cereal crop, and considered as the primary staple food for more than half of the world population, especially in Asia (Fitzgerald et al., 2009). Both abiotic and biotic factors reduce rice productivity in many tropical regions (Jena et al., 2018). The brown planthopper (BPH), [*Nilaparvata lugens* (Stål.)]

(Hemiptera: Delphacidae), a monophagous phloem sucking insect, is the most devastating pest causing significant economic losses every year in tropical, sub-tropical, and temperate rice growing areas in Asia (Jena and Kim, 2010; Pandi et al., 2016). BPH populations (both nymphs and adults) sucks the phloem sap from leaves, stems, and mainly from leaf sheath, which results in yellowing, browning, drying, and wilting of the rice, termed as "hopper burn", which leads up to 70–100% yield loss

* Corresponding author. Scientist Crop Protection Division ICAR-National Rice Research Institute, Cuttack, India, 753006.

E-mail addresses: assucoolanant@gmail.com (A.K. Anant), Guru.G@icar.gov.in, guru.g@icar.gov.in (G. Guru-Pirasanna-Pandi), mayabini.jena@gmail.com (M. Jena), gchandrakarigkv@gmail.com (G. Chandrakar), Parameswaran.C@icar.gov.in (P. Chidambaranathan), s.raghu@icar.gov.in (R. S.), basanagowda.g@icar.gov.in (G. Basana Gowda), Mahendiran.Annamalai@icar.gov.in (M. Annamalai), Nb.patil@icar.gov.in (N. Patil), totan.adak@icar.gov.in (T. Adak), naveenrk005@gmail.com (N. Ramasamy), prakash.rath@icar.gov.in (P. Chandra Rath).

<https://doi.org/10.1016/j.cropro.2021.105600>

Received 13 October 2020; Received in revised form 10 February 2021; Accepted 18 February 2021

Available online 25 February 2021

0261-2194/© 2021 Elsevier Ltd. All rights reserved.