# Evaluating Genetic Variations on Brown Plant Hopper (*Nilaparvata lugens* (Stål)) Resistance Gene *Os06g0125132* of Rice for Molecular Marker Development

R.M.S.D.L. Abeyrathne[1], H.M.N.N. Herath[1], E.Y. Fernando[2], N.H.L.D.L.D. Nanayakkara[1] and D.V. Jayatilake[1]*

[1]*Department of Agricultural Biology, Faculty of Agriculture, University of Peradeniya, Peradeniya 20400, Sri Lanka*
[2]*Department of Biological Sciences, Faculty of Applied Sciences, Rajarata University of Sri Lanka, Mihinthale 50300, Sri Lanka*
**djayatilake@agri.pdn.ac.lk*

Brown plant hopper (BPH) is the most devastating insect pest of rice (*Oryza sativa* L.). Hence, cultivation of rice varieties carrying genetic resistance to BPH is the most promising approach for mitigating its damage. BPH resistance is controlled by many genes. The expression of *Os06g0125132* was found to be significantly upregulated under BPH infection and hence, a KASP marker for marker-assisted selection (MAS) was developed targeting a SNP in the intron region. Non-synonymous sequence variations in the exons that could alter the protein structure and/or its domains could be potential target sites for the development of alternative molecular markers compatible with technology-limited setups. In the current study, to identify such genetic variations, a haplotype analysis was conducted using the coding sequence of *Os06g0125132* (177bp), retrieved from 2,804 accessions sequenced in the 3K Rice Genomes Project. The extracted sequences were aligned using UGENE and four SNPs with ≥5% occurrence frequency in the rice panel were identified (three SNPs at exon 1 and one SNP at exon 2) and three confirmed haplotypes (with ≥1% occurrence frequency) were defined using DnaSP. Given all three haplotype-defining SNPs were non-synonymous, the respective putative amino acid sequences were modeled using the *ab-initio* algorithm *TrRefineRosetta* in Robetta. The modeled output suggested that all three putative proteins would fold into alpha helical structures (confidence of ≥0.8) and with no detectable 3-D structural difference. InterPro scan of the amino acid sequences detected a TMhelix, Transmembrane, Cytoplasmic and Non cytoplasmic domain each for all three putative proteins, indicating that the three identified non-synonymous SNPs had no impact on the domains. However, given the significance of *Os06g0125132* for BPH resistance, and its potential involvement in carbohydrate metabolism *via* the tricarboxylic acid cycle, further investigation is warranted to identify alternative sites for marker development targeting users in technology limited setups.

**Keywords:** Resistance to brown plant hopper, *Os06g0125132*, Haplotyping, Protein domains, Protein modeling

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