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Elucidating *R*-gene-mediated resistance to wheat dwarf virus in *Triticum aestivum* genotypes

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Abstract

Wheat dwarf virus (WDV) poses a major limitation to global cereal production, yet reliable genetic sources of resistance remain scarce. In this study, 12 genetically diverse wheat (*Triticum aestivum* L.) genotypes exhibiting differential susceptibility to WDV were evaluated under controlled inoculation conditions. Viral titre and the expression profiles of nine candidate resistance genes – representing *NBS-LRR* family, kinase family and transcription factor families – were quantified using reverse transcription quantitative polymerase chain reaction. Phenotypic parameters, including plant height and biomass, were assessed to relate molecular responses to disease severity. Statistical analysis using one-way ANOVA revealed significant genotype-dependent differences in viral accumulation and resistance gene expression. Notably, genotype VS-H 09-4/3 exhibited an approximately 80 % reduction in virus titre relative to susceptible lines, accompanied by a 2.5-fold upregulation of key *R*-genes associated with innate immune responses. In contrast, susceptible genotypes such as Ludwig displayed elevated viral loads and downregulation of these defence-related genes. Transcriptional modulation of kinase and transcription factor genes (e.g., *MYB*, *GRAS*) further supported the involvement of complex regulatory networks in WDV resistance. Collectively, these findings reveal actionable genetic markers and distinct resistance phenotypes, providing valuable resources for marker-assisted selection aimed at developing durable WDV-resistant wheat cultivars and enhancing crop resilience under changing environmental conditions.

Keywords: Expression profile, *R*-genes, resistance, WDV