

## Loss of Function of Only One of Two CPR5 Paralogs Causes Resistance Against Rice Yellow Mottle Virus

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**Abstract :** Rice yellow mottle virus (RYMV) is one of the most important diseases affecting rice in Africa. The most promising strategy to reduce yield losses is the use of highly resistant varieties. The resistance gene RYMV2 is homolog of the Arabidopsis constitutive expression of pathogenesis related protein-5 (AtCPR5) nucleoporin gene. Resistance alleles are originating from African cultivated rice *Oryza glaberrima*, rarely cultivated, and are characterized by frameshifts or early stop codons, leading to a non-functional or truncated protein. Rice possesses two paralogs of CPR5 and function of these genes are unclear. Here, we evaluated the role of the two rice candidate nucleoporin paralogs OsCPR5.1 (pathogenesis-related gene 5; RYMV2) and OsCPR5.2 by CRISPR/Cas9 genome editing. Despite striking sequence and structural similarity, only loss-of-function of OsCPR5.1 led to full resistance, while loss-of-function *oscp5.2* mutants remained susceptible. Short N-terminal deletions in OsCPR5.1 also did not lead to resistance. In contrast to *Atcpr5* mutants, neither OsCPR5.1 nor OsCPR5.2 knock out mutants showed substantial growth defects. Taken together, the candidate nucleoporin OsCPR5.1, but not its close homolog OsCPR5.2, plays a specific role for the susceptibility to RYMV, possibly by impairing the import of viral RNA or protein into the nucleus. Whereas gene introgression from *O. glaberrima* to high yielding *O. sativa* varieties is impaired by strong sterility barriers and the negative impact of linkage drag, genome editing of OsCPR5.1, while maintaining OsCPR5.2 activity, thus provides a promising strategy to generate *O. sativa* elite lines that are resistant to RYMV.

**Keywords :** CRISPR Cas9, genome editing, knock out mutant, recessive resistance, rice yellow mottle virus

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