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Elucidating the molecular and chemical responses of resistant rice to *Fusarium fujikuroi*

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The mechanisms of rice defense against *Fusarium fujikuroi* have not yet been fully clarified. In order to elucidate the factors involved in rice resistance against bakanae disease, an RNA-seq transcriptome study was performed. The molecular events that take place during the response of the resistant 'Selenio' cultivar and susceptible 'Dorella' cultivar were identified at 21 days post germination. The basic rice resistance machinery against *F. fujikuroi* involved PR genes, glucanases and peroxidases, since they were upregulated in both the resistant and susceptible cultivars. The specialized and evolved resistance mechanisms in the resistant cultivar included WRKY transcriptional factors, MAPK cascades, and some cytochrome P450 genes. These mechanisms were further confirmed by KEGG identification of Ca²⁺-dependent protein kinase gene, JASMONATE ZIM-DOMAIN-like genes, *CEBiP*, *CERK1*, and *MYC2* genes, found only in 'Selenio'. These genes participate in one of the molecular patterns: response to chitin, jasmonic acid biosynthesis, and plant hypersensitive response. When the gibberellin production was controlled, the 'Selenio' plants activated the jasmonic acid metabolic pathway. In this way, 'Selenio' maintained its bakanae-resistance level. Increased concentrations of four rice phytoalexins were only found in 'Selenio'. The greatest increase in phytoalexin biosynthesis was observed for sakuranetin and momilactone A. The fungal pathogen in the resistant cultivar acts locally, at lower concentrations, and causes a rice hypersensitive response without any further damage to the plants.

Keywords: bakanae, jasmonic acid, *Oryza sativa*, phytoalexins, RNA-seq