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Program & Abstracts



Plant-fungal interactions

Elucidating the interactions between *Fusarium fujikuroi* and rice

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Fusarium fujikuroi, causal agent of Bakanae disease, is the main seedborne pathogen on rice. Profiles of defense-related phytohormones and phytoalexins were investigated on two rice cultivars, inoculated or not with *F. fujikuroi*. In the resistant genotype Selenio, the pathogen induced high production of phytoalexins, mainly sakuranetin, and symptoms of Bakanae were not observed. On the contrary, in the susceptible genotype Dorella, the pathogen induced the production of gibberellin and abscisic acid, inhibited jasmonic acid production, phytoalexins were very low and Bakanae symptoms were observed. A RNA-seq transcriptome study was performed. 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. The fungal pathogen in the resistant cultivar acts locally, at lower concentrations, and probably it causes a rice hypersensitive response without any further damage to the plants. In order to gain insight into secondary metabolites (SM) synthesis in *F. fujikuroi*, we sequenced the genome of three Italian strains, identified the allelic variants in the genes responsible for some SM production, and compared the pathogenicity and SM production *in vitro* and on rice. *F. fujikuroi* strains can vary deeply both in the symptoms they induce and in mycotoxins production. The significance of the findings in the genomics of *F. fujikuroi* will be discussed.