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**Minoritenkloster**  
**Tulln, AUSTRIA**

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**HR-07 Elucidating Bakanae disease resistance in japonica rice**

**Davide Spadaro**<sup>1</sup>, Slavica Matic<sup>2</sup>, Ilenia Siciliano<sup>2</sup>, Paolo Bagnaresi<sup>3</sup>, Chiara Biselli<sup>3</sup>, Luigi Orrù<sup>3</sup>, Andrea Volante<sup>4</sup>, Alessandro Tondelli<sup>3</sup>, Maria Aragona<sup>5</sup>, Maria Teresa Valente<sup>5</sup>, Francesca Desiderio<sup>3</sup>, Alessandro Infantino<sup>5</sup>, Maria Lodovica Gullino<sup>1</sup>, Giampiero Valè<sup>4</sup>

<sup>1</sup> AGROINNOVA - DISAFA, University of Torino, Italy

<sup>2</sup> AGROINNOVA, University of Turin, Largo Braccini 2, 10095 Grugliasco (TO), Italy

<sup>3</sup> Council for agricultural research and economics (CREA), Genomics Research Centre, via S. Protaso, 302 I -29017, Fiorenzuola d'Arda, PC, Italy

<sup>4</sup> Council for Agricultural Research and Economics (CREA), Rice Research Unit, S.S. 11 to Torino, Km 2.5, 13100 Vercelli, Italy

<sup>5</sup> Council for Agricultural Research and Economics (CREA), Plant Pathology Research Centre, Via Bertero 22, 00156 Roma, Italy.

*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* (Siciliano et al., 2015). In the resistant genotype Selenio, the pathogen induced high production of phytoalexins, mainly sakuranetin, and symptoms of Bakanae were not observed. 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 (Matic et al., 2016). 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 Ca<sup>2+</sup>-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, 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. A germplasm collection of japonica rice was screened for *F. fujikuroi* resistance, allowing the identification of accessions with high-to-moderate levels of resistance to bakanae (Volante et al., 2017). A GWAS approach uncovered two genomic regions highly associated with the observed phenotypic variation for response to bakanae infection. A search for candidate genes with a putative role in bakanae resistance was conducted considering all the annotated genes and *F. fujikuroi*-related DEGs included in the two genomic regions highlighting several gene functions that could be involved in resistance, thus paving the way to the functional characterization of the resistance loci.

Siciliano et al 2015. J Agr Food Chem 63, 8134-8142.

Matic et al 2016. BMC Genomics 17, 608.DOI:10.2741/E806

Volante et al 2017. Rice 10, 29.DOI:0.1186/s12284-017-0168-z