

TRANSCRIPTIONAL CHANGES IN GRAPEVINE IN RESPONSE TO BOIS NOIR INFECTION

ALBERTAZZI G.*, CAFFAGNI A.*, MILC J.*, FRANZIA E.*, RONCAGLIA E.**,
FERRARI F.***, TAGLIAFICO E.***, PECCHIONI N.*

*) Department of Agricultural and Food Sciences, University of Modena and Reggio Emilia,
Via J.F. Kennedy 17/19, 42100 Reggio Emilia (Italy)

**) Department of Biomedical Sciences, University of Modena and Reggio Emilia, Via Campi 287,
41100 Modena (Italy)

***) Department of Biology, University of Padova, Via G. Colombo 3, 35131 Padova (Italy)

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Bois Noir, a yellows disease of grapevine (*Vitis Vinifera*), is caused by a non cultivable phloem-limited phytoplasma. The physiology of its pathogenesis remains still poorly understood, and very few informations exist about the interaction with the plant. To better clarify this aspect, Affymetrix GeneChip® oligonucleotide arrays have been used to identify differentially expressed genes between infected and recovered samples from 'Chardonnay' cultivar, as well as between infected and healthy samples from 'Incrocio Manzoni' cultivar.

Nested-PCR reaction was performed to evaluate the disease status of each sample collected in the experimental field, subject to natural inoculation. Incrocio Manzoni in the field conditions showed a moderate level of tolerance, both in terms of disease severity and of number of infected plants, while Chardonnay cultivar was strongly susceptible to the disease.

Results showed that expression levels of few hundred genes were altered in infected plants, with effects on various metabolic pathways.

Genes involved in photosynthesis and lipid metabolic process were exclusively suppressed in Chardonnay plants. In both Chardonnay and Incrocio Manzoni infected plants, genes involved in cellular component organization and biogenesis, protein metabolic process and nucleobase, nucleoside, nucleotide and nucleic acid metabolic process were inhibited, while carbohydrate metabolic process were strongly affected, with some genes induced and some repressed.

The present work gives a first and detailed insight into the functional genomics of the response of grapevine to the emerging yellows disease Bois Noir.