

## COMPARATIVE TRANSCRIPTOME ANALYSIS OF FOUR OLIVE CULTIVARS IN RESPONSE TO INFECTION BY XYLELLA FASTIDIOSA

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The recent outbreak of Olive Quick Decline Syndrome (OQDS) caused by the bacterium *Xylella fastidiosa* subsp. *pauca* is radically changing agriculture on the Salento peninsula in the Apulia Region, in Southern Italy. Despite great efforts, it has not yet been possible to bring the disease under control, so a better knowledge of the mechanisms of disease ethiology is needed. The main focus of this project was a comparative transcriptome analysis of four olive cultivars known for their different susceptibility to *Xylella*: Leccino and Donna Francesca as tolerant, and Oliva Rossa and Cellina as susceptible. Olive samples were grown in certified screenhouse at DiSSPA- University of Bari Aldo Moro, and for each cultivar, three replicates from healthy plants and three replicates infected with X.f. were analysed. The total RNA was extracted from leaf and petiole tissue using a commercial kit, the RNA-seq libraries were synthesized and sequenced on Illumina platform Novaseq 6000. The analysis revealed genes with differential expression in the two resistant and the two susceptible varieties. Data analysis revealed a complex pattern of gene expression with more than 800 differentially expressed genes (DEGs) including a number of defense-related genes.