

SCREENING OF OLIVE BIODIVERSITY DEFINES GENOTYPES POTENTIALLY RESISTANT TO XYLELLA FASTIDIOSA

PAVAN S.*, VERGINE M.**, NICOLÌ F.**, SABELLA E.**, APRILE A.**, NEGRO C.**
, FANELLI V.*, SAVOIA M. A.*, MONTILON V.*, SUSCA L.*, DELVENTO C.*,
LOTTI C.***, NIGRO F.*, MONTEMURRO C.*, RICCIARDI L.*, DE BELLIS L.**,
LUVISI A.**

*) Department of Soil, Plant and Food Science, University of Bari Aldo Moro, Via Amendola 165/A, 70126 Bari, Italy

**) Department of Biological and Environmental Sciences and Technologies, University of Salento, Via Prov. le Monteroni, I-73100 Lecce, Italy

***) Department of Agriculture, Food, Natural Resources and Engineering, University of Foggia, Via Napoli 25, 71100 Foggia, Italy

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The recent outbreak of the Olive Quick Decline Syndrome (OQDS), caused by *Xylella fastidiosa* subsp. *pauca* (*Xf*), is dramatically altering ecosystem services in the peninsula of Salento (Apulia Region, southeastern Italy). Here we report the accomplishment of several exploratory missions in the Salento area, resulting in the identification of thirty paucisymptomatic or asymptomatic plants in olive orchards severely affected by the OQDS. The genetic profiles of such putatively resistant plants (PRPs), assessed by a selection of ten simple sequence repeat (SSR) markers, were compared with those of 141 Mediterranean cultivars. Most (23) PRPs formed a genetic cluster (K1) with 22 Italian cultivars, including 'Leccino' and 'FS17', previously reported as resistant to *Xf*. The remaining PRPs displayed relatedness with genetically differentiated germplasm, including a cluster of Tunisian cultivars. Markedly lower colonization levels were observed in PRPs of the cluster K1 with respect to control plants. Field evaluation of four cultivars related to PRPs allowed the definition of partial resistance in the genotypes 'Frantoio' and 'Nocellara Messinese'. Some of the PRPs identified in this study might be exploited in cultivation, or as parental clones of breeding programs. In addition, our results indicate the possibility to characterize resistance to *Xf* in cultivars genetically

related to PRPs.