

TOMATO, ARBUSCULAR MYCORRHIZAL FUNGI AND GEMINIVIRUSES: PLANT HEALTH IN A TRIPARTITE INTERACTION

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Arbuscular mycorrhizal (AM) symbiosis is one of the most widespread mutualistic associations, established between soil fungi belonging to the Glomeromycota phylum and the majority of land plants. This symbiotic association is considered a natural instrument that improves the productivity and health of host plants. Several investigations have in fact demonstrated that mycorrhizal plants often show higher tolerance to abiotic and biotic stresses, i.e. attack by bacterial and fungal pathogens. However, the impact of the AM symbiosis on the infection by viral agents is still largely unknown.

The aim of this project is to study the effects, at a phenotypic and a molecular level, of the AM symbiosis on the infection by a virus. The experimental system is: the model plant *Solanum lycopersicum* (tomato), colonized by the fungal symbiont *Glomus mosseae*, an AM fungus widespread in agricultural and natural systems, and infected by Tomato yellow leaf curl Sardinia virus (TYLCSV), an economically important DNA virus of the Geminiviridae family.

To reach our goal four biological conditions were set up: control plants (C), TYLCSV-infected plants (V), mycorrhizal plants (M) and mycorrhizal plants infected by TYLCSV (MV). Tomato seedlings were initially inoculated with *G. mosseae*. After one month, when mycorrhization was well established, plants were inoculated with TYLCSV. One month after virus inoculation a tissue print assay was performed to assess virus infection, and plants were examined for biomass, mycorrhization level, viral symptoms, and sampled for DNA and RNA extraction.

Shoot and root biomass was not significantly different in any group of plants, but V plants presented a high variability. The level of mycorrhization was comparable in M and MV plants. Viral symptom severity was lower in MV plants than in V plants.

Molecular analyses are in progress to quantify viral DNA and to monitor the expression level of important genes involved in the complex tripartite interactions.

This study will allow to extend the present knowledge on the molecular bases of plant/virus/mycorrhizal fungus interactions, and to identify key genes in the host response, candidate to represent important molecular determinants of plant health.