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Muhammad Anees, Arne Tronsmo, Véronique Edel-Hermann, Linda Gordon Hjeljord, Christian Steinberg. Characterization of field isolates of Trichoderma antagonistic towards Rhizoctonia solani. IOBC Worshop "Multitrophic interactions in soil ", Jun 2009, Uppsala, Sweden. hal-02820445

HAL Id: hal-02820445 https://hal.inrae.fr/hal-02820445v1

Submitted on 6 Jun2020

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Characterization of field isolates of *Trichoderma* antagonistic towards *Rhizoctonia solani*

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Rhizoctonia solani AG 2-2 is a phytopathogenic fungus causing damping off and root rot in sugar beet. The disease occurs in the form of patches. In monoculture, these patches are highly mobile and never occur at the same place where they were observed the previous year. The soil from within patches was found more suppressive towards the disease than soil from healthy area. Comparison of the microbial genetic structures between the different soil samples suggested that *Trichoderma* spp. were involved in the increased suppressiveness.

Trichoderma spp. are well known for their antagonistic activities. The aim of the present study was to characterize sixteen *Trichoderma* isolates isolated from within and outside the patches of disease, their antagonistic abilities, and the mechanisms involved both *in vitro* and *in vivo* against *R. solani* AG 2-2. Mycoparasitism, production of soluble antibiotics, production of volatile inhibitors and induced suppressiveness were investigated.

The isolates were identified using both molecular and morphological techniques. Molecular identification was based on sequencing of the internal transcribed spacers (ITS1 and ITS2) of the ribosomal RNA gene cluster and of the long (4th) intron of the translation elongation factor 1-alpha. Morphological identification was based on microscopic measurements of the fungal structures, and their growth rates at different temperatures on different media.

It was observed that the isolates within the patches were more antagonistic than those isolated from outside the patches. Different mechanisms were evident for different strains, including direct interaction, induced suppressiveness, production of soluble antibiotics and production of volatile inhibitors. The most antagonistic strains were identified as *T. gamsii*. The antagonistic activity was not a characteristic of a species but a characteristic of a population. Finding the marker controlling the expression of the genes involved in the antagonistic activities can be a future perspective.