

# Diversity of mycorrhizal fungi and class II fungal endophytes in chickpea, and influence of the plant genotype

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## Abstract

Chickpea (*Cicer arietinum* L.) has the ability to bring free N into cropping systems, but is only a fair rotation crop, leading to lower yield in following wheat crops, as compared to medic, vetch or lentil. The negative effects of a chickpea plant on the following wheat crops could come from chickpea root exudates, their residues or their influence on the soil microbial community. The identification of chickpea cultivars best able to promote soil biological quality and the growth of a subsequent crop in rotation will help farmers in selecting better crop rotations and, thus, will improve crop management in soil zone growing chickpea.

The global objective of this research is to improve the fitness of chickpea crops to their biological environment and to improve the ability of the plant to enhance soil biological quality. The specific objectives were (1) to verify that the productivity of chickpea and subsequent crops could be promoted through the inoculation by some indigenous endophytic fungi particularly under drought stress conditions (2) to verify the existence of variation in the rhizospheric associations of field-grown chickpea, as it is a necessary condition for the selection of genotypes with improved compatibility with beneficial microorganisms. (3) to identify the biologically active compounds present in the root extracts of chickpea cultivars with contrasting phenotypes, and assess their effect on beneficial and pathogenic soil microorganisms.

The greenhouse experiments show that inoculation with indigenous endophytes increased drought tolerance of the unifoliate Kabuli chickpea CDC Xena and the N and P nutrition of the drought stressed Desi chickpea CDC Nika. Inoculation of both Kabuli chickpea varieties with indigenous endophytes improved wheat seeds germination in tissues amended soil. Residue-free soil previously growing the unifoliate Kabuli chickpea CDC Xena strongly inhibited durum seed germination suggesting an effect of root exudates on the soil microbial community, with this Kabuli chickpea variety.

In a field experiment, the fungal diversity in cultivated Prairie dryland appeared to host a large array of fungal groups known to reduced plant nutrient, water and biotic stresses, and chickpea genotypes influenced differently the composition and biomass of the soil microbial community. The Desi chickpea CDC Anna was associated with high diversity of arbuscular mycorrhizal fungi (AMF) and culturable fungi, favored the proliferation of soil bacteria and fungal genus hosting biocontrol agents, and developed high AM root colonization level, as compared to the three Kabuli genotypes examined. The HPLC fractions of the roots of chickpea cultivar CDC Anna were recovered and the effects of these fractions on AM fungal spore germination were assayed in multi-well plates. Root extract fractions affect in a different ways the percentage of spores' germination of *Glomus etunicatum* and *Gigaspora Rosea*.

We concluded that the genotype of chickpea plants influences the composition of the associated microbial community, and this influence may be related to molecular signals produced by the plants. Furthermore, the productivity of chickpea and subsequent crops could be promoted through the inoculation with indigenous endophytic fungi.

**Keywords :** Chickpea (*Cicer arietinum* L.), genotypes, fungal diversity, symbiosis, arbuscular mycorrhizae, dark septate endophytes, drought stress, allelopathy, biologically active compounds, plant breeding.