

Biodiversity of vesicular arbuscular mycorrhizal (VAM) fungi in horticultural production system in northern Rajasthan

Vikram Kumar*, Chandra Gurnani, Shinam Mukhija, Charan Singh, Kamlesh Choure
Department of Biotechnology

Institute of Advanced Studies in Education Deemed University, Sardarshahr-331 401 (Raj) India

Abstract

The diversity of vesicular arbuscular mycorrhizal (VAM) fungi in horticultural production systems of small farmer agro systems was analysed. Vesicular arbuscular mycorrhizal fungal symbioses are playing a key role for P uptake by horticultural crops grown there. The objective of this study was to determine AM fungal community's in cropping systems and to identify soil factors affecting their frequency and diversity. Totally 4 VAM fungal species were identified. It is concluded that it will be advisable for farmers to inoculate their horticultural crops with selected Mycorrhizal inoculants during the nursery stage, as it cannot be predicted from the soil conditions whether the native vesicular arbuscular mycorrhizal fungal community is sufficient to sustain a stable horticultural production in the region.

Keywords: Glomeromycetes, Vesicular Arbuscular Mycorrhiza, soil, arid region and agro-ecosystems.

Introduction

Soil micro flora plays fundamental role for the productivity and stability of horticultural and agro ecosystems in the northern Rajasthan (Harley, 1983). Within this micro flora vesicular arbuscular mycorrhizal (VAM) fungi stand out because they are so important for the phosphate (P) nutrition of plants in this soil. They establish a mutualistic symbiosis with most of plants and this type of mycorrhiza is by far the most important worldwide. It is said that it occurs with more than 60-90% of the species of the plant kingdom (Trappe, 1987). Fungal species involved in the formation of VAM belong to the Glomeromycota (Schüssler *et al.*, 2001).

Diversity of Vesicular arbuscular mycorrhizal fungi

Among the factors influencing the vesicular arbuscular mycorrhizal fungal community dynamics and associations with plants, agricultural practices may be considered to be the most important (Bakshi *et al.*, 1974). Tillage, crop rotation sequences, and crop management systems have been reported as critical factors affecting the development, activity and diversity of VAM fungi (Oehl *et al.*, 2003; 2005). Mycorrhizal propagules can survive in the soil as spores which appear to be long-term structures of different ages, states of dormancy and germination periods and they constitute an inoculum source persisting for many years (Smith and Read, 2009). Hence, these fungal propagules represent the native mycorrhizal inoculum potential for locally grown crops. The fungal species naturally present in agro systems may be decisive for the productivity of crops. The main purpose of this study was to investigate the occurrence of AM fungi species in some horticultural ecosystems in soil of northern Rajasthan, and to determine whether there is any relation between their

occurrence and soil factors. VAM fungi are present in almost every ecosystem from tropical rain forest and grasslands to extreme environments such as semi-arid (Veenendaal *et al.* 1992) and arid deserts (Allen and Allen 1992).

Materials and Methods

The study site is situated in northern Rajasthan. The total human population of district is about 17.89 million and out of this nearly 72.6 percent in rural areas. The sampling was done in Sri Ganganagar district, which is under the influence of Great Thar desert. It is bounded on the north by Punjab state, on east by Hanumangarh district of Rajasthan, on the south by Bikaner district of Rajasthan, and on the west by Pakistan. The annual rainfall of this area is ranged between 250-300mm. The climate of this region is semi arid with extreme temperature condition in summer (up to 45 °C) and winter (up to 1°C) two agro ecosystems were selected for the study is northern part of Rajasthan: Horticultural systems habitually cropped by local farmers with vegetables, crops and fruit crops, based on cropping system. Soil samples were taken from Sri Ganga Nagar district where fruits crops are cultivated. Soil samples from the 0-10 cm horizon were taken from 10 m² plots from within the planting grows and between the rows. There were 4 replicated plots per location. Soil samples from each plot were bulked to give four replicates per ecosystem; soil samples were brought to the laboratory and stored in a freezer until analyses for separation of spores and the identification of VAM fungi species, and for soil analyses. Spores of VAM fungi were extracted and separated from the soil using the wet sieving and decanting procedure described by Sieverding (1991). For the taxonomic

*Corresponding author's e-mail: vikramhmg@gmail.com

classification main morphological spore characteristics such as colour, size, type and number of spore walls, and the morphology of the subtending hyphae at the point of spore attachment were observed. The species identification was carried out using the keys and instructions given by Schenck and Pérez (1990) and INVAM (International Culture Collection of Arbuscular and Vesicular-Arbuscular Endomycorrhizal Fungi).

Results and Discussion

Periodical survey of Sriganganagar district, northern Rajasthan was undertaken to collect and identify different VAM spores associated with fruit plants. Rhizosphere soil sample collected from various localities revealed the presence of several species of different genera. The VAM genera were identified such as *Glomus*, *Gigaspora*, *Acaulospora* and *Scutellospora* (Figure 1). In the Present study, it was established that 80-90% VAM spores accounted in Sriganganagar region. The number of species was highly variable among the horticultural production sites ranges. This may indicate that these species are fit to survive and form spores under very diverse conditions. Therefore, these fungal species can be

considered ecological generalists. In horticultural system soils presented relatively high diversity of VAM fungi. The function and importance of each of the different VAM fungal species in each ecosystem is known. In ecosystems, the horticultural and cropping systems, *Glomus* sp. represented each about 60% of all VAM fungal species found clearly the majority of the AMF community (Table 1). It is not surprising that most of VAM fungi spores owned to the *Glomus* genus because this is the prevailing genus in agricultural soils among the VAM species described so far (Jansa *et. al.*, 2003).

The results indicated that *Glomus* and *Gigaspora* were the dominant genera in Sriganganagar district, Northern Rajasthan. It has been found *Glomus* and *Gigaspora* usually produce more spores than *Acaulospora* and *Scutellospora*. Arid soil contain 7 -80 spores of VAM (*Glomus*, *Gigaspora*, *Acaulospora* and *Scutellospora*.) 100 per gram soil. Almost all plant growing in desert including Xerophyte do carry VAM fungi infection on their roots. (Kiran Bala *et. al.*, 1989) and the infection varied from plant to plant. VAM fungi also enhance nodulation and Nitrogenase activity in legumes (Tarafdar and Rao, 1997)

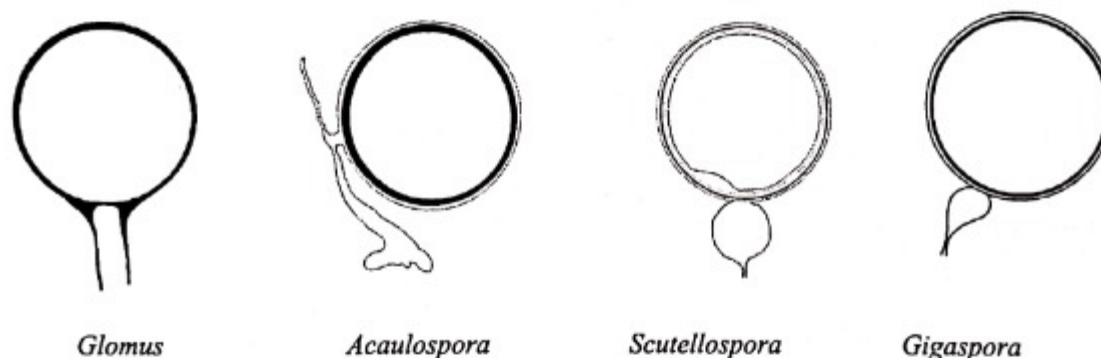


Figure : 1 showing the various genera of VAM fungi

Table 1. Showing the distribution of plants and relationship with symbiotic plants of FAM fungi

Sr. No.	VAM Fungi	Distribution of Plants	Symbiotic Plants
1	<i>Glomus</i> sp.	+++++	All kinds of Plants
2	<i>Gigaspora</i>	++++	All kinds of Plants
3	<i>Acaulospora</i>	+++	All kinds of Plants
4	<i>Scutellospora</i>	++	All kinds of Plants

(++++ maximum, +++moderate, ++less moderate, ++minimum)

The diversity of VAM fungal species is highly variable in horticultural production systems of small farmers in the Northern Rajasthan. There is no relationship between the most common soil parameters with such diversity, and the occurrence or absence of VAM fungi species is likely to depend on the divers agronomic historic inputs, that farmer apply to horticultural crops. Thus, because most of the horticultural crops depend obligatorily

for growth on mycorrhizae, in the soil of the region, it is advisable to inoculate the horticultural crops with selected highly effective mycorrhizal inoculants at the nursery stage especially in organic agriculture. This will likely give farmers a more secure and sustainable production than to depend in crop production on unknown natural VAM fungi communities.

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