EFFECT OF EDAPHIC FACTORS ON THE DIVERSITY OF VAM FUNGI

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Abstract:

The present study deals with the diversity and distribution of VAMF at different sites with different selected plants. Maximum number of VAMF species were found at site IV (57 species) out of which Glomus species was most dominant (58%), followed by Acaulospora (19%), Scutellospora (8%), Sclerocystis (4.8%) and Gigaspora (1.6%) respectively. In site II 56 species of VAMF were observed with Glomus (55%), followed by Acaulospora (22.5%), Scutellospora (8%), Gigaspora (1.6%) and Sclerocystis (3.2%) respectively. In site III 55 species of VAMF occurred with Glomus (51.6%) followed by Acaulospora (22.5%), Scutellospora (9.7%), Sclerocystis (4.8%) and Gigaspora (0%) respectively. In site I 54 species of VAMF were found; out of these Glomus was highest 53% followed by Acaulospora (22.5%), Scutellospora (5%), Sclerocystis (1.6%) and Gigaspora (1.6%) respectively. These results suggest that selected study sites are rich in VAMF frequency and diversity.The Shanon-Wiever index confirms that diversity of VAMF fungal species varies with the test plant and maximum diversity was observed with Ocimum sanctum (3.948), and Withania somnifera (3.909) respectively. Maximum ANOVA value recorded in case of and Withania somnifera (0.20) and Ocimum sanctum (0.19) respectively. Maximum richness value was observed in case of Ocimum sanctum (0.3948) and Withania somnifera (0.0391).

Keywords:

VAMF, Glomus, Diversity, Mycorrhizae, richness

Introduction:

Mycorrhizae is the mutualistic symbiosis (non-pathogenic association) between soil borne with the roots of higher plants (Quilambe., 2003), revealed that they are found in wide range of habitats usually in the roots of angiosperms, gymnosperms and pteridophytes.They also occurs in the gametophytes of some mosses, lycopods and psilotes, which are rootless (Mosse et al., 1981; Vyas et al., 2007, 2008). AMF have shown to be potentially able to take up both organic

(Hodge, Campbell & Fitter, 2001) and inorganic nitrogen from the soil (Govindarajulu et al., 2005). VAM fungi are essential components of ecosystem

for both re-vegetation of the degraded lands and maintenance of soil structure (Caravaca et al.,2005), therby reducing the risks of erosion and desertification. Soil characteristics, plant species, and climate may all regulate the arbuscular mycorrhizal (AM) fungi community. The distribution of certain VAM fungal species has been related to soil pH, phosphorus level, salinity, soil disturbance (Abbott and Robson 1991), vegetation (Johnson et al., 1992), or hydrologic condition of the soil (Ingham and Wilson, 1999; Miller and Bever, 1999). In general terms, increases in soil pH, nutrient status and salinity in soil are related to a decrease in VAM root colonisation or spore density (Abbott and Robson, 1991). Despite the importance of VAM fungi in the physiology and nutrition of plants, as well as in shaping plant communities (Grime et al., 1987; Van der Heijden et al., 1998; Smith et al,. 1999), factors affecting the presence, diversity, spore density, and root colonisation by AM fungi in soil are poorly understood. One reason is the difficulty of establishing causation from correlation of soil and plant factors with VAM fungal populations. Another reason is that AM fungi can associate with a wide range of hosts present in community, but the sporulation rates of AM fungi have been found to be host dependent (Bever et al., 1996; Lugo and Cabello, 2002). Host-dependence of VAM fungal population growth rates in soil may play an important role in the maintenance of VAM fungal species diversity in grasslands (Bever et al., 1996), and suppression of mycorrhizal symbioses may result in a decreasing of the dominant plant and an increase in species diversity (Hartnett and Wilson, 1999). In addition, plant diversity may increase or decrease if the dominant plant competitors are more weakly or more strongly mycotrophic than their neighbours (Hartnett and Wilson, 1999). An additional factor influencing populations of VAM fungi in soil, which may in turn affect the performance of plant species relative to each other, is the hydrologic condition of the soil, which may vary seasonally. The hydrologic condition of the soil plays an important role in determining plant community structure, and this effect is even more important when soils are commonly subjected to periods of dryness

and flooding (Chaneton et al., 1998). VAM fungi have been found in the roots of many plants in wetlands (Ingham and Wilson, 1999; Miller and Bever (1999), or salt marshes (Brown and Bledsoe 1996). This is relevant because the fungi are believed to require wellaerated soils, and are thought to have problems adapting to flooded conditions (Mosse et al., 1981). Nevertheless, little is known of VAM fungi patterns in wetlands or of the influence of the hydrologic condition of the soil on populations of AM fungus species. The most important and historical account of medicine in the form of „Ayurveda"(2500 t0 900 B.C.), which is considered as „Upaveda" ,Charak Samhita and Susruta Samhita" also
delt with plants related to medicine and their use in health management.These days many people cultivating medicinal plants to fulfil the increasing demands of pharmaceutical industries. The major biochemical constituents of Ashwagandha (is a small, woody shrub in the Solanaceae family) that root are steroidal alkaloids and steroidal lactones in a class of constituents called withanolides. At present, 12 alkaloids, 35 withanolides, and several sitoindosides from this plant have been isolated and studied. A sitoindoside is a withanolide containing a glucose molecule at carbon 27. Much of ashwaganda\'s pharmacological activity has been attributed to two main withanolides, withaferin A and withanolide D. Tulsi, Queen of Herbs, the legendary \

Material and Method:

For the present investigation two test sites were selected, (I) Kariaya Village (II) Jaitpur Village. The experiments were conducted for quantitative and qualitative estimation of AM fungi were done from rhizosphere and non-rhizosphere soil and roots of test plants. The rhizosphere soil and root samples of selected test medicinal plants were collected from study sites up to 0-10, 10-20, 20-30, 30-40 cm depth. The VAM spores were isolated from the collected soil samples by wet sieving and decanting method (Gerdemann and Nicolson, 1963). Mycorrhizal spores are identified according to their spore morphology by

conventional taxonomic key of Schenck and Perez (1990&http:/www.invam.cat.wu.edu). For the estimation of AM spores, a technique provided by Gour and Adholeya (1994) was followed. The soil pH was determined in 1:5 suspension of soil; deionized water ratio, electrometrically by glass electrode pH meter 335 (Jackson, 1982). Statistical analysis of data for comparison of means, analysis of variance (ANOVA), etc. was followed after Gupta and Kapoor (1997).

Result and Discussion:

The result obtained from the present study depicted in the table 1, which show the relative abundance of VAMF spores associated with test plants Withania somnifera and Ocimum sanctum, growing in the Karaiya village and Jaitpur village. Variance in relative abundance (RA) of VAMF spores along with the depths of the soil was observed. Maximum value recorded of VAMF spores was observed from the soil surface up to 10 cm length and it reduces and minimum was recorded at 30-40 cm depth. Shannon-Weaver diversity index and evenness of VAM fungi is shown in table (2). The Shannon-Weaver index value suggests that W. somnifera harbours more diverse morphotypes of O. sanctum. Comparatively soil of Jaitpur village has fairly greater number of morphotypes in W. somnifera then in the soil of Karaiya, H 2.351 and H 2.250 respectively. However, Shannon –Weaver index (H') values confirm that (VAMF) reduces whereas in contrast H' value obtained from the different depth of rhizosphere of O. sanctum growing in Jaitpur village soil showed to maximum value at the depth of 10-20 cm (2.143), and further deeper region showed linear decrease an H` value. However, O. sanctum growing Karaiya village showed maximum H` value up to 10 cm depth and below this H` value gradually decreased The value obtained for evenness (J') of VAMF with W. somnifera growing in Karaiya or Jaitpur village soil are also described in table (2). Interestingly there is little hike in J` value at 20-30 cm and 30-40 cm deep in respectively with W. somnifera plants growing in Jaitpur village soil. However, same species growing

at Karaiya village dose not show any significant difference in J` value. Evenness of VAMF J` value of O.sanctum in both the sites Karaiya village soil and Jaitpur village soil showed poorly different trend. At Kariaya village soil J` value almost remains same upto 30 cm depth, but suddenly significant reduction in J` value was observed. In contrast to this Jaitpur village soil though J` value remains same upto the depth of 30 cm but a significant increase in J` value at 40 cm depth was recorded. During the present study, a total of 27 morphologically distinct VAM species were isolated from the rhizosphere of Withania somnifera and Ocimum sanctum growing at two different sites; Karaiya village and Jaitpur village (Fig.1). Out of 27 VAM fungal species, 13 different species were found associated only with W. somnifera, six species were found only with O. sanctum and eight species were found common in both the plants. Thus, a total of 21 species associated with W. somnifera and

14 species were found associated with O. sanctum. Among the 21 VAM species found associated with W. somnifera, five VAMF species viz. Acaulospora mellea, A. scrobiculata, Glomus claroideum, G. etunicatum and G. macrocarpum were not found in Jaitpur soil, whereas A. bireticulata, A. denticulata, G. dimorphicum were not found in Jaitpur village soil (Fig. 2). Acaulospora sp., A. nicolsonii, G. clarum and G. hoi were the prominent species of the VAM fungi which were isolated from surface to 40 cm. depths in the Karaiya village soil. G. intraradices and G. mosseae were isolated from the depth of 30 cm. A. denticulata and Glomus sp. were obtained from the depths of 10-20 and 20-30 cm. G. ambisporum, and G. fasciculatum were isolated from 0-10 and 10-20 cm depths. A. bireticulata, G. australe, G. desrticola, G. dimorphicum, and G. pustolatum were isolated from 0-10 cm depth in the Karaiya village soil (Table 1). In the Jaitpur village soil, A. nicolsonii, G. clarum, G. hoi and G. intraradices were isolated from the topsoil to of 40 cm depth. G. etunicatum, G. mosseae and G. versiforme were collected from of 30 cm depth. A. mellea and G. desrticola were isolated from 0-10, 10-20, and 30-40 cm soil depth. A. scrobiculata, G. australe, G. fasciculatum, G. macrocarpum, and G.

pusotlatum were isolated from 0-10 and 10-20 cm depth. Acaulospora sp. and Glomus sp. were isolated from 0-10 and 20-30 cm depth. G. ambisporum was isolated only 10- 20 cm (Table 1). Out of 27 VAMF species, 14 species were found associated with O. sanctum in both the sites (Fig. 1). Among the 14 VAMF species, three species viz. A. foveata, Entrophospora infrequens and G. etunicatum were not found in Karaiya village soil (Fig. 2). A. nicolsonii and G. clarum were the two VAMF species found very prominent in Karaiya village soil and isolated in all measured soil depth. A. spinosa, G. fasciculatum, G. heterosporum and G. hoi were isolated from the depth of 30 cm. Whereas, A. scrobiculata, G. ambisporum and G. intraradices were isolated from the depth of 20 cm. G. botryoides was isolated in topsoil (0-10 cm) and Scutellospora pellucida was isolated from 20-30 and 30-40 cm soil depth (Table 1). In Jaitpur village soil G. clarum, G. fasciculatum and G. intraradices were isolated from 40 cm depth. A. nicolsonnii, G. heterosporum and G. hoi were collected from 30 cm depth while, A. foveata, G. ambisporum and G. etunicatum 20 cm depth. A. spinosa was isolated from 10-20, 20-30 and 30-40 cm soil depths, respectively. Here, also G. botryoides was isolated from the topsoil. E. infrequens was isolated from 20-30 and 30-40 cm depth and S. pellucida was isolated from 30-40 cm depth (Table 1). The result shown in fig.3 clearly indicate that 14 VAMF species associated with W. somnifera, commonly occurring in both the sites Karaiya village soil as well as Jaitpur village soil. Among 14 VAMF species, 11 species associated with O. sanctum. It was also observed that 6 VAMF species viz. A. nicolsonii, G. ambisporum, G. clarum, G. fasciculatum, G. hoi and G. intraradices were found associated with both the test plants at in both the sites. However, three species A. bireticulata, A. denticulata and G. desrticola which are associated with W. somnifera were found only in Karaiya village soil. A linear regression analysis with coefficient of determination (= squared correlation coefficient or r2) of VAMF spore population with soil depth, soil pH, and soil moisture per cent in W. somnifera and O. sanctum at both the sites were presented in fig. 4 (A-F) and fig. 5 (A-F).

It is clearly evident from the result that the VAMF spore population showed a strong negative correlation with soil depth, pH and moisture of the soil. It is assumed that an increase in single variable (depth pH, or moisture) resulted in decrease in VAMF spore population in both the test plants at both the sites. In Karaiya village soil, depth and moisture of rhizosphere soil of both the test plants show highly significant correlation, while, variation found in correlation between soil pH and spore population of both the plants. Here, VAMF spore population had weak correlation (r2= 0.563) with the pH of rhizosphere soil with W. somnifera in comparison to O. sanctum (r2 = 0.943). Whereas, in Jaitpur village soil, VAMF spore population showed similar trend as observed at Karaiya village soil with the depth and percent moisture of rhizosphere of both the plants. These two attributes significantly, correlated with the VAMF spore population (Fig. 5 A-F). The data presented in table (3) show the comparative analysis of average values of soil pH, soil moisture, VAMF spore population and Shannon-Weaver diversity index at four soil depths from both the sites. The mycorrhizal population dropped significantly from the upper to lower soil depth level. Both the soils showed similar relationships for depths and mean total spore population (Fig. 6). In the present study average soil moisture present initially increased two fold with the increasing depth (Fig. 7). Average soil pH found increased. Interestingly, soil pH values showed a general tendency to increase with increasing soil depth in both the site (Fig.8).

Discussion:

In the present study, the rhizosphere of two medicinal plants viz. Withania somnifera and Ocimum sanctum in different soil depth at two locations showed common as well as variant VAMF flora. Such variations in the VA mycorrhizal fungal community at differ

Conclusion:

This study shows that the frequency of genera and species of VA mycorrhizal fungi isolated from both the site varied with the above ground vegetation and with changes in soil moisture and soil pH. Currently, we have limited means

for accurately determining the complex of genera and species that forming symbiosis with host plants in natural soil and that are responsible for variations in fungal density obtained from soil samples. Recent advancements in characterizing mycorrhizae with molecular markers will greatly improve our understanding of the ecology of these fungi.

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