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○ Singh P. K., Mahendra Kumar Mishra, and Vyas, D. "Efficacy of Trichoderma spp. Strains for Control of Fusarium Wilt of tomato (Lycopersicon esculentum Mill.)". In: *Journal of Mycology and Plant Pathology*, Uadipur.

○ Singh P. K., Mahendra Kumar Mishra, and Vyas, D., Interactions of Vesicular Arbuscular Mycorrhizal Fungi with Fusarium Wilt and Growth of the Tomato (Lycopersicon esculentum Mill.). In:*Indian Phytopathology*, IARI, New Delhi.

VAM Fungi Association in Catharanthus roseus
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Abstract
Catharanthus roseus of Apocyanaceae is better known for its medicinal value particularly it's anticancerous property was studied for it's mycorrhizal association. The result obtained from our experiment suggests that VAM fungi vary at different stages of plant growth. It is clearly evident from the result that root colonization by VAM fungi occurs after 30 days of seedling transplantation. At this stage, spore population was sparsely scattered and only 3 VAM fungi was identified in the rhizosphere soil of C. roseus. Linear increases in, root colonization, spore population and VAMF species was recorded with the growth of the plant. However, arbuscules were observed between 30 to 60 days of plant growth. At later stage of plant growth arbuscules were disappeared and vesicles were appeared. When plants were uprooted after 150 days, spore populations as well as VAM fungi were found reduced.

Key words: Catharanthus/ Colonization/ Rhizosphere/ VAMFungi.

Introduction
Mycorrhizal association vary widely in structure and function, but the most common interaction is the vesicular arbuscular mycorrhizal (VAM) symbiosis which is formed between the roots of more than 90% terrestrial plants and belonging to the order Glomales. It is now well established that the VAM fungi improves plant growth. Colonization of the root system by VAM fungi confers benefits, directly to the host, plant growth and development through the acquisition of mineral nutrients from the soil. VAM fungi form critical link between the above grown plant and soil by influencing plant nutrient cycling and soil structure and make a large direct contribution to soil fertility and quality through soil organic matter. These fungi consists an integral and important component of ecosystem and may have significant applications in sustainable agricultural systems. Different plant species may respond differently to specific VAM fungal species.

Catharanthus roseus (syn. Vinca rosea) belongs to family Apocyanaceae, better known for its medicinal value particularly in Cancer treatment. It's dimeric indole alkaloids, viz. Vinblastine and Vincristine have high anti-tumor potentials. These substances mostly contained in leaves of the plant. Medicinal value in the plant depends upon the availability of nutrients in soil where they are growing. Catharanthus found growing wild as well as cultivated in botanic garden. Keeping with view that mycorrhization may influence synthesis of alkaloids in C. roseus. Therefore, we have taken this study.

Material and Methods
This study was conducted at Botanic Garden of Dr. H. S. Gour University, Sagar (M.P.). Soil and root samples were collected from the rhizosphere soil of C. roseus. The soil of this region is grayish black, sandy clay having about 7.2 pH and annual temperature is 28°C. The sampling was done in different growing intervals. VAM spore was isolated by wet-sieving and decanting method. VAM colonization in the roots determined by method of Phillips and Hayman and percent root colonization was determined after staining with Lacto-phenol cotton blue. Mycorrhizal spores are identified according to their spore morphology by conventional taxonomic key of Schenck and Perez. The data obtained from our experiment are presented in Table 1. The results suggests that 30 days of seedling plants shows 52% root.
VAM Fungi...

Table 1. VAM association with C. roseus in different growing intervals

<table>
<thead>
<tr>
<th>Growing intervals (days)</th>
<th>Root colonization (%)</th>
<th>Average no. of arbuscules (cm⁻² root bit) ND</th>
<th>Average no. of vesicles (cm⁻² root bit) ND</th>
<th>Spore population 100 g⁻¹ of Rhizospheric soil</th>
<th>Total No. of VAM fungal species</th>
<th>Name of the dominant VAM species*</th>
</tr>
</thead>
<tbody>
<tr>
<td>30</td>
<td>52</td>
<td>6</td>
<td>ND</td>
<td>104</td>
<td>3</td>
<td>ADTC, LLCT, LHOI.</td>
</tr>
<tr>
<td>60</td>
<td>71</td>
<td>10</td>
<td>ND</td>
<td>120</td>
<td>4</td>
<td>LCTC, LCLR, LHOI, LMSS.</td>
</tr>
<tr>
<td>90</td>
<td>75</td>
<td>1</td>
<td>6</td>
<td>216</td>
<td>5</td>
<td>ADLT, ASCB, LFSC, LPBS, SPCC.</td>
</tr>
<tr>
<td>120</td>
<td>85</td>
<td>ND</td>
<td>8</td>
<td>320</td>
<td>6</td>
<td>ABRT, ALCN, LCTC, LHOI, LHTS, LLPT.</td>
</tr>
<tr>
<td>150</td>
<td>70</td>
<td>ND</td>
<td>2</td>
<td>288</td>
<td>5</td>
<td>AGDM, LABS, LCRD, LFSC, LMSS.</td>
</tr>
</tbody>
</table>

* Codes as per Perez and Schenck⁵

ABRT *Acaciapora bireticulata* (Rotthwell and Trappe)
ADLT *Acaciapora dilatata* (Morton)
ADTC *Acaciapora denticulata* (Severing and Torro)
AGDM *Acaciapora gerdemanni* (Schenck and Nicolson)
ALCN *Acaciapora lacunosa* (Morton)
ASCB *Acaciapora scrobiculata* (Trappe)
LABS *Glomus ambisporum* (Smith and Schenck)
LCLR *Glomus clarum* (Nicolson and Schenck)

LCTC *Glomus citricolum* (Tang and Zang)
LFSC *Glomus fasciculatum* (Thaxter)
LHOI *Glomus hoi* (Brech and Trappe)
LHTS *Glomus heterosporum* (Smith and Schenck)
LLCT *Glomus lacteum* (Rose and Trappe)
LLPT *Glomus leptotichum* (Schenck and Smith)
LMSS *Glomus mosseae* (Gerdemann and Trappe)
LPBS *Glomus pubescens* (Trappe and Gerdemann)

Colonization, spore population 104 spores 100 gm⁻¹ of soil and 3 VAM fungal species were recorded. 60 days old plant, when examined for root colonization, 71% root colonization, 120 spores 100 gm⁻¹ of soil and 4 VAM species respectively. Further increase root colonization, spore population and VAM species was recorded in with the increase in plant growth up to 120 days. The data recorded was 75 and 85%, 216 and 320.

**Fig. 1. Root Colonization and Spore population in growing intervals of Catharanthus roseus**

![Graph showing root colonization and spore population](image)

Mycorrhization, it was observed that there was an increase in percent root colonization, VAM spore population and VAMF species. It was...
spores 100 g^{-1} of soil, 5 and 6 VAMF species respectively for 90 and 120 days. However, when 150 days old plant were uprooted and examined for mycorrhization, it was found that not only percent root colonization was reduced but also number of spores and VAM fungal species were found decreased in comparison to 120 days old plant. Arbuscules were seen with early stages of seedling plant that is up to 90 days old plant and since then arbuscules was disappeared; vesicles were appeared and found increasing up to 120 days old plant. However, at the time of uprooting they were also reduced. Dominance of *Glomus* was observed among the VAMF obtained during the study period. *Catharanthus* is a well-known medicinal plant. The occurrence of mycorrhizal fungi at early stages of growth shows it’s mycorrhizal dependency. VAM fungi are biotrophs, therefore, colonization of roots are essential for their continued occurrence in soil. VAM fungi have a number of different propagules-hyphae (in soil or within roots depending on the special intraradical structure of fungus, arbuscules and vesicles in soil or within roots). The VAM fungi species recorded during the present investigation at different intervals from the rhizosphere soil are *Acaulospora bireticulata* (ABRT), *Acaulospora dilatata* (ADLT), *Acaulospora denticulata* (ADTC), *Acaulospora gerdemanni* (AGDM), *Acaulospora lacuosa* (ALCN), *Acaulospora scrobiculata* (ASCB), *Glomus ambisporum* (LABS), *Glomus clarum* (LCLR), *Glomus claroideum* (LCRD), *Glomus citricolum* (LCTC), *Glomus fasciculatum* (LFSC), *Glomus hoi* (LHOI), *Glomus heterosporum* (LHTS), *Glomus lacteum* (LLCT), *Glomus lepiotichum* (LLPT), *Glomus mosseae* (LMSS), *Glomus pubescens* (LPBS) and *Sclerocystis pachycaulis* (SPCC). It is clearly evident from the result that *Glomus* spp. dominated in the occurrence in association with *C. roseus* at different intervals of plant growth. Interestingly, (Fig.1) the number of spores and VAMF was not as good as, it was observed earlier by us in association with other plants. However, *C. roseus* shows greater colonization in the roots suggest that host plant develop strong mutualistic association with only few VAM fungi. This may be interpreted also by other way. Probably the substances leached out in the form of root exudation might have detrimental effects on other VAM fungi until otherwise appeared with other plants of the botanic garden. 

**Acknowledgement**

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**References**

11. http://www.invam.caf.wvu.edu

Studies on mycorrhizal association in wheat

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ABSTRACT: VA mycorrhizal fungi are found associated with different cultivars of the wheat though, their distribution varies along with the wheat varieties. Among the 13 wheat varieties under study, C-306 showed maximum colonization, greater number of VAM propagules and maximum number of VAM species whereas minimum colonization was found in HI-1501. Less number of spore population was found in rhizosphere soil of variety HD-4672 and minimum number of VAM species associated with two cultivar HD-2781 and A-9-30-1. Among the VAM species isolated from rhizosphere soils of all thirteen wheat cultivars, Glomus were found dominating with recorded 13 species followed by Acaulospora 10 species, Sclerocystis and Gigaspora are found poorly distributed with single species in rhizosphere soil of wheat cultivar. Among Glomus species, LHOI (Glomus hoi) was found dominating.

Key words: Colonization, cultivar, Glomus, rhizosphere, VAM, and wheat

Arbuscular mycorrhizal fungi are most ubiquitous and form mutualistic relationship with more than 80 percent of major group of vascular plants (Brundrett, 2004). Over the past several years, there has been growing appreciation of the importance of plant and fungal interaction especially arbuscular mycorrhizal (AM) fungi on terrestrial ecosystem (Zhao et al., 2001; Muthukumar et al., 2003; Dwivedi et al., 2003). A mycorrhiza form critical link between the above ground plant and soil by influencing plant nutrient cycling especially phosphorous and soil structure (Karandashev and Bucher, 2005) and make a large direct contribution to soil fertility and quality through contribution of soil organic matter (Rilling et al., 2001).

Most natural ecosystem comprises several AMF species, forming AMF communities (Walker et al., 1982; Johnson et al. 1997). AM fungi do not have any host specificity (Fitter, 1991) and each plant species could potentially be colonized by each AMF species from that community. AMF species are known to vary in their ability to take up phosphorous from nutrient depletion zone of soil (Jakobsen et al., 1992; Karandashev and Bucher, 2005) and in their stimulation of plant growth (Haas and Krikun, 1985). Furthermore, different plant species may respond differently to specific AMF species. It is therefore hypothesized that differential response of plant species to specific AMF species exist.

Sagar is situated on the hills of Vindhyan ranges. Since wheat is one of the most cultivated crops of this region. Therefore, there is need to take close look at the nature of natural processes that help to produce crop of high yield and quality with more efficient use of nutrient inputs, reduced need for pesticides. VA mycorrhizal fungi, the 'hidden heroes' of nutrient deficient soil especially phosphorous can provide support for management of nutrients and maintenance of crop growth. Recently, Dwivedi (2003); Dwivedi et al. (2003); Vyas (2005) studied occurrence of VAM in wheat at Sagar.

Keeping this in view, the present study is undertaken to know the diversity and distribution of VA mycorrhizal fungi among the wheat cultivars grown in Sagar.
MATERIALS AND METHODS

Isolation of spore of VAM fungal species and quantification of root colonization

The rhizosphere soil and root samples of selected 13 wheat cultivars were collected from study site Ratouna agriculture station Sagar up to 10–20 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 and http://www.invam.cat.wvu.edu). VAM colonization in the roots were determined after staining with Lacto-Phenol acid fuchsin, Tryphan blue and Cotton blue, by the method of Philips and Hayman (1970). Study of spore isolation and root colonization was done during the cropping period but the results presented here are of only at the time of harvesting.

Density and frequency of VAM fungi

VAM fungal species association and their density and frequency with each wheat cultivar were calculated by following modified formula. Standard formula is used for higher plants (Ambasth 1988).

\[
F = \frac{\text{Number of cultivars in which a VAM species occurs}}{\text{Total number of wheat cultivars}} \times 100
\]

\[
D = \frac{\text{Number of individuals of VAM species occurs in all cultivars}}{\text{Total number of wheat cultivars}}
\]

where, \( F \) represents frequency and \( D \) represents Density.

RESULTS

VAM spore population

Table 1 shows the VAM spore population in rhizosphere soils of 13 different wheat cultivars and percent root colonization at the time of harvesting. The maximum spore population was found with wheat cultivar C–306 (154 spores / 50 g soil) and minimum 66 spores / 50 g soil was found with HD–4672. Others were between them [HI–1502 (117 spores), HI–1500 (98 spores), GW–1172 (75 spores), HD–2781 (104 spores), HW–2004 (89 spores), MACS–3208 (103 spores), MPO–1126 (90 spores), A–9–30–1 (108 spores), HI–1501 (86 spores), HD–4694 (105 spores) and Sujata (124 spores)].

<table>
<thead>
<tr>
<th>S. No.</th>
<th>Wheat cultivars</th>
<th>Root colonization (%)*</th>
<th>Average no. of Vesicles (cm²/root bit)*</th>
<th>Spore population (50 gm⁻¹ Rhizosphere soil)</th>
<th>Total No. of VAM fungal species</th>
<th>Dominant VAM species</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>HI–1502</td>
<td>86</td>
<td>36</td>
<td>117</td>
<td>5</td>
<td>AGDM, LABS, LCRD, LFSC, LMSS</td>
</tr>
<tr>
<td>2.</td>
<td>HI–1500</td>
<td>62</td>
<td>24</td>
<td>98</td>
<td>5</td>
<td>ABRT, ALCN, GABD, LFSC, LHCI</td>
</tr>
<tr>
<td>3.</td>
<td>GW–1172</td>
<td>ND</td>
<td>ND</td>
<td>75</td>
<td>5</td>
<td>ADLC, LABS, LHTS, LHOI, LAST</td>
</tr>
<tr>
<td>4.</td>
<td>HD–2781</td>
<td>68</td>
<td>34</td>
<td>104</td>
<td>3</td>
<td>ABRT, LHTS, LMSS</td>
</tr>
<tr>
<td>5.</td>
<td>HW–2004</td>
<td>54</td>
<td>21</td>
<td>89</td>
<td>4</td>
<td>ADLC, ALCN, LABS, LHOI</td>
</tr>
<tr>
<td>6.</td>
<td>MACS–3208</td>
<td>68</td>
<td>37</td>
<td>103</td>
<td>4</td>
<td>ABRT, LCRD, LFSC, LMSS</td>
</tr>
<tr>
<td>7.</td>
<td>MPO–1126</td>
<td>57</td>
<td>26</td>
<td>90</td>
<td>5</td>
<td>ADLT, ASCB, LFSC, LLPT, SPCC</td>
</tr>
<tr>
<td>8.</td>
<td>A–9–30–1</td>
<td>75</td>
<td>39</td>
<td>108</td>
<td>3</td>
<td>ADTC, ANCS, LLCT</td>
</tr>
<tr>
<td>9.</td>
<td>HI–1501</td>
<td>47</td>
<td>25</td>
<td>86</td>
<td>4</td>
<td>ALCN, ASPN, LHOI, LRDT</td>
</tr>
<tr>
<td>10.</td>
<td>HD–4694</td>
<td>72</td>
<td>19</td>
<td>105</td>
<td>4</td>
<td>ARHM, GABD, LHOI, LPBS</td>
</tr>
<tr>
<td>11.</td>
<td>HD–4672</td>
<td>ND</td>
<td>ND</td>
<td>66</td>
<td>4</td>
<td>ABRT, LABS, LCRD, LHOI</td>
</tr>
<tr>
<td>12.</td>
<td>C–306</td>
<td>92</td>
<td>27</td>
<td>154</td>
<td>6</td>
<td>ABRT, LBTR, LMTC, LABD, LHOI, LMSS</td>
</tr>
<tr>
<td>13.</td>
<td>Sujata</td>
<td>88</td>
<td>32</td>
<td>124</td>
<td>3</td>
<td>ADLT, ALCN, LCLR, LHOI</td>
</tr>
</tbody>
</table>
Mycorrhizal colonization

The result also showed that (Table 1) highest percent root colonization was observed with wheat cultivar C–306 (92%) and lowest was observed with HI–1501 (47%). In cultivar GW–1172 and HD–4672, the root colonization could not be detected due to absence of fine roots in their rhizosphere soils. Other wheat cultivars showed intermediate range of root colonization between higher and lower range, i.e. HI–1502 (86%), HI–1500 (62%), HD–2781 (68%), HW–2004 (54%), MACS–3208 (68%), MPO–1126 (57%), A–9–30–1 (76%), HD–4694 (72%) and Sujata (88%).

Diversity and distribution of VAM fungi

Results obtained from the experiment regarding diversity and distribution of VAM fungi were presented in Table 2. It is clearly evident from the result that number of VA mycorrhizal fungi belonging to order Glomales were found associated with different cultivars of the wheat. Interestingly, the distribution varies cultivar to cultivar. Therefore, one cannot draw any correlation between the host cultivars and mycorrhizal fungi. However, we obtained total number of 25 VAM species from the rhizosphere of all the 13 wheat cultivars. Out of 25 VAM species *Acaulospora denticulata* (ADTC), *A. nicolsonii* (ANCS) and *Glomus lacteum* (LLCT) were found associated with A–9–30–1. They are not found with any other wheat cultivar. VAM species *Acaulospora scrobiculata* (ASCB) and *Sclerocystis pachycaulis* (SPCC) were found associated singly with wheat cultivar MPO–1126, *G. botryoides* (LBTB) and *Glomus citricolum* (LCTC) with C–306, *Acaulospora spinosa* (ASPN) and *Glomus radiatum* (LRDT) were found associated with HI–1501. *Acaulospora gerdemannii* (AGDM) found associated with HI–1501, *Acaulospora rehmsii* (ARHM) with HD–4694 and *Glomus clarum* (LCRL) were found associated with Sujata, showing 7.6% frequency and 0.076 density.

VAM species *Acaulospora delicata* (ADLC) was found to be associated with two wheat cultivars viz. HW–2004 and GW–1172. *Acaulospora dilatata* (ADLT) was found associated with MPO–1126 and Sujata. *Gigaspora albida* (GABD) was found associated with HI–1500 and HD–4694, *Glomus heterosporum* (LHTS) with GW–1172 and HD–2781, *Glomus pubescens* (LPBS) with GW–1172 and HD–4694 and *Glomus pallidum* (LPLD) were associated with MPO–1126 and C–306 wheat cultivars. These species showed 15.3% frequency and 0.153 density. VAM species *Glomus claroides* (LCRD) was found to be associated with three different wheat varieties HI–1502, MACS–3208 and HD–4672 showing 23% frequency and 0.230 density. VAM species *Acaulospora lacunose* (ALCN), *Glomus fasciculatum* (LFSC) and *Glomus ambisporum* (LABS) were found to be associated with four different varieties of wheat they are HI–1500, HW–2004, HI–1501 and Sujata, HI–1502, HI–1500, MACS–3208 and MPO–1126 and HI–1502, GW–1172, HW–2004, and HD–4672 respectively, with 30.7% frequency 0.307 density. *Acaulospora bireticularata* (ABRT) and *Glomus mossae* (LMSS) were found to be associated with 5 different wheat varieties i.e. HI–1500, HD–2781, MACS–3208, HD–4694 and C–306 and HI–1502, HD–2781, MACS–3208, C–306 and Sujata respectively. Both the VAM species ABRT and LMSS have three common hosts viz. HD–2781, MACS–3208 and C–306 and two different hosts HI–1500 and HD–4694 for ABRT and HI–1502 and Sujata for LMSS. The frequency and density of both the VAMF ABRT and LMSS was recorded 38.4% and 0.38 respectively VAM species *Glomus hoi* (LHOI) was found associated with 8 wheat varieties. These are HI–1500, GW–1172, HW–2004, HI–1501, HD–4694, HD–4672, C–306 and Sujata and showing 61.5% frequency and density 0.615.

DISCUSSION

VAM fungi are worldwide in distribution and have been found on numerous plant species including many of economic importance (Gerdemann, 1968). Crop plant may benefit from the mycorrhizal association because of greater efficacy in nutrient and water uptake from soil (Daft and Nicolson, 1969; Gerdemann, 1968; Ross and Harper, 1970; Safir et al., 1970; Azcon et al., 1981). The result obtained from the study suggests that the colonization, average number of vesicle, spores population, and VAM fungal species differ with different wheat cultivars. The VAM root colonization is a dynamic process, which is influenced by several edaphic factors such as nutrients status of soil, seasons, VAM strains, soil temperature, soil pH, host cultivar susceptibility to VAM colonization and feeder root condition at the
### Table 2. Frequency and Density of VAM fungi in Wheat Cultivars

<table>
<thead>
<tr>
<th>S. No.</th>
<th>Species</th>
<th>Name of Wheat Cultivars</th>
<th>Total</th>
<th>Frequency (%)</th>
<th>Density</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>ABRT</td>
<td>+ + + + + + + +</td>
<td>5</td>
<td>38.4</td>
<td>0.384</td>
</tr>
<tr>
<td>2.</td>
<td>ADLC</td>
<td>+ + + + + + + +</td>
<td>2</td>
<td>15.3</td>
<td>0.153</td>
</tr>
<tr>
<td>3.</td>
<td>ADLT</td>
<td>+ + + + + + + +</td>
<td>2</td>
<td>15.3</td>
<td>0.153</td>
</tr>
<tr>
<td>4.</td>
<td>ADTC</td>
<td>+ + + + + + + +</td>
<td>1</td>
<td>7.6</td>
<td>0.076</td>
</tr>
<tr>
<td>5.</td>
<td>AGDM</td>
<td>+ + + + + + + +</td>
<td>1</td>
<td>7.6</td>
<td>0.076</td>
</tr>
<tr>
<td>6.</td>
<td>ALCN</td>
<td>+ + + + + + + +</td>
<td>4</td>
<td>30.7</td>
<td>0.307</td>
</tr>
<tr>
<td>7.</td>
<td>ANCS</td>
<td>+ + + + + + + +</td>
<td>1</td>
<td>7.6</td>
<td>0.076</td>
</tr>
<tr>
<td>8.</td>
<td>ARHM</td>
<td>+ + + + + + + +</td>
<td>1</td>
<td>7.6</td>
<td>0.076</td>
</tr>
<tr>
<td>9.</td>
<td>ASCB</td>
<td>+ + + + + + + +</td>
<td>1</td>
<td>7.6</td>
<td>0.076</td>
</tr>
<tr>
<td>10.</td>
<td>ASPN</td>
<td>+ + + + + + + +</td>
<td>1</td>
<td>7.6</td>
<td>0.076</td>
</tr>
<tr>
<td>11.</td>
<td>GABD</td>
<td>+ + + + + + + +</td>
<td>2</td>
<td>15.3</td>
<td>0.153</td>
</tr>
<tr>
<td>12.</td>
<td>LABS</td>
<td>+ + + + + + + +</td>
<td>4</td>
<td>30.7</td>
<td>0.307</td>
</tr>
<tr>
<td>13.</td>
<td>LBTR</td>
<td>+ + + + + + + +</td>
<td>1</td>
<td>7.6</td>
<td>0.076</td>
</tr>
<tr>
<td>14.</td>
<td>LCLR</td>
<td>+ + + + + + + +</td>
<td>1</td>
<td>7.6</td>
<td>0.076</td>
</tr>
<tr>
<td>15.</td>
<td>LCRD</td>
<td>+ + + + + + + +</td>
<td>3</td>
<td>23.0</td>
<td>0.230</td>
</tr>
<tr>
<td>16.</td>
<td>LCTC</td>
<td>+ + + + + + + +</td>
<td>4</td>
<td>30.7</td>
<td>0.307</td>
</tr>
<tr>
<td>17.</td>
<td>LFSC</td>
<td>+ + + + + + + +</td>
<td>8</td>
<td>61.5</td>
<td>0.615</td>
</tr>
<tr>
<td>18.</td>
<td>LHOI</td>
<td>+ + + + + + + +</td>
<td>2</td>
<td>15.3</td>
<td>0.153</td>
</tr>
<tr>
<td>19.</td>
<td>LHTS</td>
<td>+ + + + + + + +</td>
<td>1</td>
<td>7.6</td>
<td>0.076</td>
</tr>
<tr>
<td>20.</td>
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<td>38.4</td>
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<tr>
<td>21.</td>
<td>LMSS</td>
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<td>0.153</td>
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<tr>
<td>22.</td>
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<td>0.153</td>
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<tr>
<td>23.</td>
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<td>7.6</td>
<td>0.076</td>
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<tr>
<td>24.</td>
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<tr>
<td>25.</td>
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<td>1</td>
<td>7.6</td>
<td>0.076</td>
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</tbody>
</table>

[Species codes as per Perez and Schenck, 1990]

- ABRT : Acaulospora biculata Rothwell and Trappe
- ADLC : A. delicata Walker, Pfeiffer and Bloss
- ADLT : A. diatata Morton
- ADTC : A. denticulata Sieverding and Toro
- ACDM : A. gerdemannii Schenck and Niconson
- ALCN : A. lacunose Morton
- ANCS : A. nicolsoni Walker, Read and Sanders
- ARHM : A. rehmi Sieverding and Toro
- ASCB : A. scrobiculata Trappe
- ASPN : A. spinosa Walker and Trappe
- GABD : Gigaspora alboi Schenck and Smith
- LABS : Glomus ambisporum Smith and Schenck
- LBTR : G. botryoides Rothwell and Victor
- LCLR : G. clarum Nicolson and Schenck
- LCRD : G. clarodum Schenck and Smith
- LCTC : G. citricolum Tang and Zang
- LFSC : G. fasciculatum Thaxter
- LHII : G. hoi Brech and Trappe
- LHTS : G. heterosporum Smith and Schenck
- LLCT : G. lacteum Rose and Trappe
- LMSS : G. mossae Gerdemann and Trappe
- LPBS : G. pubescens Trappe and Gerdemann
- LPLD : G. pallidum Hall
- LRDT : G. radiatum Trappe and Gerdemann
- SPCC : Sclerocystis pachycaulis Wu and Chen

The quality and type of VAM propagules also affected the dynamics of root colonization, which were also increased by increasing the age of plant (Chandra and Jamaluddin, 1999). However, Saif and Khan (1975) found increased root colonization during the period of maximum vegetative growth and tillering of wheat plants (February – April in West Pakistan), this being directly influenced by the number of spores on the soil. However Hayman (1970) found that mycorrhizal colonization in winter wheat was sparse during the spring months, but increase during
summer months to a peak at harvest (September). While spore number in the soil increased greatly in July and decreased in September, wheat had become highly mycorrhizal only after tillering and most growth of crop has occurred. Hatrick and Bloom (1983) also found little VAM colonization of tall-planted hard red winter wheat until flowering in May after the cool soils of Kansas had warmed. Then a small amount (<1 to 10%) developed just prior to harvest. Similarly, in the Netherlands, Jakobson and Nielsen (1983) found slow and very low levels (<10%) of VAM colonization in winter cereals until mid April after which there was gradual approaching 50% at harvest 3 months later. In the present investigation all the varieties of wheat used are rainfed. During the cropping season mycorrhization of each variety was recorded and it was found that at the time of harvest in the month of March and April roots are highly colonized and spore density was also good which suggest that crop plant develop greater VAM fungal association at the time of harvest.

It is clearly evident from the results that, among the 25 species of VAM fungi obtain from the rhizosphere soil of wheat cultivars, 13 species belong to Glomus followed by 10 Acaulospora, with single species of Sclerocystis and Gigaspora. This result showed that Glomus and Acaulospora were found to dominate the wheat rhizosphere soils of Sagar. Among the Glomus species Glomus hoi (LHOI) was found much more frequent than any other species. From results we can interpretate that VAM species have preference for their association with wheat plant. High frequency and density of Glomus hoi (LHOI) suggest that it has the ability to exploit the condition prevailing in the rhizosphere of the wheat cultivars. In our earlier studies we have also observed dominance of Glomus species in the rhizosphere soil of the other plant. (Vyasa and Soni, 2004; Dwivedi et al., 2001a,b; Dwivedi et al., 2003; Dwivedi et al., 2004)

ACKNOWLEDGEMENT

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REFERENCES


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VA Mycorrhizal Fungi in Tropical Monsoon Grassland
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Mahendra Kumar Mishra, Anuradha Soni and Prashant Soni
Lab of Microbial Technology & Plant Pathology
Department of Botany, Dr. Hari Singh Gour University, Sagar (M.P.) 470003

Abstract

In the present study we have determined, diversity, richness and relative density of AM fungi associated with different forbs of tropical monsoon grassland of Dr. H. S. Gour University campus. The results obtained from the experiments, suggest that 77 – 100% root colonization found in all the 10 selected forbs. Maximum spore population 1447 spores / 100 gm of soil and 100% root colonization was recorded with Parthenium hysterophorus followed by Alysicarpus monilifera 1315 spores / 100 gm soil Malvavistum sp. 1309 spores / 100 gm soil and Euphorbia hirta 1296 spores / 100 gm of soil and root colonization recorded 100% in all the above mentioned forbs. In Tridex procumbens spore population was recorded minimum 967 spores / 100 gm. soil and lesser root colonization was 77%. Number of AM fungal spores and percent root colonization in other test forbs falls in between Euphorbia hirta and Tridex procumbens. It was also observed that species of Glomus was dominated followed by Acaulospora species of AM fungi such as Gigaspora, Scutelliforme, Scutellospora and Entrophospora were found poorly distributed among the test forbs.

Keywords: AM fungi/ forbs/Tropical monsoon grassland/ Species diversity.

Introduction

Arbuscular mycorrhizal fungi (AMF) are important biotrophic organism, which live in symbiosis with ≈ 80% of land plants, forming a mycorrhiza (i.e. root colonized by a symbiotic fungus). AMF affect plants biodiversity, as well as the variability and productivity of ecosystem. As few as ≈ 150 fungal species are known to form arbuscular mycorrhiza (AM) in the roots of a vast number of plants and varied from plants to plants. The reason within population variation in AMF has not been investigated in detail, probably due to the time-consuming methodology required to obtain a set of AMF individual in the laboratory that are representative of an AMF population. Oehl4 and Fitter5 has estimated AMF species in semi-natural grassland in Europe.

Natural grasslands occur in temperate zone with annual rainfall 25 to 28 cm, while in tropics they may be found in area receiving rainfall. The favourable conditions for development of stable grasslands are frequent rainfall and sufficient warmth during the growing season. Shukla and Chandel8 mentioned in his book that grassland in M.P. belong to Sehima-Dichanthium type grasslands having black soil environment.

The present study was conducted with a view to understand the ecological status of AM fungi found in association with different forbs of the region growing in the tropical monsoon grassland.

Materials and Methods

The experiment was carried out in 5 Km area around Dr. Hari Singh Gour University, Sagar. The soil and root samples were collected from rhizosphere of selected 10 forbs plants. The soil samples were sieved by wet sieving and decanting method. The roots were thoroughly washed in tap water and cut 1 cm long segments from root tip. The roots were stained according to modified method of Phillips and Hayman. Here we have used 10% NaOH in place of 10% KOH. VAMF species frequency, density and relative density were determined following, Phillips8. Species diversity (\(H\)) of AMF was calculated following Shannon and Weaver.

\[
H = -\sum \left( \frac{n_i}{N} \right) \ln \left( \frac{n_i}{N} \right)
\]

Where; \(H\) – Diversity Index
\(n_i\) – Number of individual species
\(N\) – Total number of species

Result and Discussion

The data are presented in table 1 show variability in the occurrence of AM fungal spores among the 10 test forbs. Maximum spore population (1447/100 gm of soil) of AM fungi were recorded with Parthenium hysterophorus and minimum was 967/100 gm of soil of Tridex procumbens percent colonization also differs in different forb plants, it was recorded 100 and 77%,
<table>
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<td>90</td>
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<td>Trides procumbens</td>
<td>967</td>
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<td>10</td>
<td>Parthenium hysterophorum</td>
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<td>0.19</td>
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</tbody>
</table>

respectively. Among the different AM fungi, Glomus and Acaulospora spp. found associated with almost all test forb plants. However, Sclerocystis spp. was found associated with Ageratum conoids, Alyscarpus monilifera, Euphorbia geniculata, Euphorbia hirta, Malvestrum sp., Parthenium hysterophorum, Phyllanthus simplex, and Trides procumbens, Gigaspora spp. show association with Ageratum conoids, Alyscarpus monilifera, Euphorbia geniculata, Malvestrum sp., Parthenium hysterophorum, Trides procumbens and Scutellospora spp. and Entrophosphora spp. were associated with least plants species.

Data of Statistical analysis of AM fungi associated with forbs are presented in Table 2, total 37 number of AMF species were found associated with forb plants. Among of 37 species, 18 species of Glomus, 10 species of Acaulospora, 4 species of Sclerocystis, 2 species of Gigaspora, 2 species of Scutellospora and one species of Entrophosphora was observed.

The density of Acaulospora spp. was 14.1 and species diversity (H) 2.24 was recorded. However the maximum density was recorded of Glomus species i.e. 31.9 and diversity index (H) 2.78 was calculated. While species density of Gigaspora was 0.20 recorded with 0.678 species diversity (H), and Sclerocystis species density was 2.8 and diversity index (H) 1.32 was estimated. The density of Scutellospora spp. was 1.8 and H - 0.686 was calculated whereas only single species of Entrophosphora was observed.

The arbucular mycorrhizal colonization and spore population of rhizosphere soils varied in different plant species raised in the grassland vegetation. AM fungi occurred in almost all terrestrial ecosystems. However, only some 150 fungal species have been described so far in contrast to over 250,000 known plant species. Typically 20-30 species of AM fungi occur in most plant communities, so that AM fungal diversity seems to be quite similar to that of plants in the same community. Niche separation between AM fungal taxa might therefore be expected yet almost nothing is known about their response to different environmental conditions, which would be required for an evaluation of such on hypothesis.

It is clearly evident from the results that Glomus spp. was dominating in the rhizosphere of test forbs followed by Acaulospora and Sclerocystis others Gigaspora, Scutellospora and Entrophosphora poorly distributed among the test forbs. These results are in with good accord of our
Table 2. A comparative study of distribution, diversity, frequency, abundance, density and relative density of AM fungi associated with different test forbs of Tropical Monsoon Cragland

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<tr>
<th>S No.</th>
<th>AMF spp.</th>
<th>1</th>
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<th>3</th>
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<td>2.24</td>
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**SE = 139**

|       | 1     | LAGR  | 1 | 2 | - | 2 | 7 | 1 | - | 2 | - | 4 | 19 | 70 | 2.4| 1.9| 5.95 | -0.16 |
| 2     | LAST   | 4 | - | 4 | 1 | - | 5 | - | 4 | - | 2 | 20 | 60 | 3.3| 2.0| 6.27 | -0.17 |
| 3     | LCRD   | 2 | - | 3 | 7 | 2 | 4 | - | - | 4 | - | 19 | 60 | 3.2| 1.9| 5.95 | -0.16 |
| 4     | LCLR   | 3 | 3 | - | 4 | 2 | 4 | - | 2 | - | - | 18 | 60 | 3.0| 1.8| 5.64 | -0.16 |
| 5     | LPDR   | - | - | 2 | 1 | 2 | 1 | 4 | - | - | 1 | 11 | 60 | 1.8| 1.1| 3.45 | -0.12 |
| 6     | LDMR   | 5 | 4 | - | - | 2 | - | 1 | - | - | - | 18 | 50 | 3.5| 1.8| 5.64 | -0.16 |
| 7     | LFSC   | 2 | 8 | 2 | 2 | - | 8 | 5 | 2 | 7 | - | 36 | 80 | 4.5| 3.6| 11.3 | -0.25 |
| 8     | LFGRG  | 2 | - | - | 6 | 3 | 1 | - | - | - | - | 16 | 60 | 2.6| 1.6| 5.0  | -0.15 |
| 9     | LFLY   | 1 | - | 5 | - | 2 | - | - | - | - | 8 | 30 | 2.6| 0.8| 2.5 | -0.09 |
| 10    | LGSP   | 4 | 2 | - | 2 | 3 | 4 | - | 2 | - | 5 | 22 | 70 | 3.1| 2.2| 6.8  | -0.18 |
| 11    | LHTS   | 1 | - | 4 | 5 | 2 | 3 | - | - | 4 | 19 | 60 | 3.1| 1.9| 5.95 | -0.16 |
| 12    | LHOI   | 3 | 3 | - | 4 | 2 | 2 | - | - | 5 | 17 | 60 | 2.8| 1.7| 5.3  | -0.15 |
| 13    | LINR   | - | - | 2 | 4 | - | 5 | - | 4 | 6 | 21 | 50 | 4.2| 2.1| 6.56 | -0.18 |
| 14    | LMCL   | 4 | - | 2 | 5 | 2 | - | - | - | - | 17 | 50 | 3.4| 1.7| 5.3  | -0.16 |
| 15    | LMSS   | 5 | 4 | 6 | - | 4 | 3 | 2 | 8 | 32 | 70 | 4.5| 3.2| 10.0 | -0.23 |
| 16    | LSMST  | 2 | 1 | - | 2 | 4 | - | 1 | - | - | - | 10 | 50 | 2.0| 1.0| 3.1  | -0.11 |
| 17    | LPST   | 2 | 1 | 2 | 1 | 1 | - | - | - | 2 | 9 | 60 | 1.5| 0.9| 2.8  | -0.10 |
| 18    | LVSF   | 1 | 3 | - | 1 | - | - | 2 | - | 7 | - | 40 | 1.75| 0.7| 2.18 | -0.08 |
|       | **Total**| 31.9| 99.7| 2.78 |   |   |   |   |   |   |   |   |   |   |   |   |   |

**SE = 1.73**

|       | 1     | GARD  | 2 | 2 | - | - | 1 | - | - | 4 | 9 | 40 | 2.2| 0.9| 69.1 | -0.35 |
| 2     | GMGRG  | - | 4 | - | 2 | - | - | 3 | - | 2 | 11 | 40 | 2.7| 0.11| 10.8 | -0.33 |
|       | **Total**| 1.01| 99.9| -0.678 |   |   |   |   |   |   |   |   |   |   |   |   |   |

**SE = 4.5**

|       | 1     | SPCC  | - | 2 | - | 4 | - | - | 1 | - | - | 7 | 30 | 2.3| 0.7| 25  | -0.35 |
| 2     | SPKS   | 2 | 4 | - | - | 2 | - | 3 | 11 | 40 | 2.5| 1.1| 39.2 | -0.37 |
| 3     | SRBF   | - | - | 1 | 2 | - | - | 2 | 3 | - | - | 8 | 30 | 1.6| 0.5| 17.85| -0.30 |
| 4     | SENS   | - | 3 | - | 2 | - | - | - | - | - | 5 | 20 | 2.5| 0.5| 17.85| -0.30 |
|       | **Total**| 2.8| 99.8| -1.32 |   |   |   |   |   |   |   |   |   |   |   |   |   |

**SE = 1.22**

|       | 1     | CPLC  | 1 | 2 | 1 | - | - | 3 | - | - | 1 | 3 | 50 | 1.6| 0.8| 44.4 | -0.36 |
| 2     | CHTG   | 4 | 2 | - | - | 2 | 1 | - | - | 1 | 10 | 50 | 2.0| 1.0| 55.5 | -0.32 |
|       | **Total**| 1.8| 99.9| -0.685 |   |   |   |   |   |   |   |   |   |   |   |   |   |

**SE = 0.71**

Note: Code of AMF species as Peretz and Schenck²; SE – Standard error; %F – Percent Frequency; A – Abundance; D – Density; RD – Relative Density; H – diversity index

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earlier findings. Chourasia and Khare have also reported AM distribution, colonization and dominance of Glomus spp in some grasses and forbs growing in this region. The dominance of Glomus in the monsoonic grassland of this region may be that Gigaspora required specific edaphic condition viz. low pH whereas most of the Glomus species are ubiquitous nature and they can be found growing in association with different host plants under different conditions.

Both the species richness and spore density of AMF depend upon the size of the area sampled, season sampled and yearly variation in precipitation and temperature. The factors like edaphic or climatic condition, host fungus compatibility, root properties and soil microorganisms might influence the abundance of spore population and mycorrhizal association with a particular plant species. A denser plant community helps the colonizing obligate AMF to spread extensively, with less propagule being lost to passive stochastic dispersal. However, plant diversity may be important in maintaining a diverse AMF community, and vice-versa. It is evident from the investigation that numbers of different AMF species are well adapted to the grassland vegetation of the region showing their high biodiversity with the soil.

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PLANT DISEASES MANAGEMENT IN SUSTAINABLE AGRICULTURE
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ABSTRACT

This article aims to demonstrate sustainable management of the fungal pathogens by regulation and exploitation of the microbial diversity without causing degradation of environment and health problems. Development of sustainable, integrated pest management (IPM) approaches for plant diseases control, ecology and characterization of plant pathogens and biocontrol agents. Restoring beneficial organisms that attack, repel, or otherwise antagonize disease-causing pathogens will render a soil disease-suppressive. Plants growing in disease-suppressive soil resist diseases much better than in soils low in biological diversity. Beneficial organisms can be added directly, or the soil environment made more favorable for them through use of compost and other organic amendments. Compost quality determines its effectiveness at suppressing soil-borne plant diseases. More recently, larger portions of the strategies utilized in agriculture have been biological control practices. In the broad sense, host genetics, soil amendments, fertilizer effects on pathogens, etc., are all part of the IPM picture.

INTRODUCTION

Sustainable Agriculture defined as an integrated system of plant production practices having a site-specific application that will, over the long term: satisfy human food and fiber needs; enhance environmental quality and the natural resource base upon which the agriculture economy depends; make the most use of nonrenewable resources and on-farm resources and integrate, where appropriate, natural biological cycles and controls; sustain the economic viability of farm operations and enhance the quality of life for farmers and ranchers and society as a whole (Gliessman, 1990; Neate, 1994).

Sustainable agriculture is a way of farming that can be carried out for
generations to come (Folgarait, 1998). This long-term approach to agriculture combines efficient production with the wise stewardship of the earth’s resources. Sustainable agriculture include the following:

- Meet human needs with a safe, high-quality and affordable supply of food and fiber.
- Protect the natural resource base and prevent the degradation of air, soil and water quality.
- Use nonrenewable resources efficiently.
- Use natural biological cycles and controls.
- Assure the economic survival of farming and the well being of farmers, their families and communities.
- Creation of institutional incentives and funding that focus public and private research, education, and technology development on integrating agricultural productivity and profitability with environmental stewardship.

New technology in all areas has improved agricultural production, thus its sustainability. Today’s agriculture is using best management practices (BMP’s), by targeting many of its applications, not broadcasting as was done in the past. New disease resistant hybrids, biological pest control, reduced fungicide use; cultural practices that reduce the incidence of diseases and better placement and reduced amounts of fertilizers are all being employed (Cook, 1994; Nisbet and Fox, 1991).

### Disease Suppressive Soils

There are two types of disease suppression, specific and general. Specific suppression results from one organism directly suppressing a known pathogen. These are cases where a biological control agent is introduced into the soil for the specific purpose of reducing disease incidence. General suppression is the result of a high biodiversity of microbial populations that create conditions unfavorable for plant disease development (Nisbet and Fox, 1991; Neate, 1994; Harrison and Frank, 1999).

Introducing a single organism to soils seldom achieves disease suppression for very long. If not already present, the new organisms may not be competitive.
with existing microorganisms. If soil conditions are inadequate, the introduced beneficial organism will not survive. This practice is not sufficient to render the soil "disease suppressive;" it is like planting flowers in the desert and expecting them to survive without water. With adequate soil conditions, inoculation with certain beneficial should only be needed once. A soil is considered suppressive when, in spite of favorable conditions for disease to occur, a pathogen either cannot become established, establishes but produces no disease, or establishes and produces disease for a short time and then declines (Schneider, 1982; Hermosa et al., 2000).

Suppressiveness is linked to the types and numbers of soil organisms, fertility level, and nature of the soil itself (drainage and texture). The mechanisms which disease suppresses organisms in these soils include induced resistance, direct parasitism (one organism consuming another), nutrient competition and direct inhibition through antibiotics secreted by beneficial organisms. Additionally, the response of plants growing in the soils contributes to suppressiveness. This is known as induced resistance and occurs when the rhizosphere (soil area around plant roots) is inoculated with a weakly virulent pathogen.

After being challenged by the weak pathogen, the plant develops the capacity for future effective response to a more virulent pathogen. In most cases, adding mature compost to a soil induces disease resistance in many plants. The level of disease suppressiveness is typically related to the level of total microbiological activity in a soil. Larger the active microbial biomass, greater the capacity to utilize carbon, nutrients and energy in the soil, thus lowering their availability to pathogens. In other words, competition for mineral nutrients is high, as most soil nutrients are tied up in microbial bodies. High competition—coupled with secretion of antibiotics by some beneficial organisms and direct parasitism by others—makes for a tough environment for the pathogen (Chen et al., 1993). Our goal is to create soil conditions with all three of these factors present.

Therefore we want high numbers and diversity of competitors, inhibitors and predators of disease organisms, as well as food sources on which these
organisms depend. The food for beneficial organisms comes either directly or indirectly from organic matter and waste products from the growth of other organisms. It should be noted that general suppression would not control all soilborne diseases. *Rhizoctonia solani* and *Sclerotium rolfsii*, for example, are not controlled by suppressive soils their large propagules make them less reliant on external energy or nutrient sources and therefore they are not susceptible to microbial competition. With these two pathogens, “specific” beneficial organisms such as *Trichoderma* and *Gliocladium* will colonize the harmful propagules and reduce the disease potential (Granatstein, 1998).

**Crop Rotation and Disease Suppression**

Avoiding disease buildup is probably the most widely emphasized benefit of crop rotation in vegetable production. Many diseases build up in the soil when the same crop is grown in the same field year after year. Rotation to a non-susceptible crop can help break this cycle by reducing pathogen levels. To be effective, rotations must be carefully planned. Since diseases usually attack plants related to each other, it is helpful to group vegetable rotations by family e.g., nightshades, alliums, cole crops, cucurbits. The susceptible crop, related plants and alternate host plants for the disease must be kept out of the field during the rotation period (Karlen *et al.*, 1994). Since plant pathogens persist in the soil for different lengths of time, the length of the rotation will vary with the disease being managed. To effectively plan a crop rotation it is essential to know what disease organisms affect what crops. In most cases, crop rotation effectively controls those pathogens that survive in soil or on crop residue. Nor will it help control pathogens that can survive long periods in the soil without a host *Fusarium*, for example. Rotation, by itself, is only effective on pathogens that can over-winter in the field or be introduced on infected seeds or transplants. Of course, disease-free transplants or seed should be used in combination with crop rotation. The period of time between susceptible crops is highly variable, depending on the disease. For example, it takes seven years without any cruciferous crops for clubfoot to dissipate. Three years between parsley is needed to avoid damping off. Three
years without tomatoes to avoid *Verticillium* wilt on potatoes. A three-year crop rotation is the standard recommendation for control of black rot (*Ceratocystis fimbriata*), stem rot (*Fusarium oxysporum*), and scurf (*Monilochaetes infuscans*) in sweet potatoes.

**Plant Nutrients and Disease Control**

Soil pH, calcium level, nitrogen form, and availability of nutrients can play a major role in disease management. Adequate crop nutrition makes plants more tolerant of or resistant to disease. Also, the nutrient status of the soil and the use of particular fertilizers and amendments can have significant impacts on the pathogen’s environment. One of the most widely recognized associations between fertility management and a crop disease is the effect of soil pH on potato scab. Potato scab is more severe in soils with pH levels above 5.2. Below 5.2 the disease is generally suppressed. Sulfur and ammonium sources of nitrogen acidify the soil, also reducing the incidence and severity of potato scab. Liming, on the other hand, increases disease severity. While lowering the pH is an effective strategy for potato scab, increasing soil pH or calcium levels may be beneficial for disease management in many other crops. Adequate levels of calcium can reduce club root in crucifer crops (broccoli, cabbage, turnips, etc.). The disease is inhibited in neutral to slightly alkaline soils (pH 6.7 to 7.2) (Campbell and Árthurl, 1990). A direct correlation between adequate calcium levels, and/or higher pH and decreasing levels of *Fusarium* occurrence has been established for a number of crops, including tomato, cotton, melons and several ornamentals (Jones *et al.*, 1989; Yamazaki and Hosina, 1995).

Calcium has also been used to control soilborne diseases caused by *Pythium*, such as damping off. Crops where this has proved effective include wheat, peanut, peas, soybeans, peppers, sugarbeet, beans, tomato, onions, and snapdragon (Ko and Ching-Wen, 1989). Researchers in Hawaii reported reduction of damping off in cucumber after amending the soil with calcium and adding alfalfa meal to increase the microbial populations (Ko and Ching-Wen, 1989). Potassium fertility is also associated with disease management. Inadequate potash levels can lead to
susceptibility to *Verticillium* wilt in cotton (Obrien-Wray, 1995). Phosphate can also be critical. Increasing phosphorus rates above the level needed to grow the crop can increase the severity of *Fusarium* wilt in cotton and muskmelon (Jones et al., 1989). In general, the combination of lime, nitrate nitrogen and low phosphorus is effective in reducing the severity of *Fusarium*.

**Biological Control**

Biological control of plant disease is defined as the involvement of the use of beneficial microorganisms, such as specialized fungi and bacteria, to attack and control plant pathogens and the diseases they cause (Lewis and Papavizas, 1991). These “specialized” fungi and bacteria are microorganisms that normally inhabit most soils. In their native habitat they compete with other microorganisms for space and food and in some cases they produce toxic substances that parasitize and/or kill other soil-inhabiting microorganisms such as *Pythium* sp., *Phytophthora* sp., *Rhizoctonia* sp., and other plant pathogens (Lorio et al., 1996). There are four different mechanisms by which biocontrol agents control other microorganisms. Most biocontrol agents apply only one of these four mechanisms, however, some may employ more than one. Direct competition with the target organism: In this case the biocontrol agent out competes the target organisms for nutrients and space.

**Antibiosis:** With antibiosis, the biocontrol agent produces a chemical compound such as an antibiotic or some type of toxin that kills or has some sort of detrimental effect on the target organism.

**Predation or parasitism of the target organism:** In this case the biocontrol agent can attack and feed directly on the target organism or the biocontrol agent can produce of enzymes and some sort of toxin that kills the target organism and then the biocontrol agent feeds on the dead target.

**Induced resistance of the host plant:** It has been know for decades that once a plant is infected with a pathogen, that infection triggers some sort of reaction in the infected host plant that helps keep it from being infected with other pathogens. The infected plant becomes more “resistant” to other infections.
In the area of greenhouse floriculture and perennial production there are about a half dozen products that are currently popular of these root shield appears to be the most widely used. Root shield is the T-22 strain of the soil inhabiting fungus *Trichoderma harzianum* (TH). It uses both antibiosis and predation against many common soil-inhabiting fungi that cause root and crown rots such as *Pythium, Rhizoctonia, Fusarium* and *Sclerotinia*. It appears to be one of the most popular bio-fungicides in the greenhouse industry and can be an asset to a disease management program if used properly. In order for any of these biological control agents to work for you, two simple rules must be followed. First off, all these products must be used in conjunction with standard disease cultural controls. Cultural controls include, growing plants in a well drained media, not over watering, keeping the greenhouse relative humidity below 85%, practicing strict sanitation and making sure that the nutrient and pH conditions of the host plant are within the ideal range for proper growth and development.

Chemical control of soil borne plant diseases is frequently ineffective because of the physical and chemical heterogeneity of the soil, which may prevent effective concentrations of the chemical from reaching the pathogen. Biological control agents colonize the rhizosphere, the site requiring protection and leave no toxic residues, as opposed to chemicals. Microorganisms have been used extensively for the biological control of soil borne plant diseases as well as for promoting plant growth. Fluorescent *Pseudomonas* are the most frequently used bacteria for biological control and plant growth promotion, but *Bacillus* and *Streptomyces* species have also been commonly used. *Trichoderma, Gliocladium* and *Coniothyrium* are the most commonly used fungal biocontrol agents (Hoitink, 1986).

Competition as a mechanism of biological control has been exploited with soil borne Plant pathogens as with the pathogens on the phylloplane. Naturally occurring, nonpathogenic strains of *Fusarium oxysporum* have been used to control wilt diseases caused by pathogenic *Fusarium* spp. Molecular techniques have also facilitated the introduction of beneficial traits into rhizosphere competent organisms to produce potential biocontrol agents. Chitin and b-(1,3) - glucan are the two
major structural components of many plant pathogenic fungi, except by oomycetes, which contain cellulose in their cell wall and no appreciable levels of chitin. Biological control of some soil borne fungal diseases has been correlated with chitinase production, bacterial producing chitinases or glucanases exhibit antagonism in vitro against fungi (Haran et al., 1996; Baek et al., 1999).

Many naturally occurring microorganisms have been used to control diseases on the aerial surfaces of plants (Elad, 2000). The most common bacterial species that have been used for the control of diseases in the phyllosphere include Pseudomonas syringae, P. fluorescens, P. cepacia, Erwinia herbicola and Bacillus subtilis. Fungal genera that have been used for the control of air borne diseases include Trichoderma, Ampelomyces and the yeasts Tilletiopsis and Sporobolomyces (Haggag and El-Gamal, 2001). Phytopathogenic bacteria possess several genes that encode phenotypes that allow them to parasitize plants and overcome defense responses elicited by the plant. In addition, phytopathogenic bacterial possess pathogenicity genes. Isogenic avirulent mutants can be produced by insertional inactivation of genes involved in pathogenicity. Nonpathogenic mutants of Erwinia amylovora, produced by transposon mutagenesis, have also been used in the biological control of fire blight. Antibiosis has been proposed as the mechanism of control of several bacterial and fungal diseases in the phyllosphere. Molecular biology techniques could be used to enhance the efficacy of biocontrol agents that use antibiosis as a more of action (Garcia et al., 1994). Biocontrol agents must normally achieve a high population in the phyllosphere to control other strains, but colonization by the agent may be reduced by competition with the indigenous microflora. Integration of chemical pesticides and biocontrol agents has been reported with Trichoderma spp. and P. syringae. Biocontrol agents tolerant to specific pesticides could be constructed using molecular techniques. Resistance to the fungicide benomyl is conferred by a single amino acid substitution in one of the B-tubulins of Trichoderma viridi. The corresponding gene they're by producing a biological control agent that could be applied simultaneously or in alternation with the fungicide.

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Inoculum products: The following is a partial list of soil inoculum and biocontrol products available for control of soil-borne diseases on a variety of plants: Liquid drench containing *Bacillus subtilis* GB03 for horticultural crops at seeding or transplanting or as a spray for turf target pathogen/disease is *Rhizoctonia, Pythium, Fusarium* and *Phytophthora*.

Peat-based dried biomass from solid fermentation; aqueous suspension of *Burkholderia cepacia* for control of *Rhizoctonia, Pythium, Fusarium* and disease caused by lesion, spiral, lance and sting nematodes. Used in alfalfa, barley, beans, clover, cotton, peas, grain sorghum, vegetable crops and wheat as a seed treatment, in drip irrigation or as a seeding drench.

Dry powder formulation of *Bacillus subtilis* for control of *Rhizoctonia solani, Fusarium* spp., *Alternaria* spp. and *Aspergillus* spp. attacking roots of cotton and legumes. Can be added to a slurry, or mixed with a chemical fungicide for commercial seed treatment. A seed inoculant of *Pseudomonas cepacia* for control of *Rhizoctonia solani, Fusarium* spp., *Pythium* spp. in corn, vegetables and cotton. *Agrobacterium radiobacter* strain K-84 for control of crow gall disease caused by *Agrobacterium tumefaciens* in fruit, nut and ornamental nursery stock. Used as a dip or spray for root, stems or cuttings.

Streptomycetes soil drench for suppression of *Fusarium, Alternaria* and *Phomopsis. Trichoderma* fungus for suppression of *Pythium, Rhizoctonia solani* and *Fusarium* spp. Applied as granules or wettable powder mixed with soil or potting medium or as a soil drench. Crops include trees, shrubs, transplants, all ornamentals, cabbage, tomato and cucumber.

*Gliocladium virens* GL-21 for damping-off and root rot pathogens especially *Rhizoctonia solani* and *Pythium* spp. of ornamental and food crop plants grown in greenhouses, nurseries, homes, and interior-scapes. Sold as granules. *Bacillus subtilis* GB03 plus chemical pesticides. Used as a dust seed treatment in the planter box for seedling pathogens of barley, beans, cotton, peanut, pea, rice and soybeans. *Trichoderma harzianum* Rifai strain KRL-AG2 for control of *Pythium* spp. *Rhizoctonia solani, Fusarium* spp. and *Sclerotinia homeocarpa* in bean, cabbage,
corn, cotton, cucumber, peanut, potato, sorghum, soybean, sugarbeet, tomato, turf and greenhouse ornamentals. Applied as in-furrow granules, broadcast to turf, mixed with greenhouse soil, or mixing powder with seeds in the planter box or in commercial seed treatment.

The *Trichoderma* system: *Trichoderma* spp. are one of a small group of beneficial fungi, which has proven commercially viable as a biological control agent. This microorganism is now registered as a bio-fungicide in India, France, the UK, Switzerland, Sweden, Belgium, Chile, New Zealand and the USA and regulations are pending in several other countries. *Trichoderma* thrives in the leaf litter or mulch in orchard situations and it requires a minimum organic carbon level of 1% to ensure proliferation in cropping locations. This species is a mycoparasite or saprophyte, which feeds on pathogenic fungi. There is now a body of photographic evidence highlighting this phenomenon where *Trichoderma* spp. are seen actively parasitic Basideomycetes including *Armillaria*, *Mellea*, *Rhizoctonia solani* and *Chondrostereum purpureum*. In fact, *Trichoderma* can control the growth of many opportunistic, wood-infecting, decay fungi, as well as many soil-borne fungi responsible for seedling wilt and damping off (e.g. *Fusarium* and *Pythium*) (Baek *et al.*, 1999; Elad, 2000). *Trichoderma* is completely safe for humans and livestock. In 55 years of research there has never been a recorded adverse reaction. The predatory qualities of *Trichoderma* are a big part of the appeal of this species of fungus for commercial applications, but there are other associated benefits that warrant consideration (Lorito *et al.*, 1996). The ability of *Trichoderma* in natural soil is important in terms of its disease control potential because the pathogen survives in soil in the form of sclerotia (Singh *et al.*, 2005).

Compost and Disease Suppression

Compost has been used effectively in the nursery industry; in high-value crops and in potting soil mixtures for control of root rot diseases (Haggag, Wafaa and Saber, 2000, 2001). Adding compost to soil may be viewed as one of a spectrum of techniques including cover cropping, crop rotations, mulching, and manuring, which add organic matter to the soil (Hoitink *et al.*, 1991; Logsdon,
The major difference between compost-amended soil and the other techniques is that organic matter in compost is already "digested". Other techniques require the digestion to take place in the soil, which allows for both anaerobic and aerobic decomposition of organic matter. Properly composted organic matter is digested chiefly through aerobic processes. These differences have important implications for soil and nutrient management, as well as plant health and pest management (Trankner, 1992; Hudson, 1994). Compost is effective because it fosters a more diverse soil environment in which a myriad of soil organisms exist. Compost acts as a food source and shelter for the antagonists that compete with plant pathogens, for those organisms that prey on and parasitize pathogens and for those beneficial that produce antibiotics. Root rots caused by Pythium and Phytophthora are generally suppressed by the high numbers and diversity of beneficial microbes found in the compost. Such beneficial prevent the germination of spores and infection of plants growing on the amended soil (Goldstein, 1998; Harrison and Frank, 1999). Systemic resistance is also induced in plants in response to compost treatments. Hoitink et al. (1997) has now established that composts and compost teas indeed activate disease resistance genes in plants. These disease resistance genes are typically "turned on" by the plant in response to the presence of a pathogen. These genes mobilize chemical defenses against the pathogen invasion, although often too late to avoid the disease.

Plants growing in compost, however, have these disease-prevention systems already running (Goldstein, 1998). Induced resistance is somewhat pathogen-specific, but it does allow an additional way to manage certain diseases through common farming practices. It has become evident that in disease management, using a "one size fits all" approach to composting will not work. Depending on feed stock, inoculum and composting process, composts have different characteristics affecting disease management potential. For example, high carbon to nitrogen ratio (C:N) tree bark compost generally works well to suppress Fusarium wilts. With lower C:N ratio composts, Fusarium wilts may become more severe as a result of the excess nitrogen, which favors Fusarium. (Hoitink et al., 1997).
Compost from sewage sludge typically has a low C:N ratio. Some of the beneficial microorganisms that re-inhabit compost from the outside edges after heating has subsided include several bacteria (Bacillus species, Flavobacterium balustinum and various Pseudomonas species) and several fungi (Streptomyces, Penicillin, Trichoderma and Gliocladium virens). The moisture content following peak heating of compost is critical to the range of organisms inhabiting the finished product. Dry composts with less than 34% moisture are likely to be colonized by fungi and therefore are conducive to Pythium diseases (Hoitink et al., 1997). Compost with at least 40 to 50% moisture will be colonized by both bacteria and fungi and will be disease suppressive (Hoitink et al., 1997). Water is typically added during the composting process to avoid a dry condition. Compost pH below 5.0 inhibits bacterial biocontrol agents. Three approaches can be utilized to increase suppressiveness of compost. First, curing the compost for four months or more; second, incorporating the compost in the field soil several months before planting and third, inoculating the compost with specific biocontrol agents (Hoitink et al., 1997). Two of the more common beneficial used to inoculate compost are strains of Trichoderma and Flavobacterium, added to suppress Rhizoctonia solani.

Trichoderma harzianum acts against a broad range of soil-borne fungal crop pathogens, including R. solani, by production of antifungal exudates. The key to disease suppression in compost is the level of decomposition as the compost matures; it becomes more suppressive. Readily available carbon compounds found in low-quality, immature compost can support Pythium and Rhizoctonia.

As these compounds are reduced during the complete composting process, saprophytic growth of these pathogens is dramatically slowed (Nelson et al., 1994). Beneficial such as Trichoderma hamatum and T. harzianum, unable to suppress Rhizoctonia in immature composts, are extremely effective when introduced into mature composts. For Pythium suppression, a direct correlation has been shown between general microbial activity and amount of microbial biomass and the degree of suppression. Pythium is a nutrient-dependent pathogen with the ability to colonize fresh plant residue, especially in soil that has been fumigated to kill all soil life. The
severity of diseases caused by *Pythium* and *R. solani* relates less to the inoculum density than to the amount of saprophytic growth the pathogen achieves before infection (Cook, 1994). Consequently, soils that are antagonistic to saprophytic growth of *Pythium* such as soils amended with fully decomposed compost will support lower disease levels. As for *Rhizoctonia*, this fungus is highly competitive in colonizing fresh organic matter (Chung et al., 1988). Its ability to colonize decomposed organic matter is decreased or non-existent. There is a direct relationship between compost’s level of decomposition and its suppression of *Rhizoctonia* again pointing to the need for high-quality, mature compost. Like compost, raw manure is conducive to diseases at first, and then becomes suppressive after decomposition. In other words: organic amendments supporting high biological activity (i.e., decomposition) are suppressive of plant-root diseases, while raw organic matter will often favor colonization by the pathogen.

It is clear that compost maturity is a key factor in its ability to suppress disease. The challenge involved in achieving and measuring that maturity is the primary reason why compost is not more widely used. Certainly, immature compost can be used in field situations, as long as it is applied well ahead of planting, allowing for eventual stabilization. However, good disease suppression may not develop because of other factors. For example, highly saline compost actually enhances *Pythium* and *Phytophthora* diseases unless applied months ahead of planting to allow for leaching. High-quality compost should contain disease-suppressive organisms and mycorrhizal inoculum (Hoitink et al., 1997).

Direct Inoculation with Beneficial Organisms

There are a number of commercial products containing beneficial, disease-suppressive organisms. These products are applied in various ways including seed treatments, compost inoculants, soil inoculants and soil drenches. Among the beneficial organisms available are *Trichoderma*, *Flavobacterium*, *Streptomyces*, *Gliocladium* spp., *Bacillus* spp., *Pseudomonas* spp. and others. A partial list of these products can be found in the resources section. These companies will send you their product and technical information upon request. Consider your cost and
overall soil health before trying these products. *Trichoderma* and *Gliocladium* are effective at parasitizing other fungi, but they stay alive only as long as they have other fungi to parasitize. In soils with low fungal biomass (soils with low organic matter and plenty of tillage) these two beneficial have nothing to feed on. Compost is a great source of both the organisms and the food they need to do their jobs. A great diversity of bacteria and fungi occur in good compost.

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DISTRIBUTION OF VAM FUNGI IN TWO DIFFERENT RICE CROP FIELDS

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ABSTRACT

The present study deals with the occurrence of VA-Mycorrhizal fungi in two different rice varieties i.e. basmati and IR-36 grown in their respective climatic conditions. Basmati worldfame rice variety was grown in crop field of Rishikesh and IR-36 was grown in Rehli. The results obtained from the experiments suggest that the association of mycorrhizal fungi with basmati rice was much higher than the association with IR-36. In basmati rice not only VAM fungal average spore population (1236 spores/100gm of soil) and average percent colonization (69%) but were higher also number of VAM species were greater in comparison to IR-36 where we observed VAM fungal average spore population was 932 spores / 100 gm of soil, and average percent root colonization was 58% and lesser number of VAMF species. As usual, during wet/flooded condition, mycorrhizal association was reduced but at maturation / harvesting phase VAMF association was found to be increased in both the rice varieties. Interesting feature of this study was the occurrence of ASPN (Acaulospora spinosa) only with IR-36 at maturation and harvesting phase whereas in basmati ADLC (Acaulospora delicata), and ALVS (Acaulospora leavis) were found associated at seedling phase. ATRP (Acaulospora trappei), LDMR (Glomus dimorphicum) and LHTS (Glomus heterosporum) were found during maturation phase. ADLC (Acaulospora delicata), LABD (Glomus albidum), LABS (Glomus ambisporum), LAST (Glomus australis) and LOCT (Glomus occultum) were found at harvesting phase.

INTRODUCTION

The distribution of VA mycorrhizal fungi is known in more than 80% of
plant species which show such symbiotic association worldwide (Smith & Read, 1997). These symbiotic AM fungi belonging to order Glomales and division Zygomycota might also be important agent promoting plants coexistence (Hart et al., 2003). The occurrence and abundance of vascular plants in a particular community may depend on the presence of one to several AM fungi (Read 1998; van der Heijden et al., 1998; Renker et al. 2005).

Rice is one of the important crops and staple food of people of our country. According to Cassman et al. (1995) the main contribution to global rice supply mostly comes from Asian wetland rice systems. These systems are excellent example of sustainable soil fertility maintenance (Datta, 1981 ). A unique feature of soils that remain flooded for prolonged periods, (for example soils that are used for continuous lowland rice cultivation) is the maintenance of soil fertility and productivity of wetland rice based production systems (Sahrawat 1994).

Upland based rice production systems have a greater tendency for unsustainability due mainly to relatively rapid loss of organic matter, degradation of soil fertility and deterioration in physical, chemical and biological properties of rice. (Sahrawat, 2005)

The traditional way of growing lowland rice involves land preparation by cultivation at the land in flooded or wet state (pudding), followed by transplanting rice seedlings into the puddled rice paddies and growing the crop in a submerged condition.

As a part of an experimental study of the ecological role of VA mycorrhiza a quantitative analysis was carried out to record the occurrence of infection of VAM in agroecosystems of Rishikesh and Rehli. Both are situated in different locations and different environmental conditions. The most demanded basmati rice is cultivated in the foot hills of Himalayas. The particular soil and climate of this region is thought to account for basmati taste and texture. The word basmati means smell of earth (bass = smell, mati = earth) is famous world over for its taste, aroma and rightly named by rice lovers around the world and considered to be the prince among 1400 cultivated varieties of rice (cultivars) available in the
world. Basmati is a long duration crop (135-140 days). IR-36 is a hybrid variety and medium duration crop (115-125 days) and can be grown in normal environmental condition. Reports on VAM fungal association with rice plants are available both with upland (Gangopadhyay et al. 1982; Amrani et al. 1985) and lowland condition (Sivaprasad et al. 1990). Since very little study has been done on the association of VAM fungi with rice crop, this study was done with a view to know whether VA mycorrhizal fungi are common in two different rice varieties grown in their respective native habitats i.e. basmati in Rishikesh and IR-36 in Rehli?

MATERIALS AND METHODS

The experiment was carried out in the rice field of Rishikesh (Uttranchal) and Rehli (Sagar). The soil and root samples were collected from the rhizosphere of basmati rice variety and IR-36 rice variety. The soil samples were sieved by wet sieving and decanting method (Gerdemann and Nicolson, 1963) to determine the chlamydospore population in soil. The roots were thoroughly washed in tap water and cut into pieces of 10 mm in length. The roots were stained according to the method of Phillips and Hayman (1970). Physico-chemical properties of soils are given in Table 1.

Table – 1 : Physico – Chemical properties of Rhizosphere Soil of IR-36 and Basmati Varieties or Rice before sowing and after harvest.

<table>
<thead>
<tr>
<th>Properties</th>
<th>Soil parameters</th>
<th>Variety basmati (Rishikesh)</th>
<th>Variety IR-36 (Rehli)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Pre sowing</td>
<td>Post harvest</td>
</tr>
<tr>
<td>Physical</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>PH</td>
<td>7.0</td>
<td>6.8</td>
</tr>
<tr>
<td></td>
<td>Conductivity (sm⁻¹)</td>
<td>0.22</td>
<td>0.30</td>
</tr>
<tr>
<td></td>
<td>Temp (°C)</td>
<td>29</td>
<td>25</td>
</tr>
<tr>
<td></td>
<td>Colour</td>
<td>Grey</td>
<td>Grey</td>
</tr>
<tr>
<td></td>
<td>Texture</td>
<td>Clay loam</td>
<td>Clay loam</td>
</tr>
<tr>
<td>Chemical</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Nitrogen kg ha⁻¹</td>
<td>305</td>
<td>319</td>
</tr>
<tr>
<td></td>
<td>Phosphorus kg ha⁻¹</td>
<td>10.2</td>
<td>9.7</td>
</tr>
<tr>
<td></td>
<td>Potassium kg ha⁻¹</td>
<td>320</td>
<td>285</td>
</tr>
</tbody>
</table>
RESULTS AND DISCUSSION

The data of spore population, percent root colonization, number of arbuscules, number of vesicles, number of VAMF species for basmati and IR-36 rice varieties are presented in Table 2. The results show that in basmati during seedling phase, spore population was 1172 spores/100 gm of soil, percent colonization was 68% and number of VAMF species was 10. During maturation phase spore population came down to 698/100 gm of soil, percent colonization reduced to 47%, and number of VAM species also declined to 8. However, at the time of harvesting not only spore population increased to 1440 spores/100 gm of soil but also number of VAMF species increased to 15 and percent colonization was 92%. Interestingly average number of arbuscules was 32/cm of root bit at the seedling phase and 491/cm root bit at the time of harvesting.

The data on spore population, percent colonization, number of arbuscules, number of vesicles and number of VAMF species for the rice variety IR-36 are also presented in same Table 2. The results show that during seedling phase spore population was 1098 spores/100 gm of soil, percent colonization was 65% and number of VAMF species was 9. During maturation phase spore population was 488 spores/100 gm of soil, percent colonization was 29% and numbers of VAMF species 6. At the time of harvesting also, similar trend was observed (1200 spores/100 gm of soil, percent colonization 80% and number of VAMF species 11).

Average number of arbuscules were 22/cm of root bit at seedling phase and 35/cm of root bit at the time of harvesting.

Total 21 VAMF species were recorded during the investigation. Among them, Glomus species dominated followed by Acaulospora species whereas Gigaspora, Sclerocystis and Scutelllospora species were poorly distributed.

Figure 1 shows common VAMF species in both the rice varieties. ABRT and LHOI species were common in all the three stages (seedling, maturation and after harvesting). No common species were found in seedling and maturation phase. However, LFSC, LMSS and SPCC species were common in seedling and harvesting phases ASCB and LAGR were common in maturation and harvesting.
Table 2: VAM association with Rice crop, Basmati variety at field of Rishikesh and IR-36, variety at field of Rehli

<table>
<thead>
<tr>
<th>Rice Variety</th>
<th>Cropping Phase</th>
<th>Spore Density / 100 gms soil</th>
<th>% Colonization</th>
<th>VAMF association</th>
<th>No. of Vesicles cm root bit</th>
<th>No. of VAM spp.</th>
<th>Name of associated VAM fungal spp.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Basmati</td>
<td>Seedling</td>
<td>1172</td>
<td>68</td>
<td>37</td>
<td>-</td>
<td>10</td>
<td>ABRT, ADLC, GABO, GRSA, LABS, LFSC, LMSS, LHDI, LGSP, SPCC</td>
</tr>
<tr>
<td></td>
<td>Maturation</td>
<td>698</td>
<td>47</td>
<td>6</td>
<td>8</td>
<td>8</td>
<td>ASCB, ABRT, ATRP, LMSS, LHDI, LAGR, LAST, LHTS</td>
</tr>
<tr>
<td></td>
<td>Harvesting</td>
<td>1440</td>
<td>92</td>
<td>-</td>
<td>46</td>
<td>15</td>
<td>ANCS, ABRT, ADLC, ASCB, GRSA, LABS, LAGR, LFSC, LMSS, LHDI, LOCR, LABO, LOMR, CPLC, SPCC</td>
</tr>
<tr>
<td></td>
<td>CD P=0.05</td>
<td>0.45</td>
<td>1.51</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ABRT, ASCB, LFSC, LMSS, LGSP, LHDI, SPCC, GABO, GRSA</td>
</tr>
<tr>
<td>IR-36</td>
<td>Seedling</td>
<td>1098</td>
<td>65</td>
<td>30</td>
<td>-</td>
<td>9</td>
<td>ASCB, ASPN, ABRT, LHDI, LAGR, LFSC,</td>
</tr>
<tr>
<td></td>
<td>Maturation</td>
<td>488</td>
<td>29</td>
<td>4</td>
<td>10</td>
<td>6</td>
<td>ABRT, ANCS, ASPN, ASCB, LMSS, LFSC, LHDI, LGSP, LAGR, SPCC, CPLC</td>
</tr>
<tr>
<td></td>
<td>Harvesting</td>
<td>1200</td>
<td>80</td>
<td>-</td>
<td>40</td>
<td>11</td>
<td></td>
</tr>
<tr>
<td></td>
<td>CD P=0.05</td>
<td>0.39</td>
<td>0.45</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td></td>
</tr>
</tbody>
</table>

ABRT  Acaulospora bireticulata (Rothwell & Trappe)  
ADLC  Acaulospora delicata (Walker, pfeiffer & Boloss)  
ANCS  Acaulospora nicolsonii (Walker, Read & Sanders)  
ASCB  Acaulospora scrobiculata (Trappe)  
ASPN  Acaulospora spinosa (Walker & Trappe)  
ATRP  Acaulospora tropaei (Ames & Linderman)  
GARD  Gingspori alobida (Walker & Sanders)  
ND  Not detected  
GRSA  Gigaspora rosea (Schenck & Smith)  
LABO  Glomus albidum (Nicolson & Schenck)  
LABS  Glomus ambisporum (Walker & Rhodes)  
LAGR  Glomus aggregatum (Smith & Schenck)  
LAST  Glomus australe (Schenck & Smith emend. Koske)  
LOCT  Glomus fasciculatum (Boyetchko & Tiwari)  
LGRM  Glomus geosporum (Thaxter)  
LHDI  Glomus hoi (Nicolson & Gerdemann, Walker)  
LHTS  Glomus heterosporum (Breach & Trappe)  
LMSS  Glomus mosseae (Smith & Schenck)  
LOCT  Glomusoccultum (Gerdemann & Trappe)  
SPCC  Sclerocystis pachycaulis (Walker)  
CPLC  Scutellospora pellucida (Wu & Che)  

Note: Code of VAM species as Perez and Schenck, 1990.
phases, GABD, GRSA, LGSP species were common in seedling phase only, CPLC and ANCS species were common only in harvesting phase.

Figure 2 shows occurrence of VAM fungi only in one rice variety either basmati or IR-36. It is clearly evident from the observation that ASPN is present only in IR-36 at maturation and harvesting phase. This VAM fungal species was not observed in basmati variety.

However, in basmati variety ADLC and LABS occurred only at seedling and harvesting phase, ATRP, LAST and LHTS occurred only at maturation phase. LABD, LDMR and LOCT occurred only at harvesting phase. All these species were not found associated with IR-36 at any phase.

The VAMF root infection is a dynamic process, which is influenced by various factors such as seasons, VAM species, soil temperature, soil PH, host cultivar susceptibility to VAM colonization and feeder root condition at tissue of sampling. The quantity and type of VAM propagates also affected the dynamic, of root infection, which increased with the age of plant (Chandra and Jamaluddin 1999). However, Saif and Khan (1975) found increased root colonization during the period of maximum vegetative growth and tillering of wheat plants (February-April in W. Pakistan).

During submerged conditions VAM fungal viability, number of VAM fungi and number of spores decreased (Ilag et al. 1987). VAM fungi require oxygen (O₂) for their metabolism which is usually lacking in saturated soils. However, a close examination of several wetland plant species revealed a surprisingly high level of mycorrhizal colonization (Stunlund and Charval, 1994). Cultivated wetland rice (Oryza sativa) is known to support and benefit from mycorrhizal fungi. (Secilia and Bagyaraj, 1992). Many aquatic plants have air channels in their stems and roots called “aerenchyma” which serve as a gas exchange tissue for submerged portions of the plants. Plants that contain these aerenchyma channels may support mycorrhizal fungi (Stenlund and Chazvat, 1994).

However, with the aging of the plants i.e. crops field started drying up resulting into increase in VAMF. Jalalludin and Anwar (1991) reported reduction in
Fig. 1 - Occurrence of VAM fungi common in both rice varieties - Basmati and IR-36
Fig. 2 - Occurrence of VAM fungi only in one rice variety either in Basmati or in IR-36
VAM fungi at seedling phase and increased population of VAMF at the time of harvesting in wheat and rice crop fields.

The uneven distribution of VAMF in two rice varieties may be attributed to the difference in physico-chemical properties of soil of Rehli and Rishikesh region. According to Dwivedi, (2003) in different wheat cultivars, concentration of K influences the occurrence of VAMF in host plants. Lower concentration favours occurrence of VAMF while higher concentration becomes detrimental for them. Here also potassium concentration of rhizosphere soil of IR-36 was higher than rhizosphere soil of basmati.

In spite of the fact that VAM fungi have very little host specificity (Hayman, 1983), the host plant appears to control in some way the rate of fungal colonization (Baath et al. 1984) and there are indications of dissimilar colonization patterns by the same fungus in different hosts (Hepper, 1985). In our recent findings we have observed that VA mycorrhizal species varied with different grasses grown in semi-natural grasslands (Vyas and Soni, 2004) and different wheat cultivars (Vyas et al., 2006)

In this study we have also observed similar results. This suggests that host as well as physico-chemical properties of rhizosphere soils play an important role in occurrence of VAM fungi in rice field.

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