List of Publications


Patterns of endorhizal fungal associations in fruit crops of southern India

Sarah Jaison¹, Krishnasamy Rajeswari¹, and Thangavelu Muthukumar¹*

¹ Root and Soil Biology Laboratory, Department of Botany, Bharathiar University, Coimbatore 641 046, Tamilnadu, India

Abstract

A survey on the endorhizal status of 39 fruit crops of 25 families, indicated that 22 fruit crops had arbuscular mycorrhizal (AM)–, four had dark septate endophyte (DSE)–fungal association, and 13 had dual colonization of AM and DSE fungi. Fruit crops were capable of forming Arum-, Paris-, or intermediate-types of AM morphologies of which intermediate-type was common. To our knowledge, we report for the first time AM in 10 fruit crops and DSE-fungal association in 17 fruit crops. The extent of AM- and DSE-fungal colonization ranged from 41% to 98% and < 1% to 89.9%, respectively, in different fruit crops. Arbuscular mycorrhizal–fungus spore numbers in the rhizosphere ranged from 6 to 61 spores per 25 g of soil. Arbuscular mycorrhizal–fungus spores belonging to Acaulospora, Glomus, and Scutellospora were isolated from the rhizosphere soil.

Key words: arbuscular mycorrhizae / Arum-type / Paris-type / dark septate endophyte fungi / fruit crops / Glomus / microsclerotia / morphology

Accepted September 9, 2011

1 Introduction

Tropics are rich in fruit species, many of which are important components of the tropical ecosystems. Many tropical fruit species are significant food and habitat resources. Only a dozen or so of the major crop plants worldwide are tropical fruits. Plants including fruit crops are associated with diverse group of soil microorganisms, which influence their survival and health in natural and man-made ecosystems. Among the different plant–microbial associations the most common and widespread types of association is arbuscular mycorrhizal (AM) association. Arbuscular mycorrhizal fungi belonging to the phylum Glomeromycota are the essential components of soil biota, which links plant community and soil in different ecosystems (Smith and Read, 2008). Their role includes improvement in plant growth through uptake of nutrients, especially P in nutrient-deficient soils. Other nonnutritional benefits include uptake of water, protection of plants against various stresses, and improvement in soil structure (Smith and Read, 2008).

Although it is assumed that > 80% of the plant species are mycorrhizal, our current knowledge on the mycorrhizal status for most plant families is based on actual examination of one or a few species. Hence, Wang and Qiu (2006) pointed out, that the first area that deserves more attention in current mycorrhizal research is the examination of more plant species for their mycorrhizal status. In addition, AM morphology within roots can vary with host species. Based on the occurrence of AM-fungal structures within roots, AM morphology has been classified as Arum-, Paris-, or intermediate types (Smith and Smith, 1997; Dickson, 2004). In Arum-type, the fungal hyphae and vesicles are intercellular whereas arbuscules are intracellular. Paris-type is characterized by intracellular fungal structures. Intermediate type of AM morphology shares the characters of both Arum- and Paris-types (Dickson, 2004). Although mycorrhizal status and morphology are reported for a wide range of crop plants (Wang and Qiu, 2006; Dickson et al., 2007; Muthukumar and Tamilselvi, 2010), information is limited with horticultural fruit plants (Wang and Qiu, 2006; Dickson et al., 2007; Khanam, 2007).

Another diverse group of fungi characterized by melanized and septate hyphae also colonize plant roots and are commonly referred to as dark septate endophyte (DSE) fungi. Although occurrence of DSE-fungal association in a wide range of hosts and habitats has been known, most of these reports are from temperate regions (Jumpponen and Trappe, 1998). The role of DSE fungi on plants range from mutualistic (Usuki and Narisawa, 2007) to pathogenic (Wilcox and Wang, 1987). Although DSE-fungal association in crop plants has been recently reported (Muthukumar and Tamilselvi, 2010), information on their occurrence in fruit crops is scarce. Therefore, the objective of the present investigation was to investigate the AM incidence, morphology, spore numbers, and DSE status of different fruit crops growing in two sites in southern India.

2 Materials and methods

2.1 Sample collection

Plant roots and soil samples of 39 fruit crops belonging to 25 families were collected during October–December 2007 at two different sites. Site A is Kallar located at the banks of river Bhavani in Mettupalayam (11°30' N, 76°95' E, 314 m asl). The mean maximum and minimum temperatures during sum-
Short communication

Assessment of metal accumulation capacity of *Brachiaria ramosa* collected from cement waste dumping area for the remediation of metal contaminated soil

P.M. Lakshmi a, Sarah Jaison b, T. Muthukumar b, M. Muthukumar a,∗

a Department of Environmental Sciences, Bharathiar University, Coimbatore 641046, Tamilnadu, India
b Department of Botany, Bharathiar University, Coimbatore 641046, Tamilnadu, India

**A R T I C L E   I N F O**

Article history:
Received 12 February 2013
Received in revised form 3 July 2013
Accepted 6 July 2013

Keywords:
Lead
Zinc
Shoot accumulation
*Brachiaria ramosa*
Remediation

**A B S T R A C T**

Plant and soil samples were collected from areas surrounding a cement factory. As the vegetation around the cement factory was predominated by *Brachiaria ramosa* (*B. ramosa*) and due to its ecological importance, it was evaluated for its metal accumulation capacity. An assessment of the plant and soil samples for metals such as Zn, Pb, Cd and Hg indicated that *B. ramosa* accumulated significant amounts of Pb and Zn in its shoot and root tissues several folds higher than their available concentration in the soil, hence, designated as an accumulator of metals. In the shoot, Pb accumulation of *B. ramosa* was found to be of great importance as it can be a promising plant for the remediation of Pb contaminated soil.

© 2013 Elsevier B.V. All rights reserved.

1. Introduction

Metals are noted environmental contaminants with recorded effects on environmental quality. Among the various sources such as mining activities, agronomic practices, application of industrial effluents for irrigating crop plants or application of sludge as manure, industrial sources predominates soil contamination with metals and thereby influence the ecosystem in its proximity. Cement factories though not in large numbers are potent sources of metals such as Cd, Hg, Zn, Pb and Cr which affects soil and aquatic ecosystem through deposition (Banat et al., 2005). The long term persistence of metals in the soil aggravates the risk it causes to human and animal health (Gupta and Sinha, 2007). Lead is a potent environmental contaminant and it alters the normal metabolic pathways in plants including photosynthesis, respiration, and other such key metabolic processes by disrupting specific cellular enzymes (Ruley et al., 2004). Similarly, excess Zn can have negative effects such as inhibition of seed germination, plant growth, root development, and causes leaf chlorosis (Nagajyoti et al., 2010). Although metal contaminated soil affect the growth of plants and soil microbes, such an environment is not totally devoid of flora and fauna, as a number of species have adapted to tolerate increased metal concentrations (Dazy et al., 2009). Therefore, presence of plants in the metalliferous soils necessarily implies that they have developed mechanisms to tolerate toxic levels of metals and may accumulate them to high concentrations, if they are accumulators or hyper accumulators. Further, several plant species are well known indicators of soil pollution by metals (Wenzel and Jockwer, 1999). Apart from this, native plants are generally more preferred than exotic species for phytoremediation as it could better adapted to the environmental conditions of the particular region. In this study, both soil and plant samples were collected from the waste dumping area of a cement factory which is highly contaminated with metals. As *B. ramosa* is a predominant plant in the area adjacent to the cement factory, and have assessed its ability to accumulate metals.

2. Materials and methods

Soil (up to 20 cm) and plant samples were collected (400 m away, in the northwest direction) from the waste dumping area of the cement factory located in the Coimbatore District (10° 12′ and 11° 24′ N, 76° 39′ and 77° 30′ E; 426–550 m a.s.l. and annual rainfall 500–700 mm) of Tamilnadu, India. The control samples were collected 1000 m away (in the same direction) from the study area. The soil samples collected were sieved through a 2 mm...
Role of Organic Amendments on Arbuscular Mycorrhizal Formation and Function

Sarah Jaison, E. Uma and T. Muthukumar
Root and Soil Biology Laboratory, Department of Botany, Bharathiar University, Coimbatore – 641 046, Tamilnadu, India

Abstract

The last two decades have seen a renewed interest in organic farming and amelioration of soils affected by conventional agriculture. Different types of organic substances like farmyard manures, green manures, composts, sludges and effluents are added to the soil to enhance fertility. These organic amendments influence soil microbial populations and function. Arbuscular mycorrhizal (AM) fungi are an integral component of most agricultural and natural systems, and provide a range of benefit to the host plant. The prime benefit of AM fungi to plants include improved nutrition especially phosphorus (P) and nitrogen (N) in nutrient stressed soils. Other non-nutritional benefits include improved water relations, enhanced resistance to soil-borne pathogens, improved drought resistance, heavy metal tolerance and soil structure. As most crop and horticultural plants are mycorrhizal any factors that influence AM fungi affects plant growth and productivity. Organic amendments improve plant mycorrhization, AM fungal spore numbers and their diversity. However, certain organic sources rich in certain chemicals like phenols inhibit mycorrhization. The effect of organic amendments on AM fungi depends on the composition of the organic sources.

Keywords: Arbuscular mycorrhizal fungi, organic farming, plant growth, soil amendments

1 corresponding author e-mail: tmkum@yahoo.com.
INFLUENCE OF ORGANIC POLLUTANTS ON ARBUCULAR MYCORRHIZAL FUNGI

Eswaranpillai Uma, Sarah Jaison and Thangavelu Muthukumar*
Root and Soil Biology Laboratory, Department of Botany, Bharathiar University, Coimbatore – 641 046, Tamilnadu, India

ABSTRACT

The numerous benefits contributed by arbuscular mycorrhizal (AM) fungi has lead to recognition of their benefits in sustainable agriculture and various natural environmental processes. Application of anthropogenic and other compounds intentionally in the form of pesticides, fungicides, fertilizers or unintentionally like polycyclic aromatic hydrocarbons (PAH) which affect soil fungi have shown varying effects on AM association. Not all organic pollutants are detrimental to AM fungi. Some fungicides such as Fludioxonil have a stimulatory effect on mycorrhizal formation and function. Rapid decrease in the metabolic activity of AM fungi, a decline in arbuscule production, which is the main site of nutrient exchange between the host plant and the fungus, reduction in the total root length colonized and slow colonization rates are the negative effects shown by certain fungicides. Pesticides generally inhibit AM colonization and spore numbers. Slow release mineral fertilizers though benefit AM fungi, their excessive use can result in suppression of the AM fungi. Certain PAH especially anthracene reduce the development of extra radical mycelium, sporulation, root colonization and spore germination. Different AM fungal species show differential sensitivity even within a particular class of organic pollutant. Caution should also be exercised while irrigating soils with effluents as these could affect AM fungi. A reduction in our dependency on conventional agricultural practices especially organic pesticides by using AM fungi as a biological tool which is possible only by maintaining low levels of organic pollutants in the soil. Minimal use of organic pollutants especially pesticides would enable the maintenance of a healthy AM fungal populations essential for sustainable plant production systems.

* Corresponding author, e-mail: tmkum@yahoo.com
Chapter 3
Role of Arbuscular Mycorrhizal Fungi in Alleviation of Acidity Stress on Plant Growth

Thangavelu Muthukumar, Perumalsamy Priyadharsini, Eswaranpillai Uma, Sarah Jaison and Radha Raman Pandey

Introduction

A large number of abiotic and biotic factors influence the establishment, health, and productivity of plants in both natural and agroecosystems. Among these, soil factors influence various plant processes to a greater extent since soil is the natural substrate for plants to anchor and take up nutrients and water. Around 30–40 % of the 1.44 billion ha arable land worldwide has suboptimal conditions for crop growth and thus has an adverse influence on agriculture (FAO 1992). Soil fertility is one of the major determinants for plant growth in both natural and agricultural ecosystems.

The adverse effects of soil fertility on plant growth and yield are mainly due to the deficiency of one or more essential nutrients necessary for plant growth. Factors such as acidity, alkalinity, salinity, erosion, and farming practices are the main causes for the decline in the availability of nutrients in the soil. Among the various factors that influence soil fertility, soil acidity is an important factor affecting plant growth worldwide (Iqbal 2012).

Soil pH is a highly sensitive factor, as it determines plant’s survival, distribution, and its interactions with microorganisms, which are rather vital for the availability of essential nutrients and soil fertility (Marschner 1995). An increase in the H⁺ ion concentration in the soil solution results in a decrease in soil pH, and soils with a pH < 5.5 or lower are categorized as acid soils. These soils occupy around 30 % (4 billion ha) of the world’s total land area and 50 % of the world’s cultivable lands (Von Uexküll and Mutert 1995; Baligar et al. 2001). Further, more than half of the world’s acid soils (60 %) occur throughout the tropics and...
GenBank Submissions
Aspergillus niger strain JE15 28S ribosomal RNA gene, partial sequence

GenBank: KJ549638.1

Fasta Graphics

Go to:

LOCUS       KJ549638                 565 bp    DNA     linear   PLN 24-MAY-2014
DEFINITION  Aspergillus niger strain JE15 28S ribosomal RNA gene, partial sequence.
ACCESSION   KJ549638
VERSION     KJ549638.1  GI:635662308
KEYWORDS    .
SOURCE      Aspergillus niger
            Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiumycetidae; Eurotiales; Aspergillaceae; Aspergillus.
REFERENCE   1  (bases 1 to 565)
            AUTHORS   Jaison,S., Muthukumar,T. and Uma,E.
            TITLE     Chromium resistant strain isolated from tannery effluent and sludge contaminated soil
            JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 565)
            AUTHORS   Jaison,S., Muthukumar,T. and Uma,E.
            TITLE     Direct Submission
            JOURNAL   Submitted (08-MAR-2014) Department of Botany, Bharathiar University, Maruthamalai Main Road, Coimbatore, Tamil Nadu 641046, India
COMMENT     ##Assembly-Data-START##
            Sequencing Technology :: Sanger dideoxy sequencing
            ##Assembly-Data-END##
FEATURES             Location/Qualifiers
            source          1..565
            /organism="Aspergillus niger"
            /mol_type="genomic DNA"
            /strain="JE15"
            /db_xref="taxon:5061"
            rRNA          <1..>565
            /product="28S ribosomal RNA"
ORIGIN
1 attgcctcag taacggcgag tgaagcggca agagctcaaa tttgaaagct ggctccttcg
61 gagtccgcat tgtaatttgc agaggatgct ttgggtgcgg cccccgtcta agtgccctgg
121 aacgggccgt cagagagggt gagaatcccg tcttgggcgg ggtgtccgtg cccgtgtaaa
181 gctccttcga cgagtcgagt tgtttgggaa tgcagctcta aatgggtggt aaatttcatc
241 taagctaaa tactggccgg agaccgatag cgcacaagta gagtgatcga aagatgaaaa
301 gcactttgaa aagagagtta aacagcacgt gaaattgttg aaagggaagc gcttgcgacc
361 agactcgccc gcggggttca gccggcattc gtgccggtgt acttccccgt gggcgggcca
421 gcgtcggttt gggcggccgg tcaaaggccc ctggaatgta gtaccctccg gggtacctta
481 tagccagggg tgcaatgcgg ccagcctgga ccgaggaacg cgcttcggca cggacgctgg
541 cataatggtc gtaaaaggcc cgtct
//

Please purchase PDF Split-Merge on www.verypdf.com to remove this watermark.
Candida parapsilosis strain JE12 28S ribosomal RNA gene, partial sequence

GenBank: KJ549639.1

**FASTA**

<table>
<thead>
<tr>
<th>LOCUS</th>
<th>KJ549639</th>
</tr>
</thead>
<tbody>
<tr>
<td>DEFINITION</td>
<td>Candida parapsilosis strain JE12 28S ribosomal RNA gene, partial sequence.</td>
</tr>
<tr>
<td>ACCESSION</td>
<td>KJ549639</td>
</tr>
<tr>
<td>VERSION</td>
<td>KJ549639.1 GI:635662309</td>
</tr>
</tbody>
</table>

**ORGANISM**

Candida parapsilosis

**COMMENT**

Sequencing Technology :: Sanger dideoxy sequencing

**ORIGIN**

```
1 tgccttagta gcggcgagtg aagcggcaaa agctcaaatt tgaaatctgg cactttcagt
61 gtccgagttg taatttgaag aaggtatctt tgggtctggc tcttgtctat gtttcttgga
121 acagaacgtc acagagggtg agaatcccgt gcgatgagat gtcccagacc tatgtaaagt
181 tccttcgaag agtcgagttg tttgggaatg cagctctaag tgggtggtaa attccatctaa
241 aagctaaata ttggcgagag accgatagcg aacaagtaca gtgatggaaa gatgaaaaga
301 actttgaaaa gagagtgaaa aagtacgtga aattgttgaa agggaagggc ttgagatcag
361 acttggtatt ttgtatgtta ctctctcggg ggtggcctct acagtttacc gggccagcat
421 cagtttgagc ggtaggataa gtgcaaagaa atgtggcact gcttcggtag tgtgttatag
481 tctttgctga tactgccagc ttagactgag gactgcggcg tcggcctagg atgttggcat
541 aatgatctta agtcgcccgt cttgag
```

Please purchase PDF Split-Merge on www.verypdf.com to remove this watermark.