

Species of Fungi and Bacteria Associated With the Genus *Bambusa*: A Review

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Abstract

The great economic, ecological and social importance of the bamboo around the world, has created the need to design strategies to reproduce quickly and economically reliably. An alternative to stimulate the growth and development of bamboo plants is, through beneficial microorganisms; Therefore, the objective of this research was to review scientific compilation on the relation between the beneficial microorganisms from the soil and the bamboo. A wide variety of fungi and bacteria which favor the growth and development of bamboo was found, mainly of genus *Glomus* and genera *Azotobacter*, *Pseudomonas* and *Bacillus*. Likewise, is evident that there are species of fungi and bacteria associated with genus *Bambusa*, with the potential to be inoculated looking beneficial effects for bamboo. In addition, there is opportunity to continue with research in areas of identification of fungal and bacteria species associated with bamboo in America, mainly in countries with productive potential like Mexico.

Keywords: Bamboo, Microorganism, Rhizosphere, Sustainable.

1. Introduction

Bamboo is classified within subfamily *Bambusoideae* (Family Poaceae or Gramineae) and is one of the most numerous and diverse grasses with around 90 genera and 1500 species (G. Wang *et al.*, 2010), being Asia, main center of origin, but with a wide distribution worldwide (DZ Li, 1998).

Bamboo is a plant species that has been an integral part of the social and economic life of many Asian countries and now also worldwide

(Thapa *et al.*, 2018). This is mainly because is a multipurpose plant; Although main application is in the construction industry, is also used in other industries such as textiles, paper, medicines, the arts, design, food, beverages, bioenergy and even in the aero-space industry (Akinlabi *et al.*, 2017; Echezuría, 2018; W. Liu *et al.*, 2018).

In this sense, some different sciences areas are investigating and using all facets of bamboo, since all parts of the plant can be harvested and used (Thapa *et al.*, 2018); This situation has caused an increase in the annual demands of bamboo making it a plant of scientific and economic importance worldwide (Akinlabi *et al.*, 2017).

From an environmental point of view, bamboo has multiple ecological functions, including avoiding erosion, helping to conserve water and capturing carbon dioxide in the soil (Maoyi and Banik, 1995). In addition, bamboo represents one of the largest renewable natural resources, because grow rapidly (García-Ramírez *et al.*, 2011) and its production is considered sustainable, contributing in this way to achievement of several of Sustainable Development Goals of UN; mainly those related to poverty reduction, use of renewable energy, combating climate change and land degradation (Echezuría *et al.*, 2018)

Soil microorganisms are essential to maintain soil fertility and plant growth, so they play an important role in the availability and cycle of nutrients (Chang and Chiu, 2015). Mainly rhizospheric microorganisms, such as the arbuscular mycorrhizal fungi (AMF), and the bacteria cataloged as plant growth promoters (BPCV), have synergistic effects, which potentiate growth and plants development (Cabrera *et al.*, 2018). Martínez and Dussán, 2018, Nath and Meena, 2018). These plant-microorganism interrelationships also occur with bamboo (Z. S. Yuan *et al.*, 2018).

In this sense, is important to get information about species of fungi and bacteria which interact with the bamboo and in turn identify which of these have potential to be used as an inoculum to enhance plant development and growth in order to improve the production of bamboo. Therefore, the objective of the present bibliographic review was to determine beneficial microorganisms (AMF and BPCV) from the soil, more common that relate to the different species of bamboo.

2. Microorganisms and their relationship with bamboo.

Different studies have shown the beneficial effects about symbiotic association between plant species and microorganisms like AMF and BPCV (Simard *et al.*, 2003). These microbial communities related with root system play important role in availability of nutrients and water absorption, through root hairs, promoting the development and plants growth (Kapoor *et al.*, 2008; Sayeed Akhtar and Siddiqui, 2008).

In general, in this exchange from the carbon assimilated by plants, AMF improve the supply plant nutrients (mainly N and P), increase the resistance of roots to infections caused by pathogens, increase the plants tolerance to toxins present in plants and, the soil, also reduce stress caused by environmental factors (Cano, 2011, Neuenkamp *et al.*, 2018).

Bacteria could be like a biological control agent, able to protect plants from infections, caused by phytopathogens and stimulate growth through mechanisms such as the synthesis of regulatory substances of plant development, nitrogen fixation and nutrient solubilization (Rosas *et al.*, 2009; Siddiqui and Shaukat, 2003).

On the other hand, bamboo also affects soil microorganisms. In this sense, several works carried out on the *Phyllostachys edulis* species (*Moso bamboo*), in natural forests and cedar plantations, both in China and Japan, showed that the invasion of this species causes a negative effect on the microbial biomass and its diversity (Cai *et al.*, 2018; Chang and Chiu, 2015; Q. Li *et al.*, 2016; X. Wang *et al.*, 2016). According to this, Chang *et al.* (2018) mention that a smaller biomass occurs in the natural forest, although the microbial community is less physiologically stressed in the soils of bamboo and cedar plantations.

On the contrary, Xu *et al.*, (2014) observed that the invasion of bamboo influenced the structure of soil community, increasing the microbial biomass

and taxonomic diversity despite the decrease in plant diversity. According to Huang *et al.*, (2014) and Chang *et al.*, (2016) the increase in microbial biomass is related to the increasing rise in sea level of the plantations of *Moso bamboo*. Same effect described by M. Liu *et al.*, (2017), in plantations of *Phyllostachys praecox* (*Bamboo Lei*) with an intensive management (organic fertilization) in China.

Xiao *et al.*, (2017) conducted a study to explore the microbial spatial patterns of six soils in *Moso bamboo* forests in southern China, the results revealed much more high network connectivity in the fungal network than in the bacterium. In this sense, the biomass of the AMF associated to the bamboo presents significant changes according to the management that is given to the forest, since, if this is intensive, the biomass is reduced (Qin, Chen, *et al.*, 2017), while which increases when the forest expands naturally (Qin, Niu, *et al.*, 2017).

2.1 Bacteria associated with bamboo.

In several Asian countries, the interaction between bacteria and bamboo has been reported; for example, Q. Li *et al.*, (2018) found in *Moso bamboo* plantations in Zhejiang Province, China; a microbial composition at the phylum level formed mainly by *Proteobacteria* (38.6%), *Acidobacteria* (23.4%), *Actino bacteria* (8.3%) and *Verrucomicrobia* (7.6%) and the dominant genera were *Acidibacter* (3.6%), *Cydatu Nitrosotalea* (2.6%), *Acidothermus* (2.6%), *Rhizomicrobium* (2.3%) and *Sphingomonas* (2.2%). In the same province China, Y. Li *et al.*, (2018), report associations between *Moso bamboo* and autotrophic bacteria (*Rhizobiales* and *Xanthomonadales*). For their part, Lin, *et al.*, (2017), found *Acidobacteria* and α -*Proteobacteria* (*Rhizobiales* and *Rhodospirillales*) associated with *Moso bamboo* in Japan.

On the other hand, Ngo *et al.*, (2014), isolated from the soil of a bamboo field in Seoul, Republic of Korea, a new species for which they propose the name *Pedobacter seoulensis* sp. Nov. Likewise Won *et al.*, (2015), finding the presence of a new bacterium of the genus *Pedobacter*, with the name of *Pedobacter Bambusae* sp. Nov. While *et al.*, (2015), analyzed endophytic bacteria related to *Moso bamboo*, finding that the main strains of endophytic bacteria of the roots were *Bacillus* and *Burkholderia*, where the strains of alkaloids and staphylococci were dominant in the rhizomes. Likewise, Han *et al.*, (2009) found in the rhizosphere, the rhizoplane and root tissues of

Moso bamboo, *Proteobacteria* and *Firmicutes*, where the most common genus was *Bacillus* and *Burkholderia*. Similarly, Sachin and Misra, (2009) suggest that *Azotobacter chroococcum* is beneficial for bamboo (*Bambusa bamboo*), since they improve growth and induce IAA production and phosphorus solubilization.

2.2 Fungi associated with bamboo.

Actually, exist just a few studies about AMF species associated with bamboo. In this sense, Sharma and Rajak, (2010), found antagonistic interactions between the rhizosphere and AMF associated with *Dendrocalamus strictus*, finding relationships between AMF like *Cantharellus tropicalis*, *Aspergillus sp.* and *Curvularia sp.* Likewise, Zhang *et al.*, (2018) report two fungi identified as *Talaromyces aurantiacus* and *Aspergillus neoniger*, in the rhizosphere of *Moso bamboo* in China.

In addition, Hazarika, (2015) found that four bamboo species (*Bambusa tulda Roxb.*, *B. nutans Wall ex Munro*, *Bambusa pallida Munro* and *B. Balcooa Roxb*) are associated with five genera of AMF (*Glomus*, *Gigaspora*, *Acaulospora*, *Sclerocystis* and an unidentified species) in five different communities in India.

While Acosta-Suárez *et al.*, (2011) identified thirteen genera of fungi (*Aspergillus*, *Botryotrichum*, *Cephalosporium*, *Cladosporium*, *Cunningamella*, *Fusarium*, *Paecilomyces*, *Penicillium*, *Pythium*, *Pyrenochaeta*, *Rizotocnia*, *Trichocladium* and *Trichoderma*), associated with various species of bamboo (*Bambusa vulgaris varvulgaris*, *Bambusa vulgaris varvittata*, *Dendrocalamus asper*, *Guadua angustifolia* and *Bambusa longispiculata*) grown in Cuba.

On the other hand, Ravikumar *et al.*, (1997) inoculated bamboo seedlings (*Dendrocalamus strictus Nees*) with three species of AMF (*Glomus aggregatum*, *G. fasciculatum* and *G. mosseae*); finding a significant increase in the rate of growth and biomass production in all relationships.

3. Conclusions

Soil microorganisms related to bamboo are varied and similar in number to other species of economic value. Within the diversity of species of AMF and BPCV associated with bamboo, was observed in the studies analyzed that AMF colonize in greater numbers than BPCV, mainly the genus *Glomus* and genera *Azotobacter*, *Pseudomonas* and *Bacillus*, respectively.

In addition, is evident that there are species of both AMF and BPCV that can be inoculated in bamboo, looking beneficial effects to improve their performance. However, information about its direct effects in the field is not enough. In this sense, there is a very broad opportunity niche to continue with a line of research in areas of identification methodologies of microorganisms related to bamboo, among others.

It is worth mentioning that most of the research related to the identification of AMF and BPCV species related to bamboo has been carried out in Asian countries, so is necessary to carry out studies in America, in countries with productive potential of bamboo, as in Mexico.

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