



FUNGAL DIVERSITY IN CHEMICALLY FERTILIZED PADDY CROP FIELDS OF BASAJHAL VILLAGE KOTA REGION OF BILASPUR DISTRICT

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ABSTRACT The Chhattisgarh state is considered as the “Rice Bowl of India” and the crop rice is a part of an ancient plant of agronomic importance globally. Around one-third of the global population relies on rice. The soil of the paddy field is an inhabitant of several microbial biomes due to the richness of organic matter and minerals. The nutritional enrichment of the soil system is directly correlated with microbial growth, especially mycoflora. The present study revealed that the dominant fungal species were *Neosartorya fischeri*, *Aspergillus niger*, *Aspergillus fumigatus*, *Aspergillus oryzae*, and *Penicillium notatum* were observed in the rice crop fields of Basajhal, Kota, Bilaspur, Chhattisgarh. This research could further be extended to explore the importance of each fungal strain in nutrient recycling in the soil system.

KEYWORDS : Fungal Diversity, Basajhal, Kota, Bilaspur, Chemically fertilized, Crop Fields

INTRODUCTION

Soil serves as a complex habitat to live and interact with diverse groups of microorganisms i.e., bacteria, archaea, algae, fungi, and protozoans that are the active biomes of the soil ecosystem (Warcup 1951). Among them, the fungal strains are playing a crucial role in nutrient cycling. The role of nutrient cycling depends upon the metabolic activity which relies on environmental factors i.e., nutrient availability, moisture content, soil porosity, pH, and temperature. The fungal hyphae often bind to the soil particles and form aggregation that helps to increase the water infiltration that induces the water-holding efficiency of soil. Moreover, the fungi act as decomposers and mutualism and cause disease as pathogens inside the plant tissue.

The mycofloral diversity is varied as per the source and ecological factors (Mishra *et al.*, 2017; Rosas-Medina *et al.*, 2019). The *Achlya*, *Aqualinderella*, and *Pythium* have been reported as common aquatic microflora (Dwivedi *et al.*, 2012) while Lall and Jadhav (2012) *Cladosporium cladosporioides*, *Aspergillus versicolor*, *Alternaria alternata*, *Aspergillus niger*, *A. citri*, and *Nigrospora oryzae* as aeromycoflora. Further, Chandrashekar *et al.* (2014) have observed *Curvularia lunata*, *Alternaria alternata*, *Penicillium fusiculosum*, *P. chrysogenum*, *Fusarium solani*, *Mucor* spp., *Aspergillus flavus*, *Aspergillus terreus* and *Aspergillus Niger* as soil flora of paddy crop fields.

The fungal strains are buoyant microbes that make organic nutrients available to crops, produce toxins to inhibit the growth of harmful plant pathogens, synthesize growth-promoting hormones, and enzymes for biodegradation or bioconversion of organic and inorganic matter of the soil, and so forth (Yuvaraj and Ramasamy, 2020). Hence, the present research work undertaken was focused on the assessment of fungal diversity in the chemically fertilized paddy crop fields of Basajhal village, Kota region of Bilaspur District of Chhattisgarh state.

MATERIALS AND METHODS

The soil sample was randomly collected from the chemically fertilized rice crop agriculture field of the Basajhal village of Kota, Bilaspur, Chhattisgarh, in sterile polyethylene bags and brought to the laboratory for evaluation of mycoflora.

Isolation and Identification of soil mycoflora

The soil sample (1.0 g) was diluted using 10 ml of double distilled water and then 1.0 ml of serially diluted (10^{-2} and 10^{-3}) sample was used for isolation of mycoflora (Lanjewar, 2019). The soil samples were plated using the Warcup method (Warcup 1951). A 100 mg of the soil sample was taken in the sterile Petri dish and poured potato dextrose agar medium (PDA) over it at 40-45°C supplemented with 1% streptomycin sulphate to prevent bacterial growth.

The inoculated plates were placed in an incubator at 25 ± 3°C for 72 hrs. The fungal colonies that appeared were counted. The pure culture of each fungal strain was stained with Lactophenol cotton blue and carried out microscopic identification. The identification parameters were followed by the works of literature viz., Kunjam and Jadhav (2020)

and Gilman, (1959). Percentage contribution was calculated using the following formula:

$$\text{Percentage Contribution} = \frac{\text{Total no. of fungal colonies of an individual species}}{\text{Total no. of fungal colonies of all species}} \times 100$$

RESULTS AND DISCUSSION

The present research work commenced with the assessment of fungal diversity in the rice crop field of Basajhal village of the Kota region of Bilaspur District of Chhattisgarh state. The mycoflora viz., *Neosartorya fischeri*, *Aspergillus niger*, *Aspergillus fumigatus*, *Aspergillus oryzae*, *Penicillium notatum*, *Fusarium Chlamydosporum*, *Trichoderma caeruloviride*, and *Trichoderma lentissimum* were observed in the samples collected from rice crop fields with a percentage contribution of 30.76, 19.23, 15.38, 7.69, 11.53, 7.69, 3.84, and 3.84 respectively (Fig. 1).

The microscopic structure of dominant fungal isolates in rice crop agriculture field are shown in Table 1. The literature i.e., Saxena and Sarabhoy (1964), Dwivedi (1965), Mohanty and Panda (1944), Tiwari (2002), Kulkarni (2011), Yadav *et al.* (2011), Mishra *et al.* (2017). have been done significant work on the assessment of soil fungi in India. Fungi are considered the fundamental biotic component of agriculture and forest soil ecosystems (Warcup, 1950). The *Aspergillus*, *Mucor*, and *Penicillium* genera were dominant in agricultural crop fields (Das, 1963; Chandrashekar *et al.*, 2014; Smily and Maghimaa, 2016). Additionally, Chandrashekar *et al.* (2014) documented *Curvularia lunata*, *Alternaria alternata*, *Penicillium fusiculosum*, *Penicillium chrysogenum*, *Fusarium solani*, *Mucor* spp., *Aspergillus flavus*, *Aspergillus terreus* and *Aspergillus Niger* in the paddy crop fields. Sun *et al.* (2004) stated that Agricultural practices and crop rotation have been found to be responsible for altered microbial community in crop fields.

The *Aspergillus*- and *Penicillium*-derived toxins prevent fungal pathogens in crop fields (Chandrashekar *et al.*, 2014). Karunaratna *et al.* (2021) have claimed that the soil microflora plays a crucial role in mineral solubilization and makes it available to the crop. Bollmann-Giolai *et al.* (2022) revealed that the mycological communities are crucial for plant health and found to be effective as biocontrol agents to suppress plant pathogens.

Sharma & Chaurasia (2019) evaluated the rhizospheric soil of rainfed paddy crop fields of Chhattisgarh (Bilaspur district) and reported *Glomus* spp. as the dominant AM fungi.

These AM fungi stimulate crop yield by supplying phosphorus (Grant *et al.*, 2005). Rangrao, J. R. (2022) observed the fungal genera viz., *Mucor*, *Rhizopus*, *Fusarium solani*, *Trichoderma*, *Aspergillus*, *Fusarium moniliforme*, *Aspergillus niger*, *Fusarium oxysporum*, *Penicillium chrysogenum*, *Chaetomium*, *Pythium*, *Rhizoctonia*, *Vaticillium*, *Phoma*, and *Nigrospora* in different sites of Kadegaon Tahsil of Sangli District in Maharashtra State. Recently, Liu *et al.* (2023) divulged that the mycological flora viz., *Sordariomycetes*, *Leotiomycetes*, *Archaeosporomycetes*, and *Agaricomycetes* as potent

nutrient cyclor.

Table 1. The microscopic structure of fungal isolates in chemically fertilized rice crop field

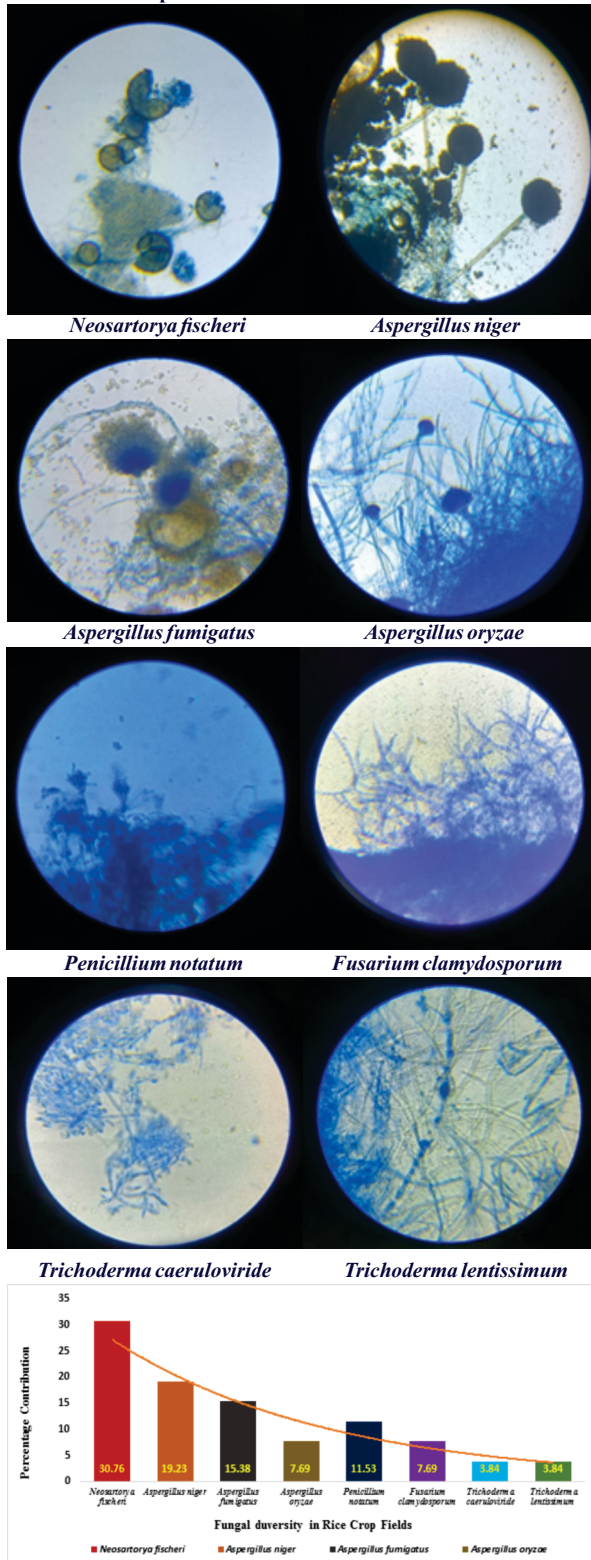


Fig. 1. The percentage contribution of fungal isolates in rice crop agriculture field

CONCLUSION

The microbial flora of the soil system plays a crucial role in maintaining biodiversity, ecological balance, and plant nutrition. The significant contribution of mycoflora in crop fields is well studied for crop growth, nutrient absorption, and nutrient recycling to increase

crop yields. The filamentous saprophytic fungi are mostly dominant in agricultural fields and synthesize a variety of enzymes that facilitate the decomposition and nutrient recycling of complex biopolymers derived from plants and animals. Additionally, the endophytes synthesize a variety of secondary metabolites of pharmaceutical importance and participate in a toxic remediation ecosystem. Moreover, they produce several mycotoxins that resist the growth of harmful fungal species. Nevertheless, the microfloral diversity in crop fields depends on the various biotic and abiotic factors.

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