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MICROBIAL DIVERSITY OF WESTERN GHATS, NORTHERN KARNATAKA, INDIA: A GIS-BASED ANALYSIS

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ABSTRACT

Besides the soil matrix, climate conditions, geomorphology and land-use information, spatial distribution and mapping of microorganisms are essential in fertility assessment of soils. Numerous studies demonstrated the key role of microorganisms in soil biogeochemical cycles and ecosystem services. However, little is known about their geographic distribution and diversity especially over the Western Ghats. The overall objectives of this study were (i) to describe the Agriculturally Important Microorganisms (AIMs) taxonomic richness variations, and to generate prediction maps adopting the geo-statistical approach, across Western Ghats (WG) region of Northern Karnataka, India. Stratified random sampling based and GPS assisted field survey was carried out, which covers 313 sites spanning 156 km^2. AIMs were determined by standard serial dilution plate count technique and related to the geomorphology for abundance and richness. Geostatistical method of Kriging was adopted in mapping the spatial distribution of AIMs according to land use land cover practices. A total of 4578 AIMs comprising eight functional groups was isolated. Mapping of AIMs revealed a heterogeneous spatial distribution, *Azotobacter* species is found to be most dominant species with the species richness (96%), while the cellulose degraders were the least dominant (*i.e.* species richness of 24%).

INTRODUCTION

Soil microorganisms are the key life forms responsible for nutrient cycling and the number of nutrients available to plants (Hernot and Robertson, 1994; Singh and Rai, 2004; Jain *et al.*, 2005). Agriculturally Important Microorganisms (AIMs) influence soil physical, chemical, and biological properties and create a complimentary medium for biological reactions and life support in the soil environment (Busse *et al.*, 2009; Ma *et al.*, 2013). A representative estimate of microbial diversity is a pre-requisite for understanding the functional activity of microorganisms in ecosystems (Zak *et al.*, 1994; Hofman *et al.*, 2004; Schulz *et al.*, 2013). Soil microbial diversity is also a good indicator of soil ecological quality (Finlay *et al.*, 1997; Winding et al., 2005), carbon sequestration (Heemsbergen *et al.*, 2004) and other environmental factors such as pH and temperature (Williamson and Wardle, 2007).

Measuring biodiversity of a habitat or community has prime importance in ecology and conservation biology since it enables the characterization of an ecosystem and helps in devising conservation strategies. A variety of indices is available to quantify the diversity of biological communities. The most popular and widely used measures are Shannon's, Simpson's, Fischer's alpha-log series (Magurron, 1988) and Avalanche index (Ganeshaiah *et al.*, 1997). Although, the majority of these techniques are used to study the diversity of plants and animals, they have also been used for studying the microbial diversity. Such type of diversity analysis using diversity indices has been carried out earlier for bacteria from soils (Torsvik *et al.*, 1990), water (Dutta and Khajuria, 2016), mycorrhizae (Beena *et al.*, 2000) and, micro-fungal populations and actinomycetes (Anand *et al.*, 2003). Hence, the scope of microbial diversity is widening and encouraging through the integration of GIS applications.

During last two decades, numerous studies were explored on microbial ecology and soil microbial diversity (Martiny *et al.*, 2006), and focused on different environmental and land use conditions (Ranjard *et al.*, 2010; Trivedi *et al.*, 2016; O'Brien *et al.*, 2016; Terrat *et al.*, 2017). However, most of the studies highlighted the lack of knowledge about the determination of microbial diversity (Baumann *et al.*, 2012; Vivant *et al.*, 2013; Fierer and Jackson, 2006). Globally, mapping of microbial distribution studies was carried-out at plot level (O'Brien *et al.*, 2016), regional (Delgado-Baquerizo et al., 2016), territorial (Griffiths *et al.*, 2011) and continental (Lauber *et al.*, 2009) scales. Fierer and Jackson (2006) demonstrated that the microbial diversity closely related to soil characteristics and land use practices. It has been recently confirmed with the studies of Delgado-Baquerizo *et al.* (2016), Griffiths *et al.* (2016) and Zhou *et al.* (2016). With these studies concludes that the ecological processes depend on the density of soil microbial organisms and the applicability of soil microbial community regulation and their diversity maps in agricultural/forestry sectors.