

INTERNATIONAL SCIENTIFIC CONFERENCE
Forest science for people and societal
challenges

The 90th "Marin Drăcea" INCDS Anniversary
2nd - 5th October 2023



Book of Abstracts

Enhancing forestry practices by leveraging Sentinel-2 satellite imagery for windfall detection	166
A Study on the Development of an UAV as a Solution to Fight Illegal Deforestation	167
Agro-ecological management strategies to improve climate change mitigation in organic fruit orchard in Italy	168
Preliminary screening of bacterial soil isolates from their antimicrobial activity against phytopathogens.....	169
Author Index	170

Preliminary screening of bacterial soil isolates from their antimicrobial activity against phytopathogens

Authors	Affiliation	Country
Stefania M MANG	School of Agricultural, Forestry, Food and Environmental Sciences (SAFE), University of Basilicata	Italy
Ippolito CAMELE	School of Agricultural, Forestry, Food and Environmental Sciences (SAFE), University of Basilicata	Italy

Abstract

Soil matrices represent a valuable resource of new microorganisms or bioactive substances derived from them which can be used against phytopathogenic bacteria and fungi. Actinomycetes are a large group of unicellular Gram-positive bacteria widely distributed, known for having a significant antimicrobial activity. Soil samples were processed to isolate microorganisms similar to Actinomycetes on artificial specific substrates such as the Starch Casein Agar (SCA) and the Actinomycete Isolation Agar Difco™. All bacterial isolates resembling Actinomycetes isolated were purified on specific culture media for Actinomycetales and preliminary morphologically identified using an optical microscope. Molecular studies were also carried out for their precise identification. For this purpose, their genomic DNA was extracted and amplified by PCR with universal primers Y1 and Y2, targeting the pectate lyase-encoding *pel* gene belonging to the *pelY* family. More than thirty microorganisms resembling Actinomycetes have been isolated from soil samples. They were initially identified at Genus level based on their morphological features. The obtained amplicons of expected size (about 350 bp) were directly sequenced using the same primers as for amplification. The nucleotide sequences were analyzed with bioinformatic tools using initially BLAST and then sequence analysis and phylogeny tools: Bioedit, MEGA X and SeaView. All taxa isolated and sequenced were identified at least at species level. A total of 21 species were identified molecularly as belonging to various species of *Bacillus*, *Streptomyces* and *Nocardia*. In particular, *Bacillus amyloliquefaciens*, *B. velezensis*, *B. cereus*, *B. brevis*, *Streptomyces thermocarboxydus* and *Nocardia farcinica* were identified showing a similarity of at least 99.50% with similar species already present into the international databases (e. g. NCBI, EMBL). Antimicrobial activity assessing for all isolates was started. More specifically, the antimicrobial activity of the 21 isolates was tested against the following 11 key fungal pathogens among them 3 species of *Fusarium* spp., *Macrophomina* spp. and some other important phytopathogens. Nearly half of the tested isolates for example *B. amyloliquefaciens* colony 4-1, *B. amyloliquefaciens* colony 4-2, *B. velezensis* colony 2 and *B. cereus* colony 1 showed, already in this preliminary phase of the research, a very good activity against one or more fungal pathogens such as *Colletotrichum* spp. and *Botrytis* being promising candidates for biocontrol. Research activities of microbial activity against *Cryphonectria parasitica*, *Gnomoniopsis* spp., *Apiognomonina* spp. and also 6 bacterial pathogens are in progress for all identified microorganisms.

Keywords

Biological control, plant pathogens, DNA, genotype, bioeconomy, ecology