

Abstract

Antimicrobial resistance (AMR) poses a severe threat to global public health, driving an urgent need for novel therapeutic agents to replace ineffective conventional antibiotics. Endophytic microorganisms, which reside within plant tissues and can synthesize diverse bioactive secondary metabolites, offer a potential source for various novel antimicrobials. In this study, Endophytic Bacterial Species were investigated from the leaves of *Piper crocatum*, which is a medicinal plant widely used in traditional medicine. Initially, the genomic DNA was extracted from endophytic bacterial isolates isolated from *Piper crocatum* leaves and subjected to Oxford Nanopore Technologies (ONT) whole-genome sequencing at IPB University. Furthermore, bioinformatic processing of raw reads was performed on the Galaxy platform using Flye for *de novo* assembly, QUAST for quality assessment, and Medaka for sequence polishing. Taxonomic identification was subsequently established using the Type (Strain) Genome Server (TYGS), BLASTn, and FastANI. Genome analysis identified three prominent endophytic strains: *Kluyvera ascorbata* strain SK, *Pseudomonas aeruginosa* strain LACPHL_BACT_2023_00013, and *Klebsiella pneumoniae* strain NK_H18_026. Furthermore, genomic mining using AntiSMASH revealed multiple biosynthetic gene clusters (BGCs) responsible for bioactive compound production. These findings highlight the rich microbial diversity within the *P. crocatum* leaf microbiome, underscoring its potential in amplifying plant development and defense, as well as a source for synthesizing various types of antibiotics.

Keywords: Endophytes, Taxonomic Identification, Biosynthetic Gene Clusters