

Abstract

Influenza viruses persist as seasonal pathogens and a continuing source of morbidity and mortality. Its RNA genome permits antigenic drift, which can reduce the effectiveness of existing antivirals and preventive strategies, motivating a search for new antiviral agents, such as those produced by endophytic bacteria in plants like *Piper crocatum*. This study used bioinformatic genome mining tools (Galaxy and antiSMASH) to analyze whole-genome sequence data from endophytic bacteria isolated from *Piper crocatum* and to identify biosynthetic gene clusters (BGCs) with potential relevance to the discovery of antiviral metabolites against influenza viruses. Across isolates, multiple BGC classes were detected, indicating a considerable degree of biosynthetic capacity. The most robust candidates were NRP-metallophore/NRPS regions containing conserved catecholate siderophore core genes, which may provide indirect antiviral capability. Other regions displayed specialized or functional potential but lacked coherent region-level reference matches and were treated as novel-like or not suitable candidates under current database constraints. Overall, the study provides putative candidate BGCs and mechanistic hypotheses for future experimental validation rather than direct evidence of anti-influenza activity.

Keywords antiSMASH; biosynthetic gene clusters; endophytic bacteria; *Piper crocatum*; influenza