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A new species of the emerging genus *Leifsonia* as a potential antagonist against phytopathogens

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The transition to sustainable agricultural models has driven the replacement of agrochemicals with biopesticides. Consequently, identifying new antagonistic bacteria is a strategic priority. The emerging genus *Leifsonia* is found in the soil microbiota and has shown promise as an antagonistic agent. Therefore, we investigated the potential for biological control of the PARNA 1/14 strain, whose genome was previously phylogenetically analyzed in a prior study by the research group, which detected that the isolate was a new species of the genus *Leifsonia*. The present work aims to detect enzymes capable of degrading the cell wall of phytopathogens. To this end, the isolate's genome was annotated using Bakta and subjected to DbCAN3 and MEROPSHit via METABOLIC to detect carbohydrate-active enzymes (CAZymes) and peptidases, respectively. Genomic analyses revealed that the PARNA 1/14 isolate possesses six CAZyme families, AA, CBM, CE, GH, GT, and PL, and 59 different types of peptidase, with the most abundant families being M38, M20D, M29, and C26. The CAZyme and peptidase families found are widely associated with biocontrol in the literature, such as the CE4 family of CAZymes, involved in chitin deacetylation, which disrupts the cell wall of phytopathogens such as nematodes, insects, and fungi. The M20 peptidase family is involved in host/pathogen interaction. Therefore, with the detected potential for biocontrol, the next steps are to perform *in vitro* and *in vivo* validation of the use of PARNA 1/14 as a biocontrol agent, supporting the transformation toward sustainable agricultural practices.

KEYWORDS: CAZymes, Sustainability, Peptidases, Biopesticides, Chitinase.

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