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Genome mining approaches reveal secondary metabolites in *Streptomyces* sp. related to biocontrol activity

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Streptomyces are a large and valuable resource of biocontrol agents, bioactive and complex secondary metabolites with a wide range of applications. Genomic information can critically guide functional studies to understand phenotypic characters and to propose valid hypotheses on the related mechanisms. Phylogenetic and functional genome analysis was carried out to explain the endophytic lifestyle, the biocontrol activity of *Streptomyces* sp. DEF48 in reducing *Fusarium graminearum* infection and deoxynivalenol contamination in wheat. The genome of DEF48 was sequenced using Illumina technology. The complete genome of the strain DEF48 consists of 9,147,966 bp (71.26 mol% GC content). Phylogenetic analyses revealed that *Streptomyces* sp. DEF48 was closely related to *Streptomyces griseoviridis*. Interestingly, functional annotation highlighted the presence of genes involved in plant growth promotion and biocontrol activity. The presented approach aids to explain the capability of DEF48 to directly antagonize *Fusarium graminearum*, confirming the effectiveness of genomics studies.