Draft genome of *Serratia marcescens* UENF 22-GI: a plant growth promoting bacterium isolated from vermicompost

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The ongoing increase in world's population and adoption of intensive farming results in large amounts of organic waste and enviromental contamination. In order to mitigate these damages sustainable approaches are being tested worldwide, many of these focused on soil management. Biological properties concerning a healthy soil are still to be uncovered, nevertheless using soil's native organisms to supply human needs in agriculture is a promisinig strategy. In this context vermicomposting is a widely known practice to biologically stabilize green wastes using earthworms to perform waste stabilization, promote aeration and substrate fragmentation, thereby drastically increasing the microbial activity specially in the drilosphere. Further, vermicompost has been demonstrated to be a rich source of microbial diversity, notably plant growth promoting rhizobacteria (PGPR). These bacteria are able to promot plant growth both directly or indirectly. In this work we report the sequencing and analysis of *Serratia marcescens* (strain UENF-22GI) isolated from vermicomposted material. 21,445,242 paired-end reads were sequenced in a Illumina HiSeq 2500 platform and assembled using Velvet, resulting in a 5,001,584 Mb assembly with 3,0 Mb N50. By annotating the genome with RAST, we found 4662 genes, 30 pseudogenes, 6 rRNAs, 84 tRNAs. We did a comparative genome analysis and phylogenetics reconstruction using other publicly available *Serratia marcescens* genomes, we also performed extensive manual curation to find genes potentially responsible for plant growth-promoting properties observed in vitro. As a whole, our results indicate a biotechnological potential of *S. marcescens* in plant growth promoting products. Financial support CAPES, FAPERJ.