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Sequence of the color purple

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Sequencing the genomes of organisms can give insights into potential gene products and regulatory mechanisms that may yield biotechnological products. The free-living, gram-negative bacterium *Chromobacterium violaceum* - native to tropical and subtropical aquatic environments - produces compounds of known biotechnological importance. One of these is the violet pigment violacein, produced in response to [quorum sensing](#) (the ability of bacteria to coordinate gene expression in a bacteria density - dependent manner), but the potential of this organism has been incompletely explored. Ana Tereza Ribeiro de Vasconcelos at the [Laboratorio Nacional de Computacao Cientifica](#) in Brazil, together with over a hundred members of the Brazilian National Genome Project Consortium - comprising 29 sequencing and bioinformatics centers - report the full genome sequence of *C. violaceum* in the September 8 early edition of [Proceedings of the National Academy of Sciences USA](#) (*Proc Natl Acad Sci USA* 2003, DOI:10.1073/pnas.1832124100).

The consortium sequenced *C. violaceum* strain ATCC 12472 using cosmid libraries in Lawrist 4 and pUC18 and annotated the sequence using their own software that automatically identified genome landmarks before assigning putative functions using BLAST searches and a variety of programs for identification of protein sequences. The genome consists of a single circular chromosome 4.8 Kb in length and has a G+C content of approximately 65%. The authors identified 4431 uniformly distributed open reading frames (ORFs) having an average length of 954 bp, of which 2717 encode proteins of known function. Comparison with other organisms showed that 17.4% of the ORFs show similarity to those in *Ralstonia solanaceae* - a soil-borne pathogen - and that the majority of these encode gene products closely associated with a soil-dwelling lifestyle (e.g., cell motility and inorganic ion transport).

The authors also showed that the bacterium can metabolize both aerobically and anaerobically and revealed information on its ability to adapt to changing environments, on the widespread use of quorum sensing to regulate gene expression, and on the basis for its occasional human pathogenicity, as well as on novel proteins induced in response to a variety of environmental chemical stresses.

The sequencing of more, similar, free-living tropical bacteria could lead to "the production of industrially useful genes, enzymes, and secondary metabolites [that] would [not only] benefit... the biotechnological and pharmaceutical industries in the developing world, where most tropical diversity is located, but would also provide a further stimulus to the preservation of the precious ecosystems where these organisms are found," the authors conclude.

References

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