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Microbial Envirogenomics

Status	Past
Competition	I
Sector	Environment
Genome Centre	Genome British Columbia
Project Leader	Julian Davies, Lindsay Eltis and William Mohn

Project Description

The first complete sequence of a free-living organism to be determined completely was that of the bacterium *Haemophilus influenzae* in 1995. This was followed by a veritable flood of bacterial sequences and now more than 1000 have been completed; this establishes the power of shotgun sequencing which has been successfully applied to many organisms, including humans, apes, horses, dogs, and other forms of life. Notable among the bacterial sequences is that of *Rhodococcus jostii* RHA1, which was the first genome sequence to be determined in Canada and, until recently, the largest bacterial genome (9.7 Mb, >9,000 genes) elucidated. This project began in 2000 and was entirely carried out by the team at UBC, including sequencing, bioinformatics and functional genomic analyses, such as transcriptome and proteome studies.

R. jostii RHA1 is noteworthy because it is an environmental microbe of great utility. It has been called a "powerhouse" of degradative functions, since it is capable of metabolizing a very large range of organic molecules. Over the course of the project, we and our collaborators established the basis of *R. jostii* RHA1's ability to degrade a wide range of pollutants including polychlorinated biphenyls (PCBs), nitriles, phthalates, *N*-nitrosodimethylamine, and polybrominated diphenyl ethers (PBDPEs). The availability of the complete sequence has revealed the potential of *R. jostii* RHA1 for many other applications, including commercial applications in environmental clean-up and in biotransformations of important commodities such as steroids.

An unexpected benefit of the genomic studies of *R. jostii* RHA1 was the recognition of a cluster of genes implicated in the degradation of cholesterol, a widely distributed type of steroid. Detailed analysis revealed that this gene cluster was nearly identical to one present in the genome of the bacterium *Mycobacterium tuberculosis*, the deadly pathogen that has killed more humans than any other disease-producing organism. The identification of cholesterol-degrading functions in the causative agent for TB has opened up the potential for novel therapies for this terrible affliction.

R. jostii RHA1 offers potential for other applications, such as a surrogate host for the production of antibiotics and the exploration of genes from uncultured organisms in diverse

environments. RHA1 is also being further explored as the UBC team continues their studies of this fascinating microbe. The public release the sequence and related information is being exploited by numerous scientists worldwide and there are many more applications and surprises yet to come from this research!

Fast Facts

<i>Highlighted outcome:</i>	Creation of a body of knowledge about microorganisms that are important for industrial chemistry and the removal of environmentally toxic compounds
<i>Number of research personnel employed by the project:</i>	~ 51 person-years
<i>Number of patents in process or obtained:</i>	2 provisional patents applications
<i>Resources generated:</i>	The genomic sequence of two microorganisms, genome fragments for future molecular biology studies, public databases of experimental results

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