Genomics and proteomics of polar microorganisms: deciphering the cellular basis of life at low temperatures

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General context

More than three quarters of the Earth's surface is occupied by permanently cold ecosystems including the ocean depths, polar and alpine regions. These permanently cold environments have been successfully colonized by a special class of extremophilic microorganisms referred to as psychrophiles (literally cold-loving). The ability to thrive at temperatures close to or below the freezing point of water requires a vast array of adaptations to maintain metabolic rates and sustained growth compatible with life in these severe environmental conditions. Previous studies have mainly addressed the problem of maintenance of enzyme catalysis and of membrane fluidity at low temperatures. However, most cellular adaptations to cold remain largely unknown. Deciphering these adaptive mechanisms is the central theme of this project because such mechanisms have significant implications in fundamental and applied research.

The recent development in genome-wide technologies allows the analysis of these biological processes in a comprehensive manner. In this respect, proteome analysis, which makes possible the study of total protein extracts by two-dimensional electrophoresis or chromatography coupled with the identification of the proteins of interest by mass spectrometry, and transcriptome analysis, which corresponds to gene expression profiling using DNA arrays, constitute the basis of global approaches towards the understanding of cellular networks.

Considering the large sequencing and bioinformatics facilities made available at the international level for previous projects as well as the fast development in proteomic technology, it can be anticipated that the genome and proteome analyses of selected polar microorganisms will lead to clear advances in understanding the cellular basis of life at low temperatures. In order to reach this goal, an international and multidisciplinary consortium of laboratories will use genomic and proteomic approaches, including bioinformatics, molecular biology, biophysics and biochemistry. The mechanisms of thermal adaptation will be analyzed by comparative genomics. Most of the research effort will be devoted to the identification, isolation and functional characterization of the structural and regulatory factors permanently synthesized by the cold-adapted microorganisms that allow the maintenance of life at low temperatures.

Relevance to the IPY 2007/8 General Principles

This proposal meets the IPY major themes "Exploration of New Frontiers" and in particular "Polar regions are home to unique organisms adapted to the demanding environment, offering incredible opportunities to understand evolution and other biological and ecological questions, especially given the tools of modern bioscience".

- Such research activity will be multidisciplinary as it involves several domains of life sciences.

- It addresses compelling science issues as geno-proteomics of polar psychrophilic microorganisms is still in its infancy.
- It will lay foundation for long-term commitments as the data acquired will stimulate further international collaborations.
- It is build on and enhance existing programs because it will be possible to compare genomic and proteomic data of cold-adapted microorganisms with those already available for mesophilic and thermophilic microorganisms, therefore covering the whole range of temperatures compatible with life.
- It will attract and develop next generation of polar scientists through the training of young scientists in the various techniques and concept involved in these approaches and will promote the career of young scientists in this fast-growing field.
- It is challenging but achievable given the current tools of geno-proteomics and the size of microbial genomes (as compared with cold-adapted invertebrates or fish).

Added value

Fundamental research
This research activity will provide an integrated model of molecular and cellular adaptations to cold and by comparison with thermophiles, it will be possible to understand how cells adapt to extreme temperatures. These results will also contribute to prepare the exploration of our solar system for life forms or remnants of living cells.

Applied research
Using the genome sequence data of cold-adapted microorganisms, it will be possible to exploit their biotechnological potential by creating a new know-how. For instance, by identification and production of industrially relevant, novel enzymes that can be used in processes requiring low temperatures or a fast thermal inactivation, as well as by discovering pathways that are responsible for the synthesis of unique organic compounds e.g. novel lipids, compatible solutes, bioactive substances and anti-microbial agents.

Education
It is expected that the type of training required by this activity will fulfil the need for scientists combining a thorough mastering of very specialized techniques with a sufficient understanding of related areas to be able to act as efficient team leaders. The present project offers a domain of choice for the application of these principles and for the training of a breed of scientist which will certainly be in great demand in the near future

Cross-cutting activities

The proposed research activity does not require field campaigns because the best currently studied cold-adapted microorganisms will be selected for genomic and proteomic investigations.
It is expected that similar and related proposals from other Nations will form the body of a larger project that will be structured after reception of the various expressions of interest.

The Belgian contribution
The contact person coordinates an informal network of collaboration focused on genomics and proteomics of an Antarctic bacterium. These groups from France, Germany and Italy have already agreed to contribute to IPY 2007/8.

At the Belgian level, the CIP (Centre for Protein Engineering, http://www.ulg.ac.be/cingprot/index.htm) and the GIGA (Interdisciplinary Cluster of Applied Geno-Proteomics, http://www.gigaresearch.com/) have also agreed to contribute to IPY 2007/8.