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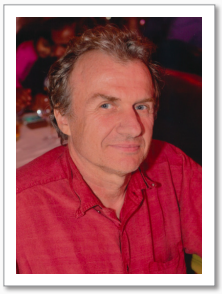

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Integrating structural bioinformatics and functional genomics to characterize novel protein in cell death and viral immunity

Identifying new genes and members of a protein family and characterizing their structure and function is fundamental to obtaining a complete list of the components that constitute our genomes. One important area of research towards this goal has been to develop more sensitive bioinformatics tools that identify distant relationships between sequence and/or structures. Once the relationship between two sequences or structures is established, one can then infer structural or functional information, develop hypotheses testable in the laboratory, and eventually annotate the function of the newly uncharacterized genes. Existing families can be expanded by adding the newly characterized members. My laboratory has worked extensively at developing new bioinformatics tools and integrative strategies towards this goal. In particular, we focused on a protein superfamily highly represented in the cell death machinery called death domain. In this talk, we will illustrate by a few examples how structural bioinformatics, biochemical and reverse genetics approaches can be integrated to identify and characterize new candidate proteins. The major findings presented will include the discovery of the death domain subfamily PAAD and the functional characterization of some members of the HIN200 family that are novel components of viral innate immunity. Finally, we will present our progress towards the identification of novel OB fold containing genes and their role in viral immunity in C. elegans using a promotor :: GFP gene fusion screen.

Biography

Frederic Pio, obtained his Ph.D degree from Pasteur Institute, University of Lille, France in 1990. He was a graduate student from the European Communauty in Structural Bioinformatics and Proteomics with Shoshana Wodak. After a postdoctoral degree in Molecular Biology and Cell Biology in the Laboratory of Rosenfeld and Steinberg at UCSD in San Diego, he joined in 1992 the Burnham Institute to work on the ETS family of transcription factor with Richard Maki. During that time he solved by X-ray macromolecular crystallography the ETS-PU.1 DNA binding domain complexed to DNA. It was the first structure of a protein-DNA complex in the family and was published in the journal nature. In 1998 he joined Dr John Reed laboratory to conduct bioinformatics studies aimed at discovering new genes and families in apoptosis. Since 2000, he has been an Associate Professor in Structural Bioinformatics and Proteomics at Simon Fraser University and has identified the new death domain subfamily PAAD and characterized some new genes in apoptosis and inflammation. He is currently developing new bioinformatics tools and approaches to gain more insight into the structure and function of the Death domain subfamilies PAAD and CARD. He is a mentor of the Canadian Institute for Health Research-Graduate training program in bioinformatics. He has advised and supervised numerous students in the field of Structural Bioinformatics Proteomics and Functional Genomics.

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