

National University of Singapore

Office of Life Sciences

OLS DISTINGUISHED LECTURE SERIES

**“Large-scale screening for new viruses; towards the sequencing
of the human virome”**

by

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Chaired by

Prof Wong Lim Soon
Bioinformatics & Computational Biology Programme
Department of Computer Science

Date: Wednesday, 7 March 2007

Time: 4.00 - 5.00pm
5.00 - 5.30pm (Meet the speaker/Tea session)

Venue: National University of Singapore
Centre for Life Sciences (CeLS) Auditorium, Level 1
28 Medical Drive S(117456)

Abstract:

Virus infections cause many of the largest health problems in the world. It is likely that there is a multitude of unknown viruses that infect humans and it has been suggested that viruses are involved in causing many common diseases, such as diabetes and MS. The discovery rate of new viruses has until now been slow. Initial results from a project will be presented to further develop and use a strategy for virus discovery using a genomics/bioinformatics approach. The project has resulted in the development of a pipeline to discover unknown viruses in patient samples and the characterization of several new viruses. The methods include enrichment of virus particles, shotgun sequencing and bioinformatics analyses. The methods have been proven to work efficiently and that they are ready for scaling up to characterize the “human virome”. Individual virus discoveries will lead to new clinical insights, therapies and diagnostic tools, and we aim to develop this protocol further with the goal of providing a broader picture of human virus infections in relation to disease. The analysis of the sequence data accumulated thus far will be presented, including the characterization of two new human viruses, Human Bocavirus and KI Polyomavirus, and a broader description of the known and novel viruses, bacterial, phage and

human sequences and completely unknown sequences found in samples of different clinical origin.

Biography:

Björn Andersson is professor of Genome analysis at the Department of Cell and Molecular Biology, Karolinska Institutet, Stockholm, Sweden. Dr. Andersson's research group has been active for over ten years and it was formed around a genome sequencing activity, following his involvement in the early stages of the human genome project. The two main sequencing projects were initially the *Trypanosoma cruzi* genome project and a project for comparative human sequencing in selected loci, including MAO, CXCR-1 and serotonin receptor 2C. *T. cruzi* is a protozoan parasite that is the causative agent of Chagas disease, which is a severe infectious disorder that affects millions of people in South and Central America. The complete genome sequence was published in a theme issue of Science in July 2005. This is being continued by functional genomics studies in this parasite. The focus is on the proteome of the parasite with the aim to characterize protein expression and localization. A major activity in the group involves the development of new algorithms, programs and databases for the analysis of genome sequences. Several new projects have been established in the last three years. These include genome analysis in domestic animals and the discovery and sequencing of new human viruses, the human virome. The latter has resulted in the discovery of several new viruses.

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