

THE UNIVERSITY



OF HONG KONG

Institute of Mathematical Research

Department of Mathematics

WORKING SEMINAR

Professor Antoine Danchin

President, AMAbiotics SAS (a biotech company), France

Member of the French Academy of Sciences

November 3, 2017 (Friday), 4:00 – 5:00pm

Rm 210, Run Run Shaw Building, HKU

Natural selection attempts to favour large genomes

Abstract

Common knowledge assumes that constructing genomes is costly, especially when genes are expressed. As a consequence there should be a tendency to streamline genomes, deleting genes that are not used in stable environments. Yet, one observes repeatedly that genomes are full of sequences that have often been deemed to be “junk” and are apparently useless. Indeed a genome is not simply the carrier of a program allowing cell to multiply and occupy a niche, it is also a store of energy-rich nucleotides. Indeed when there is a strong pressure on energy sparing, genomes have a tendency to be shorter in animals that fly as compared to their terrestrial counterparts. However genomes remain still long entities, that occupy a significant amount of the cell's volume. Exploring metabolic constraints, coupled to the need for growth associated to the requirement for multiplication, I will discuss the inevitable consequence of making genomes long as well as solutions uncovered when DNA appeared to streamline them. In conclusion I will discuss how this allowed cells to carry over the possibility of innovation for management of an unpredictable future.

All are welcome