NUS National University of Singapore | Department of Biological Sciences, Faculty of Science

BIOLOGY COLLOQUIUM

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Hosted by A/P Ganesh Anand

The slow-evolving genome of elephant shark



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The extant jawed vertebrates (Gnathostomes) are divided into two major groups: the cartilaginous fishes (Chondrichthyes) and bony vertebrates (Osteichthyes). Cartilaginous fishes comprise chimaeras, sharks and rays whereas bony vertebrates include ray-finned fishes, lobe-finned fishes and land animals. We proposed elephant shark (*Callorhinchus milii*), a holocephalan chimaera, as a model cartilaginous fish genome because of its relatively small genome (1 Gb). Sequencing and comparative analysis of the elephant shark genome revealed that the molecular evolutionary rate of the elephant shark is the slowest among the analyzed vertebrates. Furthermore, elephant shark genome has undergone a relatively low rate of inter-chromosomal rearrangements. The endoskeleton of cartilaginous fishes is made up of cartilage in contrast to the ossified skeleton of bony vertebrates. Analysis of the genes involved in bone formation revealed that elephant shark lacks a crucial family of genes present in bony vertebrates. Knockdown of a member of this gene family in zebrafish resulted in reduced bone formation, lending support to the conclusion that the absence of this gene family explains the cartilaginous skeleton of elephant shark. The adaptive immune system of elephant shark is unusual - certain co-receptors, transcription factors and cytokines/cytokine receptors are either atypical or absent, indicating that it possesses a primordial adaptive immune system. The slow evolutionary rate and the unique phylogenetic position of elephant shark make it a valuable reference genome in comparative genomics.

Artwork by Ann Nee, DBS, NUS