



City University of Hong Kong
Department of Biomedical Sciences

presents a seminar on

Comparative population genetics of purebred and village dogs

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Date: 26 September 2014 (Friday)

Time: 11:00 am – 12:00 noon

Venue: B6605 (CSE Conference Room), Blue Zone (near Lift 3)
6/F Academic 1, City University of Hong Kong, Kowloon Tong

Abstract

The history of domesticated animals involves a loss of genetic diversity, first during the domestication process and later through strong artificial selection and genetic drift in relatively small, homogeneous breed populations. The effects of these processes reshape the genetic architecture of traits and diseases in companion animals, offering opportunities for genetic insights into disease mapping and evolutionary mechanisms of adaptation.

The dog is the oldest and most phenotypically diverse domesticated species, making it uniquely suited for studying the impact of domestication and artificial selection on genetic diversity and the genes underlying extreme morphological and behavioral diversity. Using genetic analysis of purebred dogs and free-ranging “village” dog populations throughout the world, I explore the population history of the domestic dog, the degree of inbreeding found in modern purebred lines, and genes and traits showing evidence of positive selection in natural and purebred dog populations. Whereas the genetic structure of purebred dogs simplifies the discovery of genetic variants underlying phenotypic variation, the genetic diversity and wide geographic distribution of village dogs is particularly useful for understanding the evolutionary process of domestication and, for some traits, the fine-mapping of genetic associations. Where practical, combined analysis of domesticated and feral lineages can enhance our understanding of the history and evolution of adaptive traits and genetic disease.

General Enquiry: 3442-4538

All are welcome