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ASIA EDITION

New study contributes to clinical diagnosis and intervention in mite allergies in China

17 June 2022 | News

CUHK unveils the evolutionary history of medically important mites

The medically important astigmatic mites have long been known as the major cause of human allergies. Recently, a groundbreaking study led by The Chinese University of Hong Kong (CUHK)'s Faculty of Medicine (CU Medicine) with researchers from universities in Guangzhou, Shenzhen, Wuxi, Macao, Thailand, South Korea and Singapore, has revealed their divergent evolution. The findings lay the genomics groundwork for diagnosis of and intervention in mite allergy, and have been published in *Molecular Biology and Evolution*, a prestigious international scientific journal.

In Hong Kong, over 50% of the population have at least one form of allergic disease; in particular, the number of children (under 14 years old) suffering from allergies has continued to soar in recent decades. House dust mites are the predominant triggers in about 40% to 60% allergic individuals in Hong Kong.

The research group led by Professor Stephen Kwok Wing TSUI, Professor of the School of Biomedical Sciences at CU Medicine, has been working diligently for over a decade on mite genomics, revealing the comparative genomics of astigmatic mites using six high-quality genomes and cracking their evolutionary history, from emergence to extreme diversification.

The collaborative research group hopes that this pioneering comparative genomics study not only expands our knowledge of astigmatic mites and provides comprehensive genomic resources for scientific researchers in this field, but also ultimately contributes to the clinical diagnosis of and intervention in mite allergies.