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

ON-SITE BIOLOGY COLLOQUIUM

Friday, 23 Oct 2026 | 4 pm | S3 05-02 Conference Room 1

Hosted by Professor Antonia Monteiro

Map to Block S3

Deciphering the Mechanisms of Domestication Selection and Genetic Diversity Evolution in Silkworms Based on Pan-genome



Xiaoling Tong

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The silkworm (Bombyx mori) is the only fully domesticated economic insect. After 5,000 years of artificial domestication and directional breeding, it has evolved from wild silkworm into a specialized industrial insect with high and stable yield and unique traits. To reveal how genetic diversity evolves under intense artificial selection during domestication from wild to domestic silkworm, we performed large-scale genomic analyses of silkworm germplasms. We conducted deep resequencing of more than 1,000 silkworm accessions and long-read third-generation sequencing of 545 samples, and constructed a silkworm super pan-genome. Using population genomic approaches, we systematically identified selected key genes and structural variations associated with domestication and improvement, dissected the molecular basis of core domesticated traits, and detected selection signatures. Our work clarifies how artificial selection remodels the silkworm genome, purges deleterious variants and fixes favorable traits. This study uncovers the genetic blueprint of silkworm domestication and breeding, and provides critical theoretical foundations for molecular design breeding, germplasm innovation and conservation of silkworm genetic resources.

About the Speaker

Xiaoling Tong is Professor at the State Key Laboratory of Resource Insects, Southwest University. She is Director of the Key Laboratory of Sericultural Biology and Genetic Breeding (MARA), position scientist of the National Sericulture Industrial Technology System, and Vice Chair of the Entomological Society of Chongqing. She holds honours including the Young Yangtze River Scholar, Academic and Technical Leader of Chongqing and the National Outstanding Agricultural Research Talents. Her research focuses on silkworm genetic development, germplasm innovation, molecular design breeding, insect comparative genomics and evolutionary developmental biology. She led the Thousand Silkworm Pan-genome Project and built the SilkMeta database. Her group revealed molecular mechanisms of green cocoon formation, sex determination and silk yield, creating over 20 innovative silkworm germplasms and three new varieties. Her work aims to decode the genetic rules of key silkworm traits, establish molecular breeding systems and promote high-quality sericulture development.