中央研究院生物多樣性研究中心
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02-2789-9621

Microbial Diversity and Bioinformatics

The Genomic Basis of Pathogenicity in *Fusarium solani* Species Complex Infecting Sea Turtle

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Venue: Auditorium, 1st Floor,
Interdisciplinary Research Building
跨領域科技研究大樓1樓演講廳

Host: Dr. Isheng Jason Tsai 蔡怡陞副研究員

Doctoral Dissertation Defense Presentation

~Attendee must wear mask~
~與會者請配戴口罩~

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Abstract

Fungi from the genus *Fusarium* is a common pathogen that infects multi-kingdom hosts. In particular, *Fusarium solani* species complex (FSSC) associated diseases were increasingly reported in domestic, captive and wild animals in recent decades. However, most reports were only able to identify the disease causative agent and the pathology is less known. Sea turtle egg fusariosis (STEF) has been reported around the globe and has caused huge mortality in this endangered animal. Yet, little is known regarding the ecology and pathology of STEF. The establishment of hatchery is part of the conservation works to protect sea turtle eggs. But a particular hatchery practice – reusing sand for egg incubation – is to be suspected for inducing higher FSSC infection risk in incubating eggs. Hence, this study determined the microbial diversity and pathogen abundance of nest sand (Chapter 1). Distinct microbiota and a higher relative abundance of FSSC were found in hatcheries' reused-sand compared to the nesting beach. This work emphasizes that stringency in hatchery management must be maintained for the efforts of conservation to not be in vain.

Besides the field survey, this study determined the genomic basis of pathogenicity in FSSC isolated from various host types (Chapter 2). Highly contiguated assemblies of six FSSC strains were produced and compared, revealing a spectrum of conservation patterns in chromosome which can be categorised into three compartments: core, fast-core (FC), and lineage-specific (LS). Each chromosome type varied in structural architectures, with FC and LS chromosomes containing a significantly higher proportion of repetitive elements and enriched in functions related to pathogenicity and niche expansion. These findings show that genome compartmentalisation was the outcome of multi-speed evolution amongst FSSC chromosomes, which is in contrast to the commonly recognized "two-speed" genome concept in fungal pathogens.

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In addition to the classification of FSSC's genomic characteristics, experiments were conducted to observe the infection scenarios and described the transcriptome responses of FSSC pathogens and Chinese soft-shelled turtle *Pelodiscus sinensis* eggs post-inoculation (Chapter 3). The experiments demonstrated that *F. falciforme* and *F. keratoplasticum* can penetrate eggshells and colonise egg inclusions, indicating FSSC are opportunistic pathogens toward eggs and identified differentially genes also associated with plant pathogenicity, including the most upregulated genes encoding the CFEM (Common in Fungal Extracellular Membrane) domain.

The outcome of this dissertation should allow the gain of fundamental knowledge regarding the pathology behind FSSC on eggs, which represents the beginning of critical steps towards the management of epidemics to reduce disease occurrences in the wild and man-managed settings. Moreover, this study establishes genomic resources and an animal model for fungal pathogens of the trans-kingdom hosts.