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Microbial Diversity and Bioinformatics

Comparative Genomics Delimit *Aphelenchoides besseyi* Species Complex and Pinpoint Horizontal Gene Transfer Events in Clade IV Nematodes

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Time: 2022. 11. 14 Mon. 10:00
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

~Attendee must wear mask~
~與會者請配戴口罩~

Abstract

Horizontal gene transfer (HHT) is an important process for plant parasitic nematodes (PPNs) acquired essential genes to infect plants. In this study, we sequenced the species complex of *Aphelenchoides besseyi.* By comparing these genomics with other nematodes, we found genome size of *A. besseyi* are amongst the smallest in PPNs. Phylogenomic analysis shows the *A. besseyi* species complex can be successfully divived into two groups according to their host plants. Synteny analyses between reference genomes indicated that three chromosomes in *A. besseyi* were derived from multiple fusion and fission events. In addition, the major HGT events were acquired from the last common ancestors of clade IV, and most of these HGT were acquired from bacteria. The acquisition and maintenance of HGT genes may have shaped the lifestyle of PPNs.