CHIBA UNIVERSITY

Medical Mycology Research Center

Medical Mycology Research Center Monthly Seminar

April 12(Wed), 2017　16:00～17:30

Main conference room, Medical Mycology Research Center, Chiba University

"The pigment producing, antagonistic *Metschnikowia* yeasts pose a challenge to rDNA barcoding"

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DNA barcoding is a molecular method using short, standardized and variable DNA sequences (barcodes) for the rapid identification of the taxonomic affiliation of organisms. In principle, any region of the genome can serve as a barcode if its interspecies diversity exceeds sufficiently its intraspecies diversity to generate gaps (barcoding gaps) between species. The presence of such gaps assures that the DNA sequence distances can be used to assign species names to specimens/strains. In fungi, the ITS region of the rDNA repeat was proposed as the primary fungal barcode. The available results show that the ITS-regions are sufficient to correctly identify most of the medically relevant fungal species but may be insufficient for taxonomic identification in other groups of fungi, which can cause difficulties e.g. in metabarcoding analysis of fungal communities in environmental and clinical samples. We found that the pigment producing *Metschnikowia* strains which show strong antimicrobial antagonism cannot be assigned to species because their rDNA arrays are not homogenised. The repeats in the arrays have highly diverse ITS and D1/D2 sequences. The sequences differed within the genomes of certain strains by up to 30 substitutions and certain repeats were more similar to certain repeats of other species than to the repeats of their own array. The variable sites were concentrated in regions that corresponded to back-folding stretches of hairpin loops in the predicted secondary structures of the RNA molecules. The neighbour-net analysis of the sequences showed that the six antagonistic *Metschnikowia* species shared a continuous pool of diverse repeats. The phylogenetic and network analyses further revealed that their rDNA arrays had not evolved in a vertical tree-like way but by reticulation.

Organized by Medical Mycology Research Center, Chiba University

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