The extremely halotolerant black yeast Hortaea werneckii - a model for intraspecific hybridization in clonal fungi

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The polymorphic black yeast Hortaea werneckii (Capnodiales, Ascomycota) is extremely halotolerant (growth from 0 to 30% [w/v] NaCl) and has been extensively studied as a model for halotolerance in Eukaryotes for over two decades. Its most frequent sources are hypersaline environments and adjacent sea-water habitats in temperate, subtropical and tropical climates. Although typically saprobic, H. werneckii can also act as a commensal coloniser on human skin, causing tinea nigra on hands and soles. Here, we report that addition of NaCl to culture media expands the growth range of H. werneckii to 37 °C, which explains its colonisation of human skin, with its increased salinity. The morphological and physiological plasticity/ versatility of H. werneckii indicate that a species complex might be involved. This was investigated in this polyphasic taxonomic analysis based on the global diversity of H. werneckii strains collected from hypersaline environments, and from humans and animals. Analysis of D1/D2domains of 28S and internal transcribed spacer rDNA revealed 10 and 17 genotypes, respectively, that were not always compliant. The genotypes have global distributions. Human and environmental strains with the same genotypes are intermingled. Due to the limited number of phylogenetically informative characters in the ribosomal DNA dataset, the partial genes encoding for ?-tubulin (BTB) and mini-chromosome maintenance protein (MCM7) were also sequenced. The use of these genes was hampered by ambiguous sequences obtained by Sanger sequencing, as a consequence of the diploid and highly heterozygous genome of many H. werneckii strains. Analysis of the BTB and MCM7 genes showed that in some cases two copies of the gene from the same genome are positioned in distant phylogenetic clusters of the intraspecific gene tree. Analysis of whole-genome sequences of selected H. werneckii strains generally confirmed the phylogenetic distances estimated on the basis of ribosomal genes, but also showed substantial reticulation within the phylogenetic history of the strains. This is in line with the hypothesis that the diploid genomes of H. werneckii were formed by hybridizations, which have sometimes occurred between relatively divergent strains.

BTB

Clustering

D1/D2 rDNA

Genomes

ITS

MCM7

Morphology

NaCl tolerant enyzmes