

Comparative Genomics of Hemiascomycete Yeasts

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Eukaryotic molecular evolution proceeds through a succession of distinct events that leave only distorted and superimposed traces in living genomes. The hemiascomycete yeasts, with their compact genomes but distinct physiologies, provide a unique opportunity for unravelling the traces of these events and understanding the history of individual lineages. After our first survey of Hemiascomycete genomic diversity using low coverage sequencing (Souciet *et al.*, 2000), we have now completed the sequences of four yeast species, selected to represent a broad evolutionary range that *a posteriori* proved to be comparable to that of the entire phylum of Chordates. *Candida glabrata*, the second causative agent of human candidiasis, is a pathogenic yeast phylogenetically related to *S. cerevisiae*. *Kluyveromyces lactis* is an industrial yeast commonly used for genetic studies. *Debaryomyces hansenii* is a halotolerant yeast phylogenetically related to *Candida albicans* and other pathogenic yeasts. *Yarrowia lipolytica* is a very distantly-related yeast that shares a number of properties with filamentous fungi. The genomes of the four species contain a total of *ca.* 24,500 genes whose translation products have been annotated and classified into families together with *S. cerevisiae* proteins. A significant proportion of these families appear specific to Hemiascomycetes, and a number of physiologically significant family-size expansions and specific gene losses were found. Comparisons of chromosome maps and genome redundancies reveal that the different yeast lineages have evolved through a remarkable interplay between several distinct mechanisms, including tandem gene repeat formation, massive genome duplication, segmental duplications and gene loss. Results of this large scale comparative analysis will be discussed in the light of recent experiments performed in *S. cerevisiae* (Kozul *et al.*, 2004).

Souciet, J. L. *et al.* Genomic exploration of the hemiascomycetous yeasts. *FEBS Lett.* 487, 3-147 (2000).

Kozul, R., Caburet, S., Dujon, B. and Fischer, G. Eucaryotic genome evolution through the spontaneous duplication of large chromosomal segments. *EMBO J.* 23, 234-243 (2004).

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