

## **Computational identification of fungal genomes by an innovative methodology.**

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The wide number of fungal genomes whose sequence has been completed throughput screens at nucleotide and protein levels. This also provides the information regarding partially sequenced sequences of fungal species. Analysis of the sequence of the 16 chromosomes of *S.cerevisiae* revealed the existence of numerous pairs of chromosomal homologous regions. We have developed a comparative method for the analysis of genome of the fungal species. The amount of data thus obtained provides information on evolutionary relationship between the yeast species. Comparative genome analysis not only improves the recognition of true ORFs, but also yields much more accurate definition of gene structure, translation start, stop codons and intron boundaries. Interrelation between the ORF is seen in phylogenetically closely species and is lost in distantly related species. We have applied a similar approach to investigate the protein function constrains evolution. The compilation of the interactive proteins with that of other yeast proteins were performed. Computational analysis of small genomes has been successfully used to identify regulatory elements associated with known sets of related species. Genome wide exhaustive search for all regulatory motifs resulted in the discovery of conserved motifs, which includes most previously identified motifs. We found a strong overlap with functional sets for most of the genome-wide motifs, and discover novel motif functions.