

## Comparative genomics and genome wide analysis of bidirectional promoters in *Candida albicans*

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**Introduction:** With the increasing number of genome sequencing data, it is critically needed to understand the coordination among various functional classes of genes. A genome wide analysis of gene organization and their promoter functions can give a significant insight into the working of functionally related genes as gene networks. So, with the object of identifying such organization, we have investigated the genome of *Candida albicans* for bidirectional promoters and compared it with the data of bidirectional promoters of human genome.

**Summary of Results:** Cluster of functionally related genes, which is also called “Operon”, is a general feature of bacteria and other prokaryotes but such gene organizations are much less investigated in eukaryotes. The completion of *Candida albicans* genome sequencing project provided an unique opportunity to study the distribution of genes throughout the genome. By analysing the intergenic distances between 6,094 open reading frames, we have identified a class of divergently transcribed gene pairs, representing more than 20% of the genes in the genome, whose translational start sites are separated by less than 1000 base pairs. Upon comparative analysis it was found that, it was significant proportion than bidirectional promoters present in human genome. Although, this bidirectional arrangement has been previously described in various species, the prevalence of bidirectional gene pairs in *C. albicans* is striking. Our work also shows that these gene pairs have a variety of functional categories with more than fifty percent of them having a role in cellular metabolisms such DNA repair. Microarray database analysis indicated that many bidirectional pairs are co-expressed where they were tend to have positive Pearson correlation coefficient scores. Further, as a validation of computationally predicted bidirectional promoters, we constructed a dual reporter assay by which we show that promoter sequence between Nag1 and Dac1 initiate transcription in both directions.

**Conclusion:** These findings demonstrate that a bidirectional arrangement provides a unique mechanism of regulation and metabolic adaptation for a significant number of *Candida albicans* species.

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