CONCLUSIONS AND FUTURE PERSPECTIVES
VII. CONCLUSIONS AND FUTURE PERSPECTIVES

We have carried out a comprehensive identification of transcriptional regulators from the proteomes of 62 dikary fungi. A total of 47 TF families were identified and their distribution in the 62 genomes revealed several striking features. The most abundant TF family in all the fungal genomes was the Zinc finger C6 family. We found examples of TF families which were clade-specific while others were specific to particular fungal lineages. Also, certain TF families were found to be expanded in the genomes of specific organisms. Unexpectedly, a number of metazoan-specific TF families like LAG1, CP2, and the plant TF families like WRKY and EF2 were also found in the dikary fungal genomes except those of Hemiascomycota. In general, evolutionary conservation within the TF DNA binding domain was substantially higher than at the whole protein level. Moreover, comparative analyses of the two major clades- the *Saccharomyces* and the *Candida* revealed striking differences in the repertoire of their TF families. These computational screens provided a large collection of novel and unique TFs for experimental investigation and functional characterization.

Our analysis of the GATA factor families in *Candida* clade identified four transcription factors that were not present in *Saccharomyces* clade. We selected one of these putative GATA factors, called GAT9 (C. albicans orf19.4301), which has an unusual GATA zinc finger DBD for functional characterization. We found that GAT9 is an essential gene in *C. albicans*, and repression of GAT9 expression caused pseudohyphal morphology (associated with cell cycle defects), impaired growth at high and low temperatures and sensitivity to cadmium. The cadmium sensitivity is indicative of defects in the DNA repair machinery implicating a possible role for Gat9p in this process. The sequence analysis also revealed homology of the Gat9p N-terminal region to that of *S. cerevisiae* Spt21p and *S. pombe* Ams2 providing another possible link to
Gat9p function in chromosome assembly and segregation. We would like to examine the molecular mechanisms of the role of Gat9p in DNA repair, cell cycle regulation and chromosome segregation. Further insights into these connections would be obtained by examining protein-protein interactions of Gat9p, whole genome expression profiling and genetic suppression analysis.