

Abstract

Functional and Structural Annotation of Uncharacterized Lysine Methyltransferase Proteins in *Candida auris*[†]

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1. Introduction

Candida auris is a fungal pathogen that has emerged as a global threat in recent years due to its resistance to multiple antifungal drugs and its ability to cause invasive infections, especially in immunosuppressed patients. Understanding the molecular mechanisms of pathogenesis and drug resistance in *Candida auris* is crucial for the development of effective treatment strategies. The role of lysine methyltransferases, particularly the SMYD family, in the regulation of gene expression and protein function is of great interest in the context of fungal pathogenesis. Investigating the potential involvement of SMYD proteins in *Candida auris* could provide valuable information on the mechanisms underlying its virulence and drug resistance.

2. Methods

In this paper, the uncharacterized SMYD family proteins of *Candida auris* are considered for in silico functional and structural characterizations. Using a combination of sequence analysis, structural modeling, and phylogenetic profiling tools, the intricate annotation process of lysine methyltransferases will be thoroughly explored.

3. Results

The structural similarities between the SMYD members in *Saccharomyces cerevisiae*, *Candida albicans*, and their human counterparts suggest that studying the function of Set5 and Set6 in yeast could provide relevant information about the role of SMYD proteins in chromatin association, genome stability, and gene expression regulation. Further, the *Candida auris* SMYD family was expanded with a novel, uncharacterized member. This member was functionally characterized using protein sequences, phylogeny, structural modelling, and binding studies.

4. Conclusions

The study provides knowledge about SMYD methyltransferase proteins in *Candida auris* using in silico approaches, shedding light on their physiological roles. In conclusion, the emerging role of SMYD proteins in various physiological processes and their implications in cancer pathophysiology, combined with their potential involvement in fungal pathogenesis, highlight the importance of further research on members of the SMYD protein family in various biological systems.

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