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Determining the role of epigenetic factors in antifungal drug resistance

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ABSTRACT

Epigenetic factors are proteins that regulate gene expression by altering transcriptional machinery access to nucleosomes, DNA wrapped around histone proteins. Two classes of epigenetic factors are ATP-dependent chromatin remodelers and histone modifiers such as histone methyltransferases (HMTs), proteins that add methyl groups to histone tails. This study focuses on AIF4 (Antifungal-Induced Factor 4), a possible HMT induced upon neutral lipid depletion that we hypothesize is regulating antifungal drug resistance genes. Overexpression of AIF4 results in hypersensitivity to antifungal drugs. Studying epigenetic factors in the yeast Saccharomyces cerevisiae, including AIF4, can lead to better understanding of cell adaptation to their environments and insight into antifungal drug resistance of pathogenic yeast. This project will focus on identifying suppressors of AIF4's hypersensitive phenotype and exploring whether genes in the neutral lipid pathway are necessary for AIF4 expression. To support our hypothesis, I will grow yeast colonies with overexpressed AIF4 on media containing antifungal drugs. Overexpressing AIF4 strains exposed to antifungal drugs over time suppressed the grow defect. Re-plating the suppressor colonies showed drug resistance, suggesting that a genetic mutation(s) occurred. Suppressor colonies will be analyzed for AIF4 expression and genome-wide sequencing to identify the suppressor mutation(s). In addition, I have generated deletions for genes that encode neutral lipid production enzymes, and I will determine if AIF4 expression is affected. Single and double deletions will determine if a particular neutral lipid is required for the expression of AIF4. Overall, my work will help to characterize a pathway required for AIF4 expression and drug resistance.

KEYWORDS

Saccharomyces cerevisiae, epigenetics, gene expression, drug resistance