CALIFORNIA STATE SCIENCE FAIR
2008 PROJECT SUMMARY

Name(s)
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Project Number
S0409

Project Title
Identifying Functions of Novel Transcripts in S. cerevisiae

Abstract

Objectives/Goals
Identify the functions of five novel transcripts by replacing with a selectable marker gene (Geneticin resistance). Compare cell growth rate of those with to those without the novel transcript in their genome.

Methods/Materials
1)Select the transcripts to study; Microarray charts used to locate position of transcripts on DNA strand.
2)Knock out transcripts with Geneticin resistance gene:
a.Amplify the Geneticin resistance gene with primers specific for each transcript, so Geneticin resistance gene would line up and recombine in correct place.
b.Transform Geneticin gene into yeast cells. Standard lab transformation protocol followed. Encountered several challenges while working, and had to try five different methods to get it to work.
c.Transformation checked by exposure to Geneticin and gel electrophoresis.
3)Analyze and compare the growth phenotypes of the wild type cells and the transformants:
a.Tetrad dissection: Break up tetrad (four sister spores) and start a new colony resulting from each spore.
b.The deletion found in two of the four spores; yeast cells are diploid, and knockout takes place in only one chromosome. Distinguish between deletion and wildtype by repica-plate exposure to Geneticin.
c.Subject both wild type and transformants to different growth conditions and analyze their growth rates.

Results
We found several differences in growth phenotypes by comparing cell doubling times. However, it is difficult to say if these phenotypes are a result of our knockout or an artifact of the experiment.

Conclusions/Discussion
The biggest challenge of this project was getting the transformation to work. We spent countless hours troubleshooting and revising our procedure. We realized that this process of constantly revising our methods and looking at the problem from different angles is what science is all about. It made our project interesting, not just a project from a textbook. This realization is what made this project so meaningful to us.

Because of time spent on troubleshooting, we did not get to test all the growth conditions we had hoped to. To continue experimenting, we will test the wild type and deletion cells in these other growth conditions in addition to further analyzing the growth phenotype differences we found.

Summary Statement
In order to determine the functions of five novel transcripts in S. cerevisiae, we deleted these transcripts by a gene knockout and compared the growth phenotypes of the control cells to the deletion strain cells.

Help Received
Used lab equipment at Stanford University under the supervision of Dr. Albert Lee.