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Counting "Shmoos:" Identifying the Missing Yeast Mating Gene

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This lab module using the response of budding yeast (*S. cerevisiae*) to mating pheromone was designed for students in a sophomore-level genetics laboratory to formulate and test a hypothesis in two lab sessions. During week 1, students are given two cultures of yeast treated with a low concentration of mating pheromone: one culture is a "wild type" strain for mating response and the second strain has a gene deletion for bar1 which encodes an enzyme responsible for degrading the mating pheromone, rendering the cells more sensitive to the pheromone. Students are not told the specific genetic difference between the two strains of yeast, only that one is "wild type" and the other contains a single gene deletion. Students collect data in week 1 to develop and test a hypothesis to determine the function and identity of the deleted gene. Students use microscopes to count the % of yeast cells responding to the mating pheromone in each strain by: 1) the presence of mating projections or "shmoo" shaped cells, and 2) "G1 arrest" calculated as a change in the % of cells with buds representing cell cycle progress towards mitosis. Students average data for each of the two quantitative measurements of mating response among their group and formulate a hypothesis about the phenotypic and genotypic difference between the two strains of yeast. They then design a simple experiment including positive and negative controls in which they modify one variable from week 1 (usually time exposed to pheromone or concentration of pheromone) for the following lab session which will test their hypothesis. The instructor gives feedback on both the hypothesis and experimental design during the first week. In week 2, students perform their independent experiment, collecting and analyzing quantitative data to determine if they have supported their hypothesis. Students are challenged to describe the function/identity of the deleted gene. This lab module can be enhanced in either week 1 or week 2 by allowing students to perform bioinformatic research using the Yeast Genome site (**www.yeastgenome.org**) in which keyword searches can be used to look for similar gene deletion phenotypes for one or more mating-relevant genes

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