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Yeast Mating Report

Introduction:

Yeast can be either haploid or diploid in throughout their lifecycle. Haploid cells have one copy of each chromosome and diploid cells have two copies of each chromosome. Haploid cells can only mate with other haploid cells of opposite mating types, inducing sporulation with a bulge called “schmoo” (Dickinson & Schweizer 1999). The two opposite mating types alleles are either a or α determined by the expression of that allele on the MAT loci on chromosome III (Strathern, et al. 1982). The rationale of this experiment is to practice and understand basic genetic inheritance in a eukaryotic organism. Yeast was used because it mirrors the mating and fertilization of more complex multicellular eukaryotic organisms such as humans (Swanson, et. al. 2011). A monohybrid cross between two heterozygotes will result in a phenotypic ratio of 3:1 due to complete dominance as described by the principles of genetic inheritance.

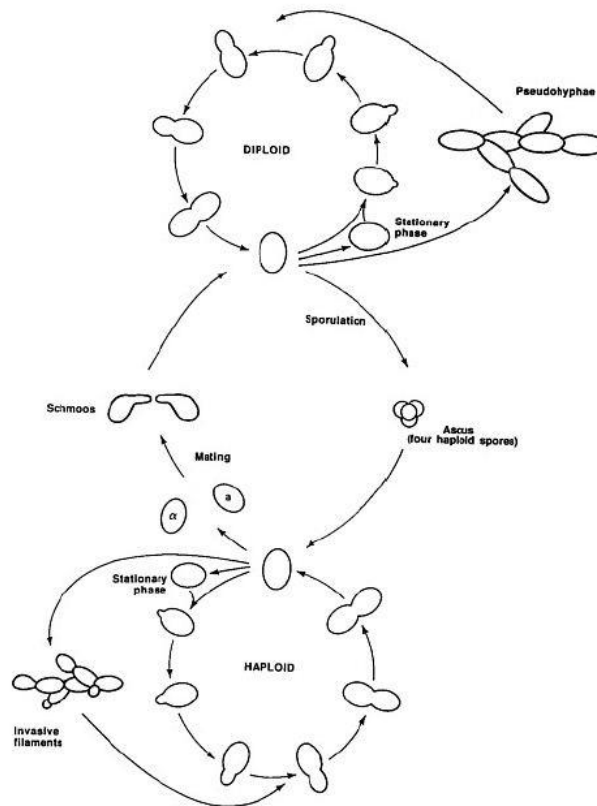


Figure 1: Generational haploid-diploid life cycle of *Saccharomyces cerevisiae* yeast cells (Dickinson & Schweizer 1999).

Methods:

- Haploid alpha and α strains are grown in a mating grid.
- Haploid cells (α 1R, α 2r, alpha1R, alpha2r) are collected and implemented on the agar with sterile toothpicks.
- The finished agar is placed in the incubator for 48 hours and at 30° Celsius.
- From the plate, the group collected haploid alpha1R cells and haploid α 1R cells and fused the two cells in the top left section of the mating grid.
- These steps are repeated for Alpha/ α 1R, Alpha1R/ α 2r, Alpha2r/ α 2r.
- The mated yeast cells are placed in the incubator at 30° Celsius for 48 hours.
- The final haploid cells are grown.
- The final product of the cells are observed and recorded.
- The colors of each strain are recorded and analyzed.

Results:

		<i>alpha</i> Haploid cells	
		<i>alpha</i> 1 R	<i>alpha</i> 2 r
<i>alpha</i> Haploid cells	<i>alpha</i> 1 R	RR	Rr
	<i>alpha</i> 1 r	Rr	rr

Figure 2: Yeast mating grid predicted genotypes

This yeast mating shows the cross between two heterozygous dominant haploid alpha. This means that each mating alpha cell contains one dominant allele and one recessive allele. The cell also contains n number of chromosomes. The resulting Punnett square follows the Mendel's ratio of 1:2:1 (Wolyniak 2013). In the 1:2:1 ratio, one of the resulting daughter cells is homozygous dominant, two are heterozygous dominant, and one homozygous recessive. The resulting phenotypes will cause three daughter cells to display the dominant trait - white. The one daughter cell, which is homozygous recessive, displays the recessive trait - red.

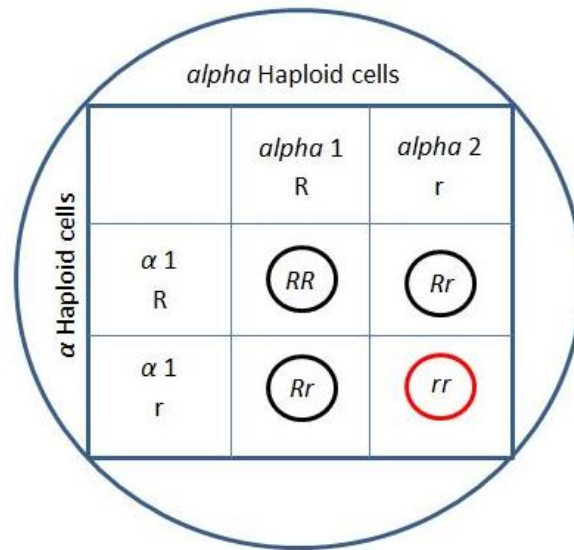


Figure 3: Yeast mating grid with predicted phenotypes

The predicted phenotypes are depicted by the colored rings around the predicted genotypes (Figure 3). The allele for white color is dominant in these cells. For this reason, the daughter cells that contain a dominant R allele will be in white color. Conversely, following the rules of Mendelian genetics, if two recessive traits are presented, like the daughter cell in the bottom right corner, then the cell will show the recessive phenotype for color – the color red (Figure 3) (Wolyniak 2013).

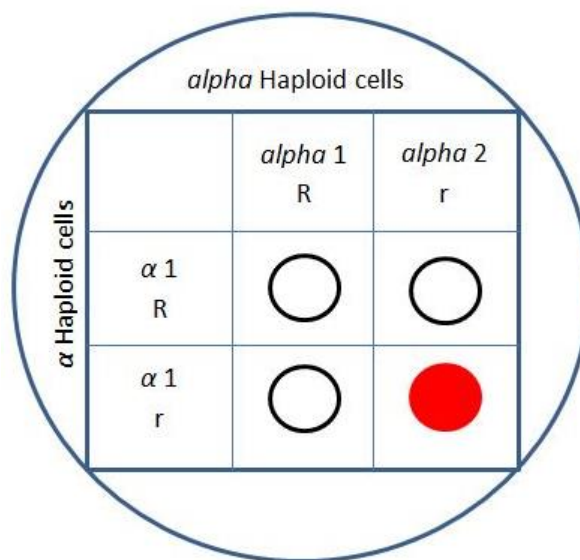


Figure 4: Yeast mating grid with observed phenotypes

The observed phenotypes are depicted by the colored circles (Figure 4). The grid demonstrates the observed daughter cells from the experimental cross, completed in lab. The experimental cross between the two haploid alpha cells follow the predicted of phenotypes (Figure 3). The resulting daughter cells from this experiment follow the prediction because the genotypes are not directly shown (Figure 2).

Conclusion:

The results obtains matched the predicted results. The monohybrid cross between two heterozygotes resulted in a phenotypic ratio of 3:1 due to complete dominance as described by the principles of genetic inheritance. Three of the four resulting strains appeared white and one appeared red in the results (Figure 4). The experimental phenotypic results match the predicted phenotypic results (Figure 3). It is unknown if the genotypic ratios match the predicted genotypes but could be determined by a test cross between the heterozygote F1 generation and a parent cell (Figure 2).

References:

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Strathern, J. N., A. J. S. Klar, J. B. Hicks, J. A. Abraham, J. M. Ivy et al. 1982. Homothallic switching of yeast mating type cassettes is initiated by a double-stranded cut in the MAT locus. *Cell* **31**: 183–192.

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