Halotolerance of Saccharomyces Cerevisiae

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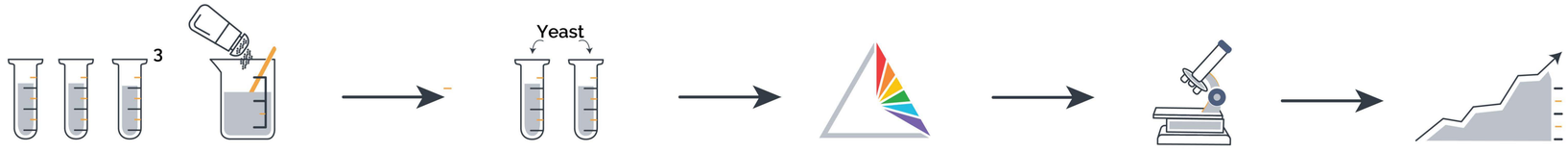
Background

Agricultural irrigation in the bread baskets of the world have contributed to an ever-increasing soil salinity. Irrigation from aquafers and rivers that flow from mineral rich mountains to the sea, spread this sodium into the soil where it accumulates over time. When sodium concentration reaches a critical point, agriculture in many cases is negatively affected.

The focus of our study is the adaptation of eukaryotes to these higher salt concentrations. We used *S. Cerevisiae* (brewer's yeast) in this study due to its ability to change gene expression and modulate enzymes when under osmotic stress (Blomberg, 2000). This can be viewed through the lens of transgenerational epigenetic inheritance, where genes inherited from preceding generations can be expressed differently due to environmental factors, such as increased NaCl (Bošković & Rando, 2018). We hypothesize that *S. Cerevisiae* has genes that can allow for increased halotolerance.



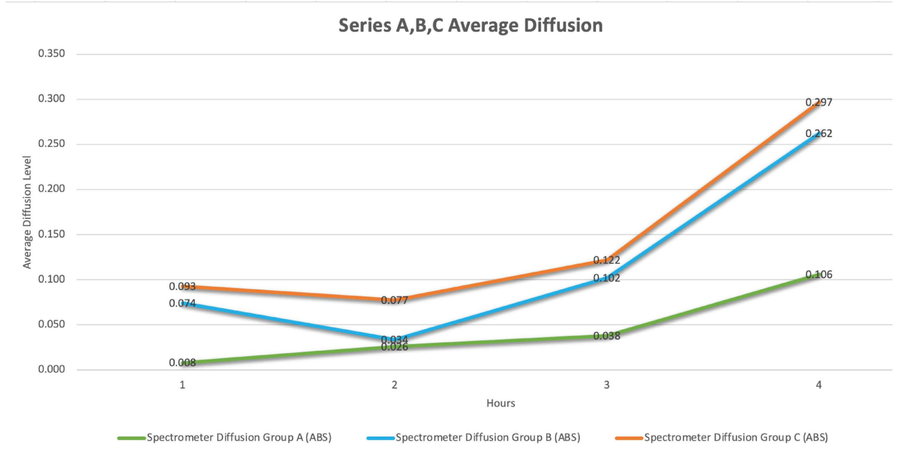
Method

1. A series of 12 test tubes were prepared with 15.2 mL grow solution and staged for inoculation. Nine tubes were labeled for culture. Three tubes were set aside as controls.
2. Three groups of t-tubes with increasing NaCl concentrations were inoculated with 1mL yeast solution except for the controls in each group. A sample of 300 µL was extracted from each and transferred to cuvettes for spectrophotometer readings.
3. All cuvette samples were analyzed for cell viability using microscope and documented.
4. Samples of the highest surviving salinity were stored in t-streaks for the following run.
5. This process was repeated in two successive runs using the most viable culture and increasing salinity each run with the intent of reaching maximum halotolerance.

Results

After 2 successful runs, our team was unable to reach the maximum halotolerance of our strain. In hindsight, higher starting concentrations of salinity should be used. No significant decline in viability ratios were recorded in each run, however, a statistically significant increase in cell division occurred as salinity was increased in each group as shown below.

Spectrometer Diffusion Group A (ABS)					Spectrometer Diffusion Group B (ABS)					Spectrometer Diffusion Group C (ABS)				
Hours	0	1	2	3	Hours	0	1	2	3	Hours	0	1	2	3
A1	0.004	0.034	0.025	0.157	B1	0.097	0.048	0.138	0.317	C1	0.08	0.063	0.109	0.281
A2	0.014	0.036	0.04	0.119	B2	0.065	0.023	0.048	0.129	C2	0.129	0.083	0.125	0.373
A3	0.006	0.007	0.048	0.041	B3	0.06	0.03	0.12	0.341	C3	0.069	0.086	0.132	0.237
A-B	0	0	0	0	B-B	0	0	0	0	C-B	0	0	0	0
AVRG.	0.008	0.026	0.038	0.106	AVRG.	0.074	0.034	0.102	0.262	AVRG.	0.093	0.077	0.122	0.297



Conclusion

Due to limitations in experimental design, further experiments are required to reach the maximum halotolerance of *S. Cerevisiae*. However, it did not escape our notice that *S. Cerevisiae* flourished with higher salinity concentrations. T-tests on our diffusion data, revealed an increased yeast mitotic rate by a factor of 3 between the lowest and highest NaCl group with highly significant p-values of less than .002. This finding was supported by a published paper (Bošković & Rando, 2018). This insight could inform various fields, including biotechnology, food science, and environmental microbiology, where yeast plays a significant role.

References

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