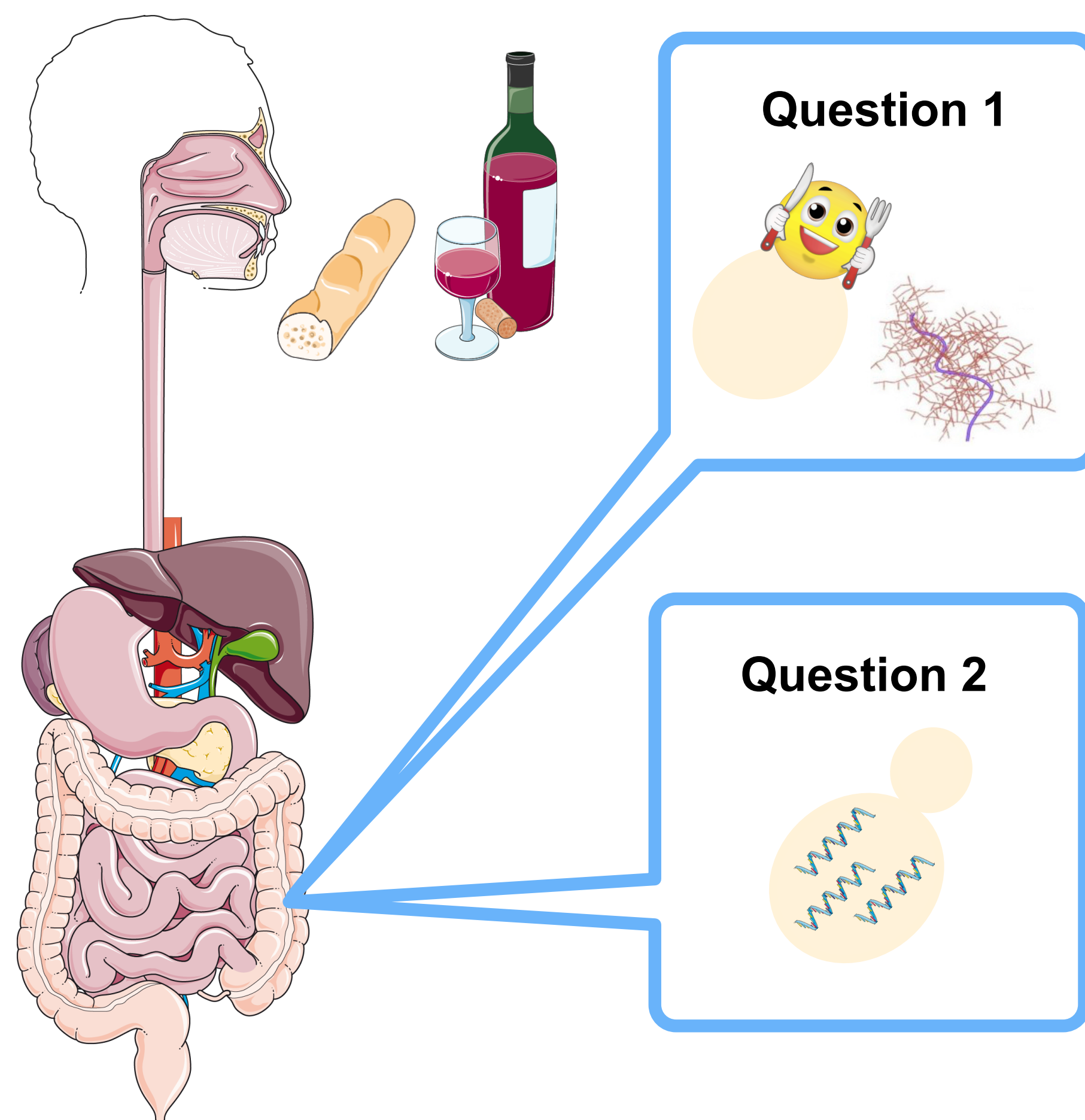


Identifying genes required for *Saccharomyces cerevisiae* growth in mucin

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Introduction



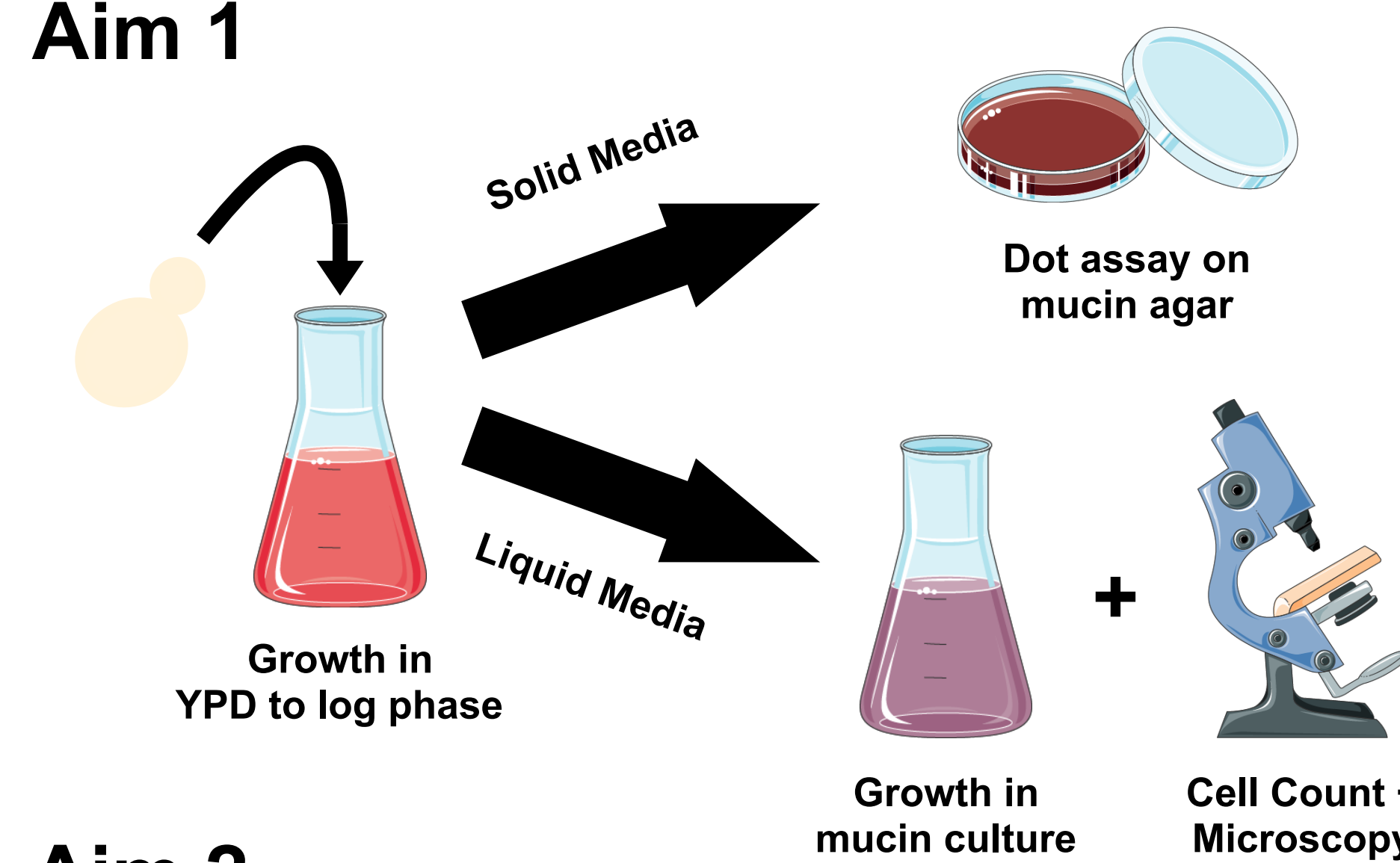
Saccharomyces cerevisiae is one of our most commonly ingested dietary fungi. Despite the detection of its DNA in gut microbiome studies, it is not known whether *S. cerevisiae* can survive and colonize the human gut. To do so, fungi must be able to metabolize mucin: large, highly glycosylated proteins that are the main carbohydrate source in the gut mucosa. Like its close relative and known gut colonizer *Candida albicans*, it is unknown whether 1) *S. cerevisiae* can utilize mucin as a carbon source, and whether 2) it possesses genes involved in breaking down this energy source for easier uptake from the environment.

Hypothesis

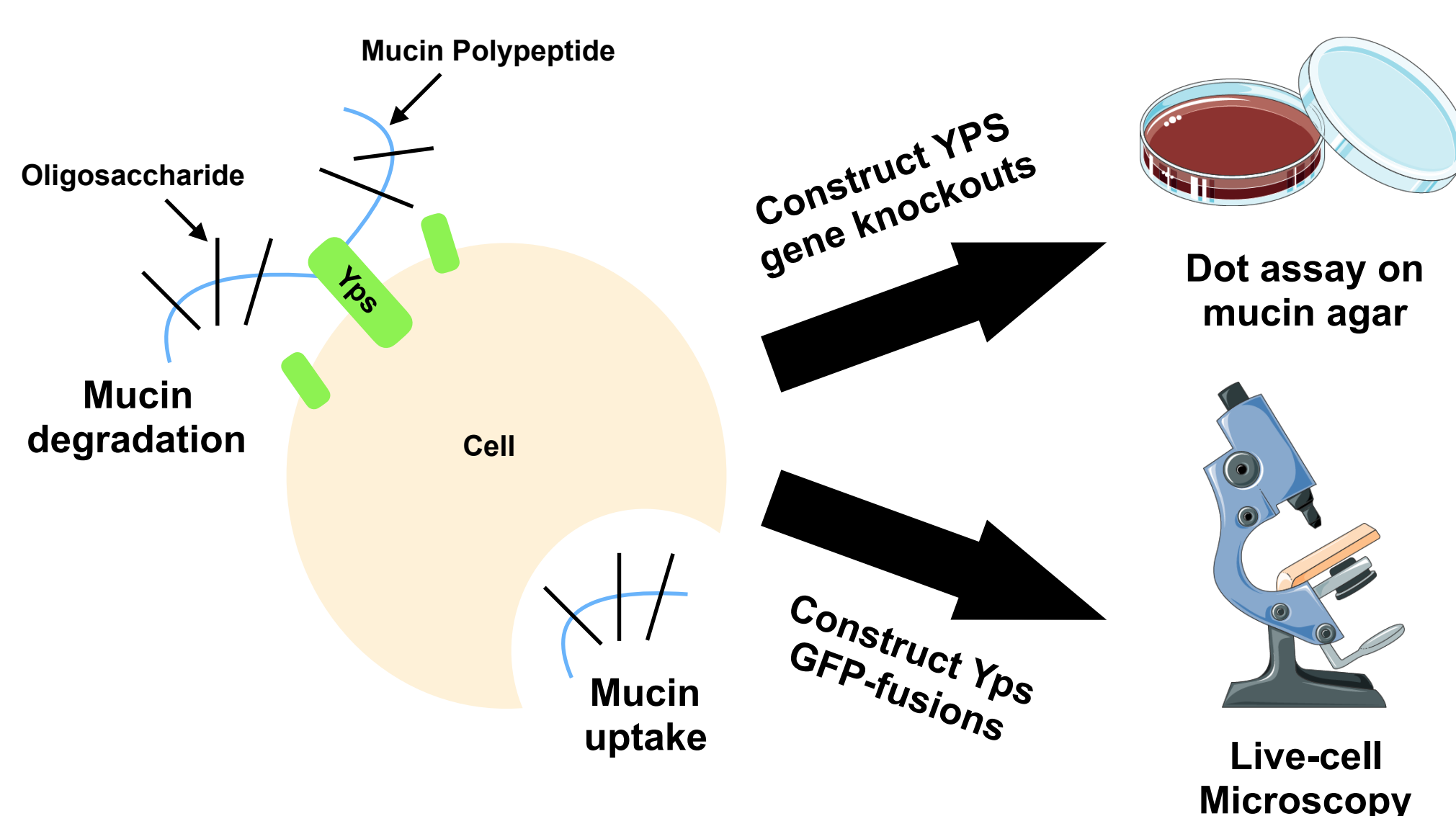
S. cerevisiae can grow in a mucin environment through the up regulation of mucin degrading proteases.

Methodology

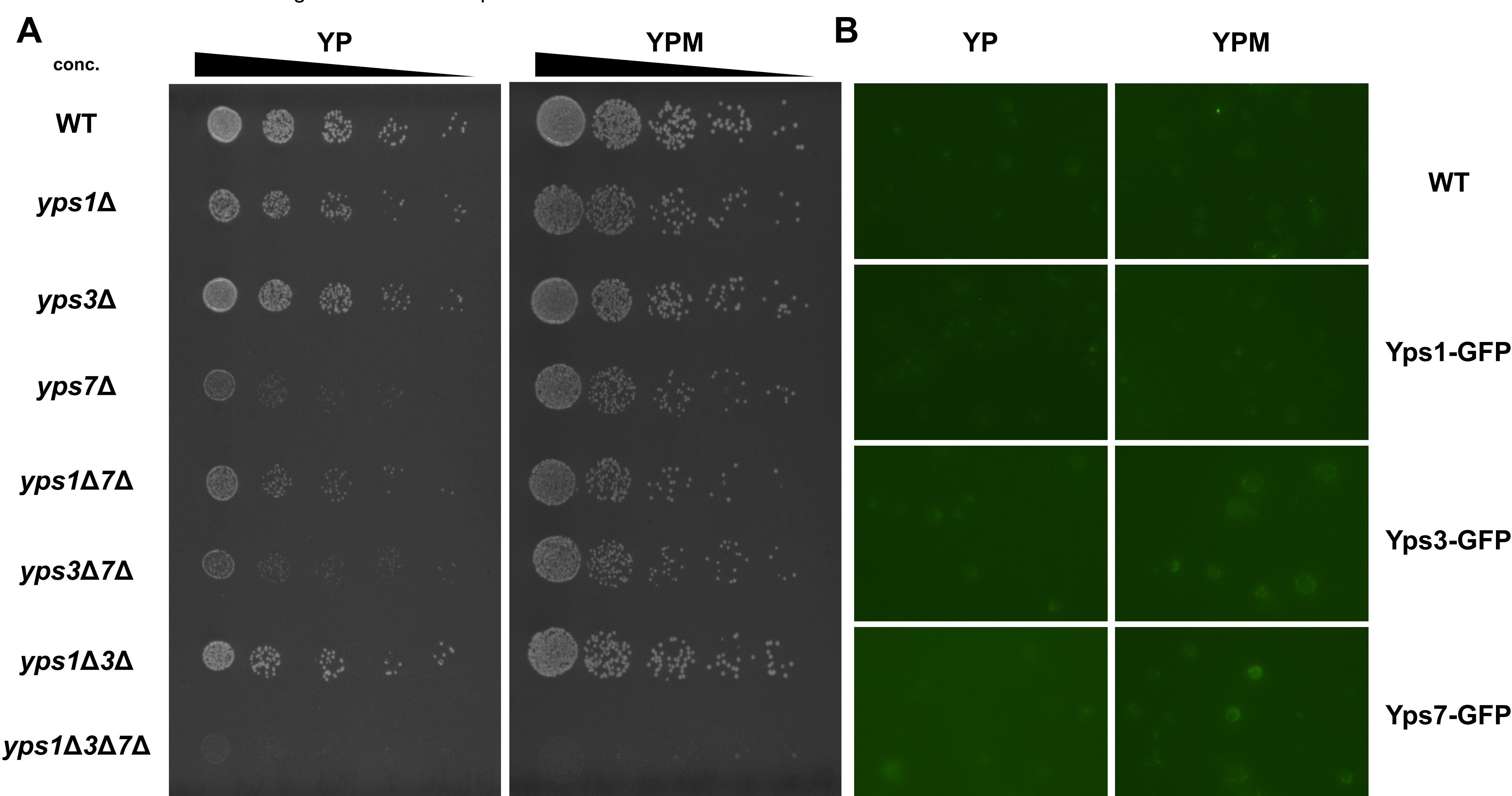
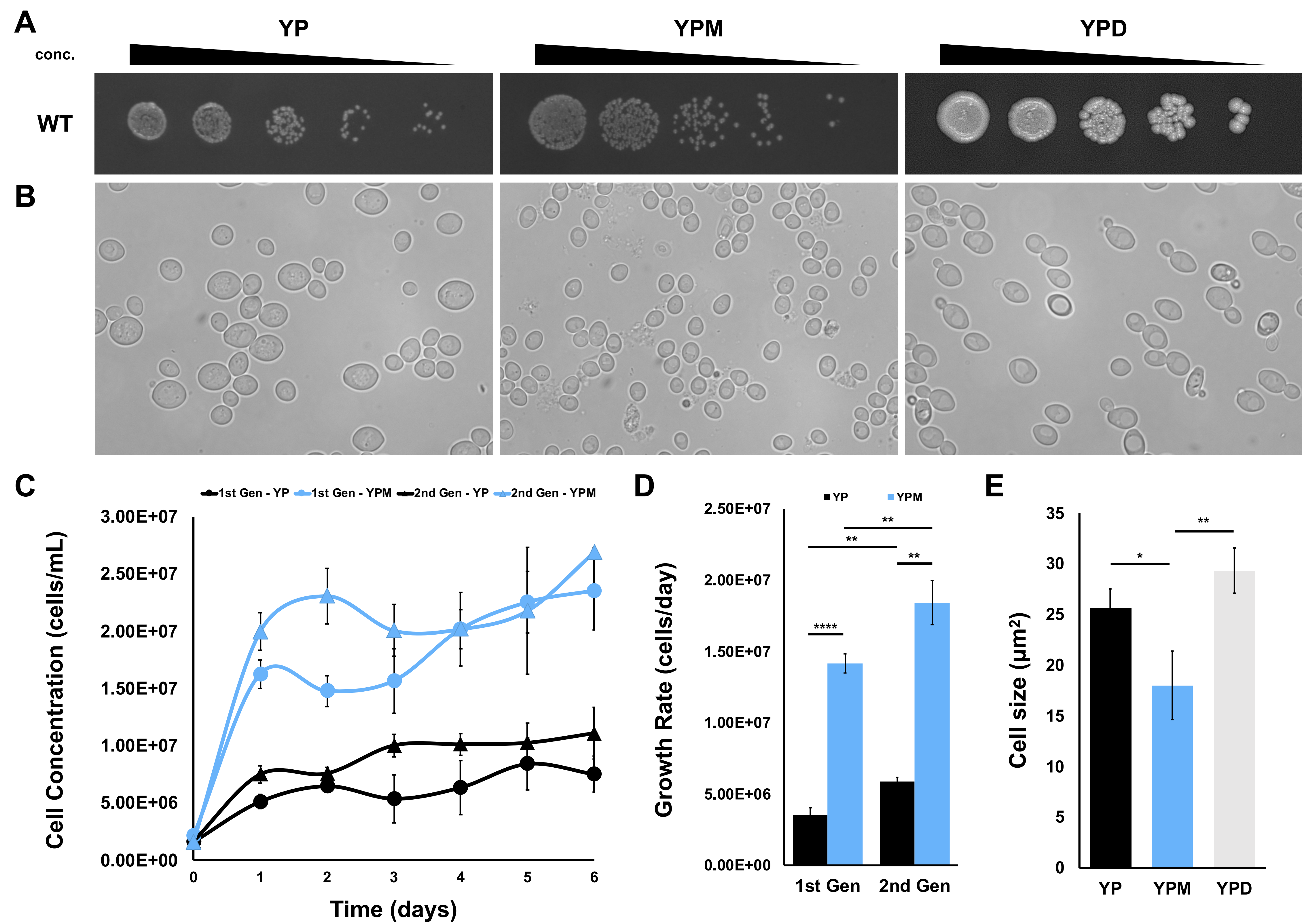
Aim 1



Aim 2



Results



Acknowledgements

Conclusions & Future Directions

- S. cerevisiae* can **grow and adapt** to mucin media, with a significant **decrease in cell size**
- Deletion of the uncharacterized **YPS7** leads to an observable growth defect in limited carbon conditions
- Greater fluorescence of **Yps3 + Yps7** GFP-fusions in mucin media, with localization to the cell periphery
- Future Directions:** Western blot for Yps protein quantification and untargeted transcriptome analysis