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Taylor Award

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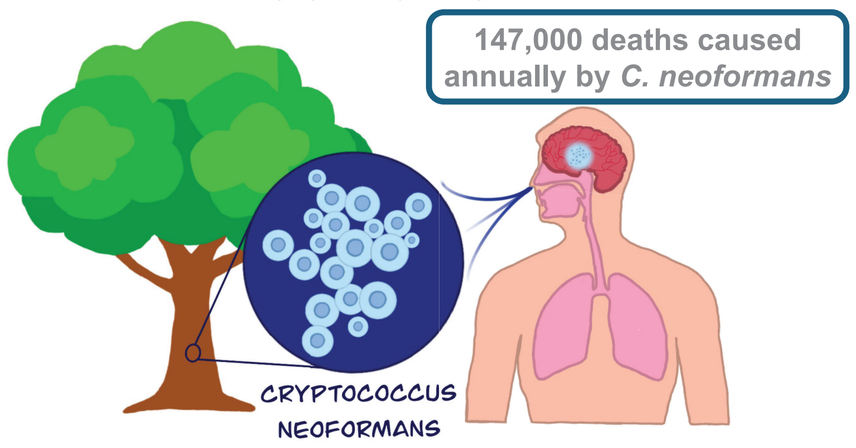
1785

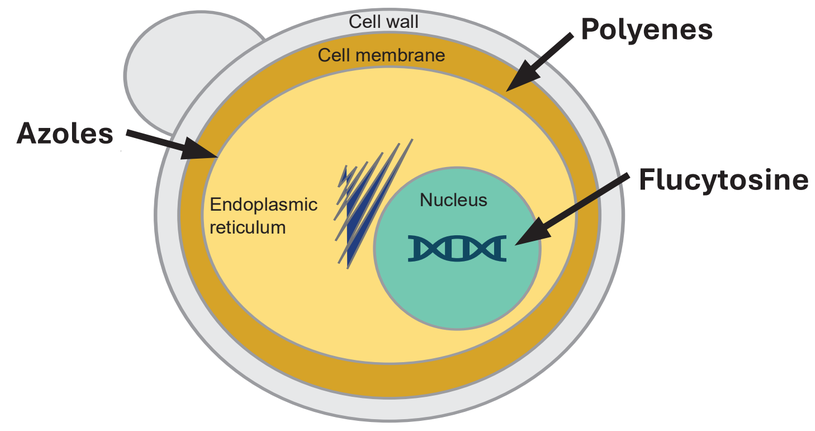
Uncovering the connection between genomic content changes and drug resistance in a human fungal pathogen.

My research aims to understand the human fungal pathogen C. neoformans as a population, through genomic analysis of 384 unique C. neoformans strains. I aim to define the genetic diversity of C. neoformans and understand how genomic content relates to antifungal drug resistance.

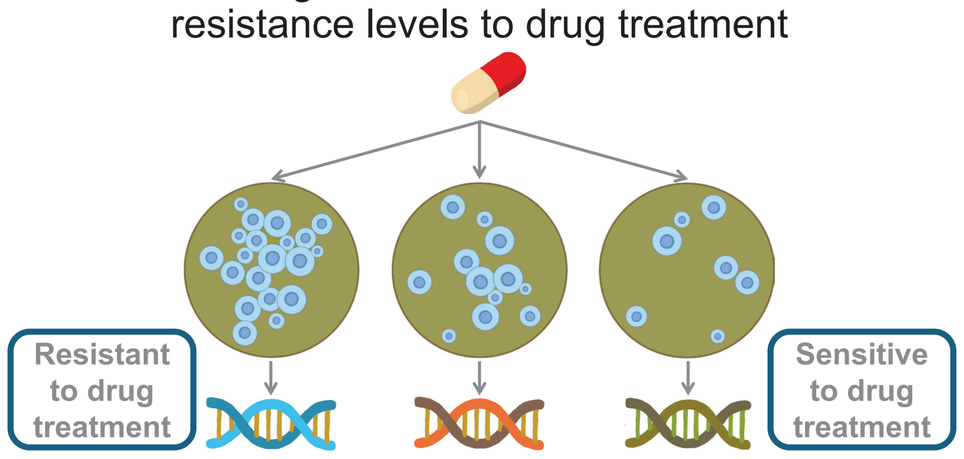
Cryptococcus neoformans commonly lives in the environment



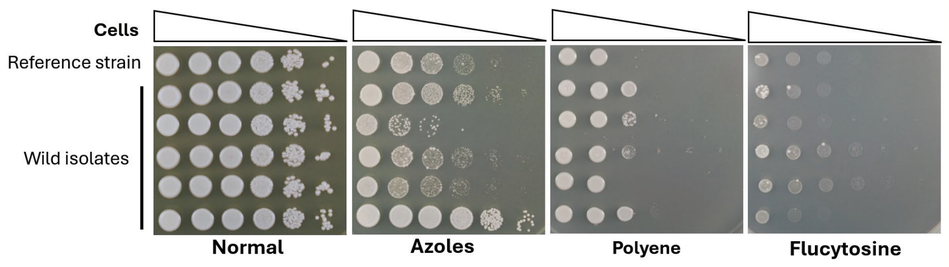
Few treatment options available for *C. neoformans*



Different genetic variants have different resistance levels to drug treatment

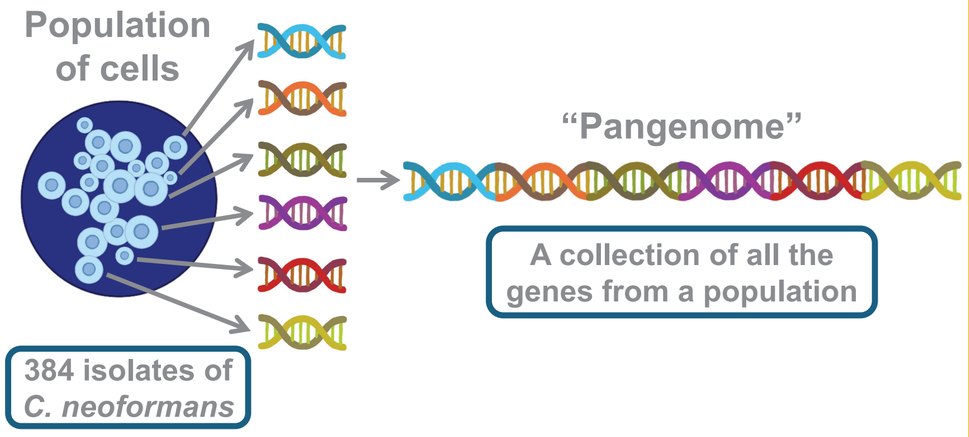


C. neoformans isolates grow differently on antifungal treatments

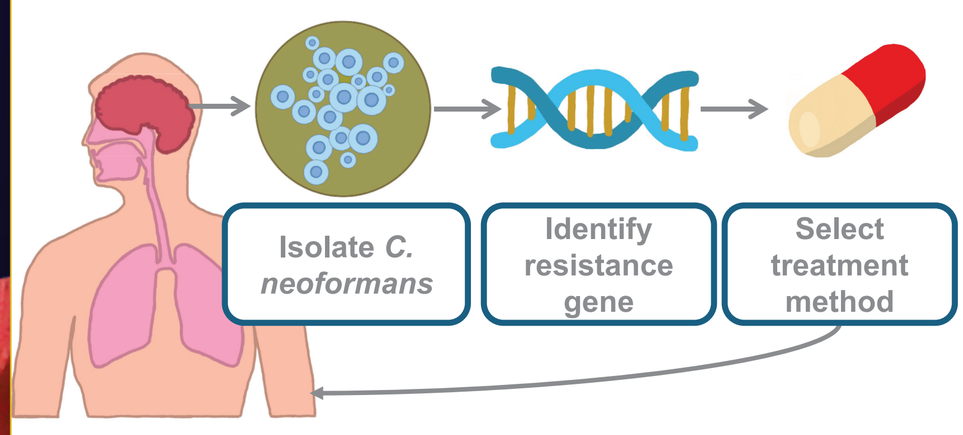


- **10.6% of incident isolates are resistant to azoles**
- **24.1% of relapse isolates are resistant to azoles**

Analyzing all genomic information of *C. neoformans* strains



Applications of my research in treatment of infected patients



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