Leveraging Comparative Population Genomics to Dissect the Mechanisms of *Issatchenkia orientalis* Fluconazole Resistance

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Project Goals: Short statement of goals. (Limit to 1000 characters)

Issachenkia orientalis is an emerging non-model ascomycetes yeast with unparalleled ability to tolerate multiple stresses, including extremely low pH, high temperature, and high concentrations of lignocellulosic inhibitors, salts, alcohols, and organic acids. These unique characteristics may make *I. orientalis* an attractive chassis for producing biofuels and bioproducts directly from lignocellulosic hydrolysates. Understanding how *I. orientalis* evolved to tolerate multiple stresses may allow engineering of a strain more suitable for industrial use than natural isolates are. We performed a population genomics study of 162 strains collected from various habitats and identified 305,435 single nucleotide polymorphism (SNPs), 16,177 insertions and deletions (indels), and other genetic variations, including ploidy, gene copy number, and pan-genome variations. We are currently working on genome-wide association study (GWAS) to understand genetic variations underlying various phenotypes. Here we discuss the results for fluconazole resistance, an unfavorable characteristic for industrial utilization of microbes.

References

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