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Poster Abstract Funding Area: Bioenergy Research Center
Abstract file naming convention: DeLucia_**Yoshikuni**.pdf

Title: Population Genomics of *Issatchenkia orientalis* Reveals the Genetic Mechanisms of its Multi-Stress Tolerance

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Project Goals: We aim to use population genomics analysis to understand how multi-stress tolerance evolved in *Issatchenkia orientalis* so that this non-model yeast may be further developed for biotechnology applications.

Issatchenkia orientalis is an emerging non-model ascomycetes yeast that has unparalleled ability to tolerate multiple stresses, including low pH and high concentrations of lignocellulosic inhibitors. Because of these unique characteristics, CABB I considers *I. orientalis* one of its flagship yeast species and is exploring development of *I. orientalis* as a chassis for production of bioproducts from lignocellulosic biomass. To understand how this species evolved to acquire multi-stress tolerance ability, we are performing population genomics analyses. First, we collected 160 *I. orientalis* strains globally and re-sequenced them using the sequencing pipeline at the JGI. Subsequent sequence analyses identified an initial set of 298,334 SNPs and 24,414 InDels. Our pilot analysis of 30 strains indicated that 21% of these strains are triploids and 79% are diploids. CNVs of large chromosome fragments (>80kb) were shown in 4 of the 30 strains. Loss of heterozygosity (LOH) events were detected among some strains. The next step of our project is to perform GWAS. We expect that GWAS will help us identify functionally important genetic variants and provide insights into how to further develop *I. orientalis* strains more suitable for biotechnological applications.

Funding statement: This work was funded by the DOE Center for Advanced Bioenergy and Bioproducts Innovation (U.S. Department of Energy, Office of Science, Office of Biological and Environmental Research under Award Number DE-SC0018420). Any opinions, findings, and conclusions or recommendations expressed in this publication are those of the authors and do not necessarily reflect the views of the U.S. Department of Energy.