New modern era of yeast genomics: annotation of multiple *Saccharomyces cerevisiae* strains at SGD

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The first completed eukaryotic genome sequence was that of the yeast *Saccharomyces cerevisiae*, and the *Saccharomyces* Genome Database (SGD; http://www.yeastgenome.org/) is the original model organism database. SGD remains the authoritative community resource for the *S. cerevisiae* reference genome sequence and its annotation, and continues to provide comprehensive biological information correlated with *S. cerevisiae* genes and their products. A diverse set of yeast strains have been sequenced to explore commercial and laboratory applications, and a brief history of those strains is provided. The publication of these new genomes has motivated the creation of new tools, and SGD will annotate and provide comparative analyses of these sequences, correlating changes with variations in strain phenotypes and protein function. We are entering a new era at SGD, as we incorporate these new sequences and make them accessible to the scientific community, all in an effort to continue in our mission of educating students, enabling bench researchers and facilitating scientific discovery.

**Additional genomes incorporated into SGD**

**In the years since the publication of the S288C genome, dozens of complete yeast genome sequences have been published**

**SGD tools provide access to strain genomes**

Coming soon to SGD! Select your reference strain...SEY6210, Cen.PK2, J9-3d, SK1, W303, Sigma1278b, FL100...

Questions? Contact us! sgd-helpdesk@lists.stanford.edu