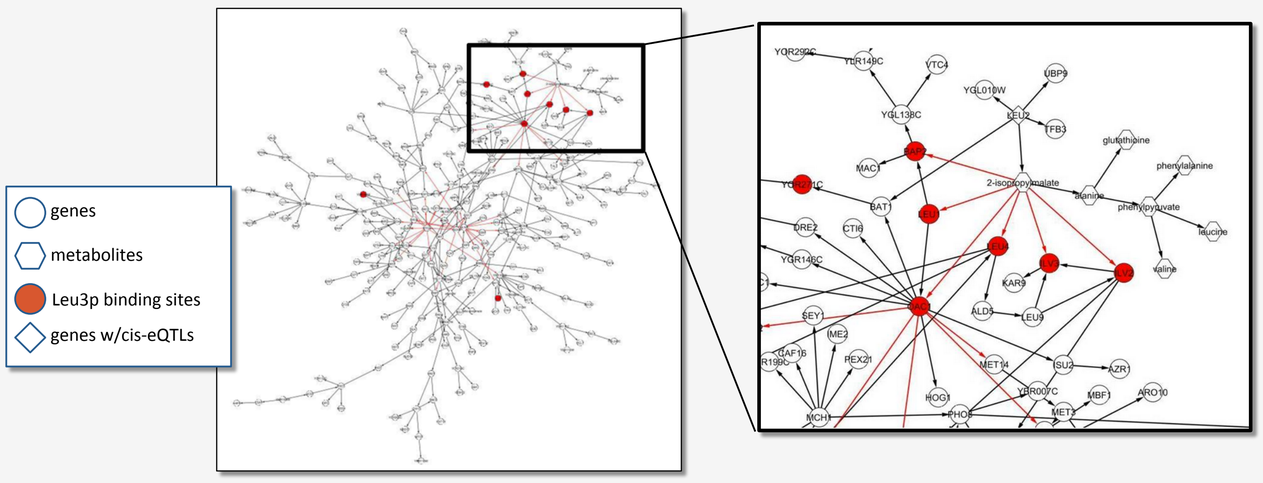
Yeast – why it simply has a lot to say about human disease

Selina S. Dwight, Kalpana Karra, J. Michael Cherry, and the SGD Project
Department of Genetics, Stanford University, Stanford, CA 94305, USA

Science has long approached a complex system by exploring a simpler system that exhibits similar functionality. What happens when the complex system itself becomes more penetrable? Human gene products have been known for decades to have counterparts in *S. cerevisiae*, and detailed knowledge about these *S. cerevisiae* genes has provided clues to basic cellular functions in humans and other higher organisms. In the past decade, however, technological advances in genomic sequencing and other methods have allowed more direct studies in human cells. Contrary to what might be expected, the result is not that budding yeast is less consequential as a model organism, but that increasing information about human genes verifies and expands the connections between the two organisms, allowing human research to more readily leverage yeast knowledge. For instance, identification of regions in human genes with similarity to yeast prion-like domains led to the discovery of a mutation in an evolutionarily conserved residue in a gene that co-segregates with ALS. Conversely, increasing knowledge about human biological processes also suggests areas for further study in yeast. As an example, mutation of mitochondrial DNA associated with aging, disease, and anticancer agents has prompted studies of pathways in yeast that sense the nutritional state of the cell and affect mitochondrial function. Lastly, while yeast may be a relatively simple system, yeast research has witnessed its own advances in technology that serve to further its relevance as a model organism, such as chemogenomic profiling of systematic deletion strains to identify potential drug targets and the mechanisms of action by which compounds exert their effects on disease. As researchers continue to elucidate functional homology between yeast and humans, and to employ yeast as a tool for discovery, it becomes increasingly important to highlight and connect this information. The *Saccharomyces* Genome Database (SGD, www.yeastgenome.org) is building a new class of information called "Species Connections" towards this goal through the incorporation of OMIM homologs and phenotypes, phenologs, drug interactions, and functional homology studies.

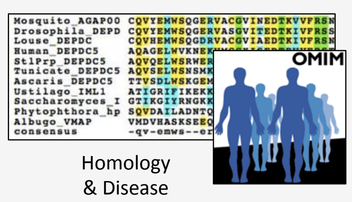
Genetic mutations identified in human disorders

A richness of data allows yeast to tell a multi-dimensional story

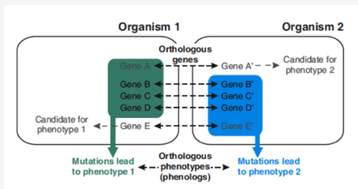


Zhu, et al. (2012), *Stitching together multiple data dimensions reveals interacting metabolomic and transcriptomic networks that modulate cell regulation*. PLoS Biology

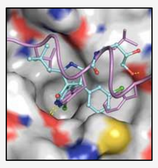
Human connections into SGD



Homology & Disease

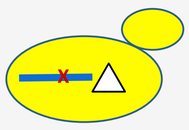


Phenotypes & Orthology



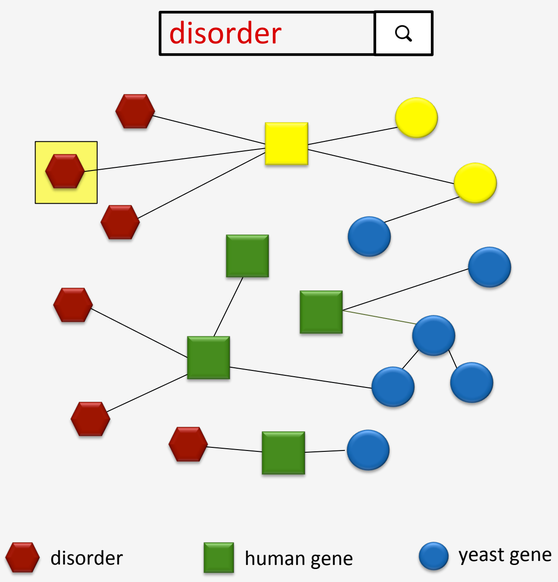
Drug Interactions

Literature

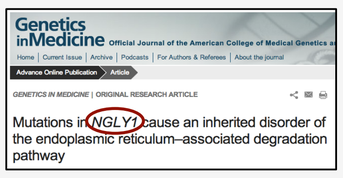


Functional Complementation

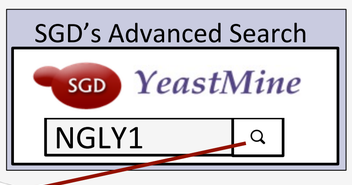
Searchable connections

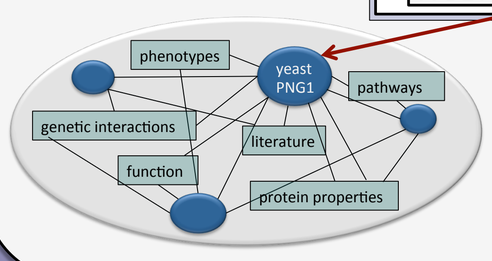


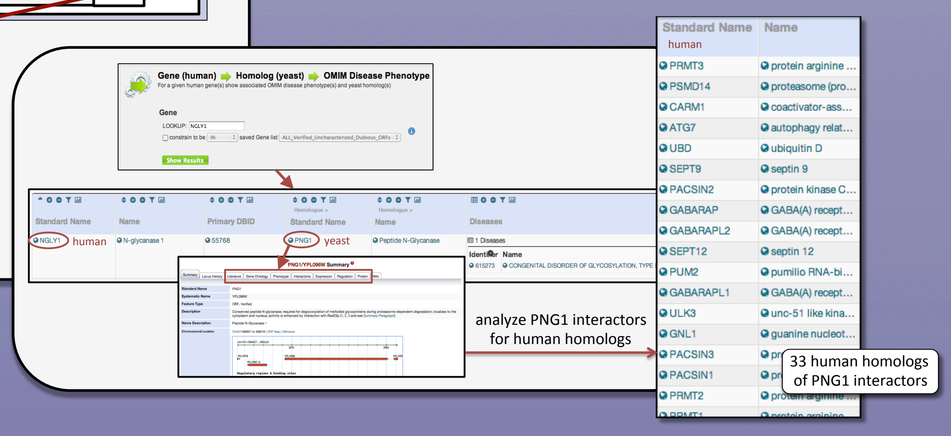
A real and present connection



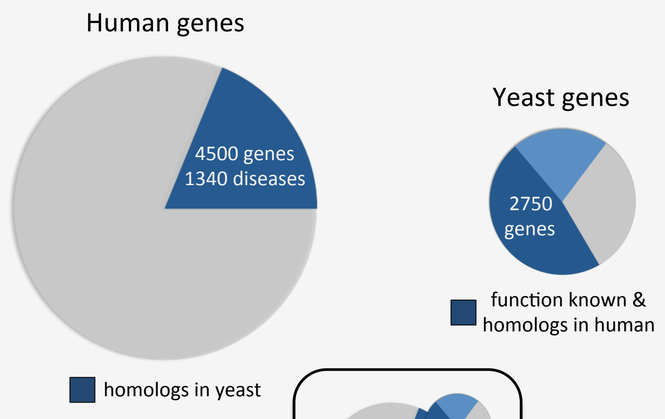
SGD's Advanced Search







Half of all yeast genes have a known function and at least one human counterpart



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