

P022 Using high-throughput data to imply gene function: assessment of selected genes for roles in meiotic and mitotic DNA processing

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The large volume of data generated in high-throughput studies of the 6200 genes of *Saccharomyces cerevisiae* provides a valuable resource. An *in-silico* screen, mining existing data-sets including interaction, expression, localisation and phenotype data was developed with the aim of selecting partially uncharacterised genes involved in DNA processing

Our selection procedure yielded 57 genes for which deletion mutants were constructed and analysed for phenotypic abnormalities. During vegetative growth 12 of these mutants showed hypersensitivity to hydroxyurea, four to methyl methanesulfonate and four to ionizing radiation. During meiosis three mutants were identified with reduced gene conversion and one with increased levels of chromosomal nondisjunction, while six mutants showed very low levels of nuclear divisions. Of those six, five showed a significant delay in initiation and progression of pre-meiotic DNA replication, while one did not initiate. Among these five, one displayed inefficient synapsis between homologs. Finally, a mutant was identified to produce up to eight inviable spores per ascus.

We identified 16 genes with properties in DNA processing from 57 selected using high-throughput data (28%). This represents an example of how existing data sets may be used to define gene sets, enriched for roles in specified biological processes.