Genomic profiling of drug sensitivities via induced haploinsufficiency

Guri Giaever[1], Daniel D. Shoemaker[2], Ted W. Jones[3], Hong Liang[1], Elizabeth A. Winzeler[1], Anna Astromoff[1] & Ronald W. Davis[1,3]

Lowering the dosage of a single gene from two copies to one copy in diploid yeast results in a heterozygote that is sensitized to any drug that acts on the product of this gene. This haploinsufficient phenotype thereby identifies the gene product of the heterozygous locus as the likely drug target. We exploited this finding in a genomic approach to drug-target identification. Genome sequence information was used to generate molecularly tagged heterozygous yeast strains that were pooled, grown competitively in drug and analysed for drug sensitivity using high-density oligonucleotide arrays. Individual heterozygous strain analysis verified six known drug targets. Parallel analysis identified the known target and two hypersensitive loci in a mixed culture of 233 strains in the presence of the drug tunicamycin. Our discovery that both drug target and hypersensitive loci exhibit drug-induced haploinsufficiency may have important consequences in pharmacogenomics and variable drug toxicity observed in human populations.

Introduction

It is often assumed that one copy of a gene is adequate for the normal function of diploid organisms in all but a few cases. This assumption is based primarily on the fact that haploinsufficiency, in which loss of function of one gene copy leads to an abnormal phenotype, is rarely observed. In humans, for example, only a handful of genes have been identified as haploinsufficient[1]. These were identified because they resulted in developmental abnormalities or other severe disease. In a genome-wide analysis of *Drosophila melanogaster*, 56 haploinsufficient loci (approximately 0.4% of the *Drosophila* coding capacity) exhibited lethality or abnormality[2]. These examples demonstrate that, regardless of their frequency, haploinsufficient loci define a set of genes whose dosage and function are critical to the organism. In this study, we designed experiments to allow identification of haploinsufficient genes in yeast in a whole-genome manner. In addition to the identification of haploinsufficient genes under optimal growth conditions, we identified a class of genes that are haploinsufficient only under stressed conditions. This study focuses on the haploinsufficiency induced in the presence of a drug that targets the gene product of the heterozygous locus. In these experiments, the primary effect of drug is to decrease further gene function in heterozygous strains by inhibiting the remaining gene product, effectively widening the phenotypic window for identification of haploinsufficient genes.

The yeast *Saccharomyces cerevisiae* is a model organism for the study of haploinsufficiency due to its ease of genetic manipulation and the availability of genome sequence information, which allows for the systematic construction of heterozygous deletion strains in any essential or nonessential gene. Although comprehensive genome-wide surveys of gene dosage in yeast have not been performed, evidence that gene dosage can alter drug sensitivity has been demonstrated. Specifically, increased gene dosage (on the order of ten copies per cell) of a drug target has been shown to increase resistance of a yeast strain to the corresponding drug[3,4]. Here, the converse is demonstrated: decreased gene dosage of a drug target from two copies to one copy in heterozygous strains results in increased sensitivity, or drug-induced haploinsufficiency. Although the idea of increasing or decreasing copy number is not new, the study of heterozygous yeast strains with decreased copy number of a single gene has been largely unexplored due to the lack of discernable phenotypes in most heterozygous strains. We first performed a feasibility study to confirm increased sensitivity in individual strains, and then used this phenotype to screen heterozygous strains in parallel for drug sensitivity. The success of the parallel approach using 233 strains encourages efforts to scale to a genome-wide level.

Results

Individual heterozygous deletion strains exhibit drug-induced haploinsufficiencies

We constructed a set of heterozygous yeast strains carrying deletions in genes encoding known drug targets. The genes used in this study, which encode essential proteins involved in diverse cellular processes, include: *HIS3*, required for histidine biosynthesis; *ALG7*, required for glycosylation; *RNR2*, required for deoxyribonucleotide biosynthesis; *TUB1* and *TUB2*, encoding tubulin subunits essential for cell division; and *ERG11*, crucial for ergosterol biosynthesis (Table 1). Each heterozygous strain was grown in the presence of sublethal concentrations of the drug that directly targets the protein encoded by the heterozygous locus. The growth rate of each heterozygote with respect to wild type provides a measure of the relative fitness, or sensitivity, of a strain in the presence of a drug. In these experiments, haploinsufficiency is manifested as a reduced fitness of a heterozygous strain compared with the wild-type strain under the same conditions.

[1]*Department of Biochemistry, Stanford University School of Medicine, Stanford, California 94305-5307, USA.* [2]*Rosetta Inpharmatics, 12040 115th Ave NE, Kirkland, Washington 98034, USA.* [3]*Stanford DNA Sequencing and Technology Center, 855 California Ave, Palo Alto, California 94394, USA. Correspondence should be addressed to G.G. (e-mail: ggiaever@cmgm.stanford.edu).*

Table 1 • Genes encoding known drug targets used in individual strain analysis

Gene	Protein; protein function	Inhibited by	Haplo-insufficiency*
HIS3	imidazoleglycerol-phosphate dehydratase; required for histidine biosynthesis	3-amino-triazole[21]	100 mM
ALG7	Asn-linked glycosyl transferase; required for Asn-linked glycosylation	tunicamycin[9]	0.6 μM
RNR2	small subunit of ribonucleotide reductase; required for nucleotide biosynthesis	hydroxyurea[22]	50 mM
TUB1	α-tubulin structural protein; essential component of mitotic apparatus	benomyl[7]	85 μM
TUB2	β-tubulin structural protein; essential component of mitotic apparatus	benomyl[7]	85 μM
ERG11	cytochrome P450 lanosterol 14a-demethylase; required for biosynthesis of ergosterol	fluconazole[23]	40 μM

*Haploinsufficiency: concentration of drug where $O.D._{600}$ wild type/$O.D._{600}$ heterozygote was greatest. Gene information obtained from the Saccharomyces Genome Database (http://genome-www.stanford.edu/Saccharomyces).

As increased gene dosage of *ALG7* is known to confer increased resistance to tunicamycin[5,6], we predicted that the decreased gene dosage in the *alg7/ALG7* heterozygous strain would confer increased sensitivity to tunicamycin. In the absence of tunicamycin, both *alg7/ALG7* and wild-type strains grew equally well, with a generation time of approximately 2 hours (Fig. 1*a*), whereas high concentrations of tunicamycin (2 μg/ml) prevented growth of both strains (Fig. 1*c*). At intermediate drug concentrations (0.5 μg/ml), however, we saw a difference in growth rate between the *alg7/ALG7* strain and wild type (Fig. 1*b*), demonstrating that the *alg7/ALG7* strain was more sensitive to tunicamycin than wild type.

We also tested the effects of the microtubule-depolymerizing agent benomyl on a *tub1/TUB1* heterozygote strain. In the absence of benomyl, the *tub1/TUB1* strain grew slower than the wild-type strain (Fig. 2*a*), as previously reported[7]. Hence, the level of Tub1p in the heterozygote is not sufficient for wild-type growth, and this strain is haploinsufficient for growth in the absence of benomyl. This inherent haploinsufficiency does not affect our analysis, however, as at intermediate concentrations of drug (in this example 25 μg/ml benomyl) growth of wild type is minimally affected, whereas growth of the *tub1/TUB1* strain is inhibited (Fig. 2*b*).

We carried out similar growth rate analyses for several other heterozygous strains using known inhibitors (Table 1). Each experiment was tested using at least two individual transformants, which all showed induced haploinsufficiency in response to the appropriate drug. Furthermore, when the *his3/HIS3* heterozygote strain was transformed with a single copy of plasmid-borne *HIS3*, it became more resistant to the inhibitor 3-amino-triazole, confirming that the affected locus is responsible for the observed phenotype (data not shown). These results demonstrate that increasing or decreasing gene dosage by a single gene copy results in detectable phenotypes.

Parallel identification of drug targets

The results from the individual strain study suggest that if a heterozygous strain exhibits increased sensitivity to a drug, then the heterozygous gene may encode the drug target. We incorporated this prediction into a parallel screen for the identification of drug-sensitive strains. Mixed cultures of heterozygous deletion strains were grown in the presence of drug. Strains that grew more slowly with respect to wild type represented those most sensitive to drug and indicated the possible identification of a drug target. We tested the feasibility of this parallel approach using strains tagged with 'molecular bar codes' that allow quantitative measurement of individual fitness when strains are grown competitively[8].

We analysed a pool of 12 heterozygous strains in the presence of the drug tunicamycin, a well-characterized glycosylation inhibitor[9]. Each strain was uniquely tagged using a 20-base oligonucleotide bar code, as previously described[8] (Fig. 3). Equal numbers of cells from each of 12 heterozygous strains were pooled and grown in rich medium in the presence or absence of 0.5 μg/ml tunicamycin (the concentration at which there was the greatest fitness differential between the individual *alg7/ALG7* strain and wild type). Aliquots of cells were taken from the pool over time and genomic DNA was isolated and used as template for PCR amplification of the oligonucleotide tags by two common primers, one incorporating a 5′ fluorescent label in the process. Subsequent hybridization of the DNA tags to a oligonucleotide array, followed by laser scanning, allowed quantitative analysis of the relative abundance of each strain in the pool. Each position on the oligonucleotide array contains a complementary oligonucleotide corresponding to a unique heterozygote strain, and the fluorescence intensity at this position reflects the relative abundance of each individual heterozygous strain.

At time zero in the 12-strain experiment, each strain was present in equal amounts and the fluorescent signals on the oligonucleotide array were of approximately equal intensity (Fig. 4). In

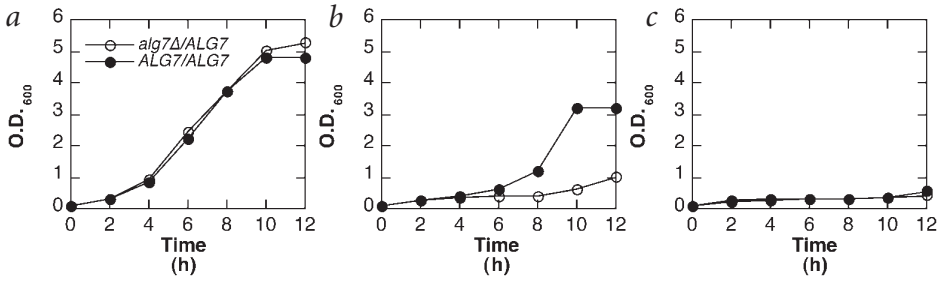

Fig. 1 Tunicamycin sensitivity of *alg7/ALG7*. Growth of *alg7/ALG7* and *ALG7/ALG7* wild-type strains ($O.D._{600}$) as a function of time. ***a***, 0 μg/ml tunicamycin; ***b***, 0.5 μg/ml tunicamycin; ***c***, 2.0 μg/ml tunicamycin. Drug-induced haploinsufficiency is seen in (*b*), where an intermediate concentration of 0.5 μg/ml tunicamycin reveals a difference in drug response between the two strains.

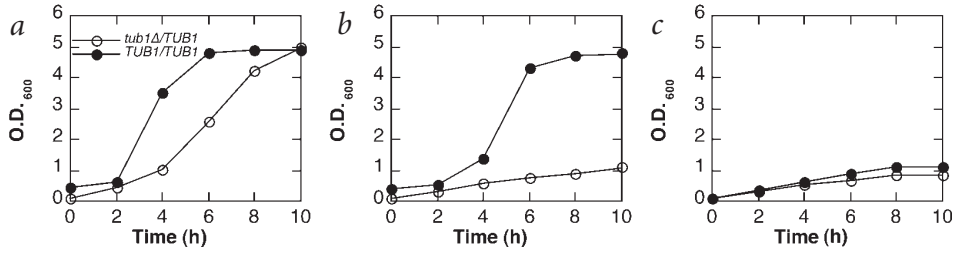

Fig. 2 Benomyl sensitivity of *tub1/TUB1*. Growth of *tub1/TUB1* and *TUB1/TUB1* wild-type strains ($O.D._{600}$) as a function of time (h). ***a***, 0 μg/ml benomyl; ***b***, 25 μg/ml benomyl; ***c***, 50 μg/ml benomyl. Drug-induced haploinsufficiency is seen in (*b*), where at an intermediate concentration of benomyl growth of wild type is minimally affected, whereas the *tub1/TUB1* strain is inhibited.

the 0.5-μg/ml tunicamycin culture, the hybridization signal on the oligonucleotide array representing the *alg7/ALG7* strain was diminished at 22 hours, and undetectable by 48 hours. All other strains in the pool remained at equal intensity (and therefore equal abundance) over the course of the experiment, indicating that they were relatively unaffected by the drug. These results demonstrated that a known drug target could be identified in a pool of 12 heterozygous strains.

The 12-strain study was expanded using a set of 233 unique heterozygous yeast strains constructed by a consortium of laboratories (E.A.W. *et al.*, manuscript in preparation; http://sequence-www.stanford.edu/group/yeast_deletion_project/deletions3.html) and was performed in the same manner as the 12-strain pool experiment. The analysed data from this study are shown (Fig. 5). Each bar in the graph reflects the sensitivity of a heterozygous strain grown with and without 0.5 μg/ml tunicamycin. The greater the negative value of the bar, the greater the rate the strain is diminishing from the pool. The greater the positive value of the bar, the greater the rate the strain is increasing in the pool. The unlabelled positive and negative bars (Fig. 5) define the background fluctuation in a given experiment due to natural variation of growth rates combined with experimental noise. In the absence of drug (Fig. 5, top), one strain (*ymr242c/YMR242C*) showed a significantly reduced growth rate and was thereby identified as haploinsufficient. *YMR242C* codes for a protein that has been classified by sequence as a cytoplasmic ribosomal protein[10]. In the presence of 0.5 μg/ml tunicamycin (Fig. 5, bottom), 3 of 233 strains were significantly diminished in relative abundance in the pool during the time period tested, therefore identifying these strains as drug-induced haploinsufficient. These three strains were *alg7/ALG7*, *ymr007w/YMR007w* (both of which diminished in the pool at a rate approximately five times that of any other strain) and *ymr266w/YMR266w* (which diminished in the pool at an intermediate rate).

To further characterize the newly identified *YMR007w* and *YMR266w* genes, we studied individual growth of the heterozygous and homozygous strains. The heterozygous strains showed drug-induced haploinsufficiency at growth rates consistent with their behaviour in the pool (data not shown). Both the *ymr007w/ymr007w* and the *ymr266w/ymr266w* homozygous strains exhibited increased sensitivity to tunicamycin, with the *ymr007w/ymr007w* strain being the more sensitive of the two. Neither strain exhibited increased sensitivity to the unrelated drugs hygromycin B and fluconazole. A conventional halo assay revealed extreme sensitivity to tunicamycin for *ymr007w/YMR007W*, but relatively little increased sensitivity for the *alg7/ALG7* and *ymr266w/YMR266W* strains (Fig. 6). The discrepancy between the relative sensitivities of the strains in liquid culture versus growth on plates probably reflects the increased sensitivity of the direct competitive growth in combination with the differences in the physiological state of the cells. It should be noted that the amount of drug used for the plate assay was 40 times that used for the liquid culture assay.

Discussion

We tested six heterozygous strains carrying deletions in known drug targets for induced haploinsufficiency, all of which revealed induced haploinsufficiency in the presence of a drug that targets the gene product of the heterozygous locus. In each case, the result was highly specific, as we saw no haploinsufficiency when these strains were tested with other drugs. These strains define a class of genes that exhibit induced haploinsufficiency in the presence of a drug. Induced haploinsufficiency may also be revealed under other general stress conditions, as well as in conditions that specifically stress a particular gene product. This suggests that a variety of environmental perturbations, when combined with genetic lesions, will reveal previously undetected haploinsufficiencies.

Drug-sensitivity profiling of 233 heterozygous strains in the presence of tunicamycin identified three drug-sensitive loci: (i) the *ALG7* locus, encoding the known target of tunicamycin; (ii) *YMR007W*, encoding a 126-aa protein of unknown function; and (iii) *YMR266W*, encoding a 953-aa protein with homology to the multi-facilitator superfamily[11] (MFS). Because both the *ymr007w/ymr007w* and *ymr266w/ymr266w* strains were also

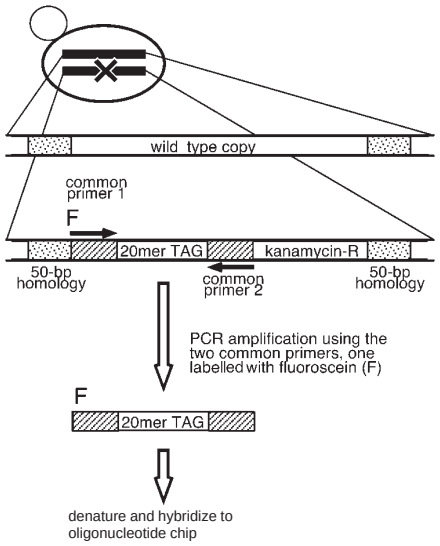

Fig. 3 Heterozygote deletion construct. The gene transplacement cassettes used for precise deletion of each yeast ORF were designed such that they contain unique 20-base bar codes. This oligonucleotide serves as the gene-specific (and therefore strain-specific) hybridization tag. The tag is flanked by two common priming sites, allowing PCR amplification of any unique tag and incorporating a 5′-fluoroscein label in the process. The disruption cassettes contain a kanamycin gene to allow for selection of yeast transformants by G418 resistance and two 50-bp sequence at both ends homologous to upstream and downstream sequences that flank the ORF of the target gene, allowing for site-specific mitotic recombination[20]. DNA was extracted and all tags were amplified in a single PCR reaction using common primers. These PCR products were then hybridized to an oligonucleotide array carrying the complement of each tag to determine the relative abundance of each strain in the pool (Fig. 4).

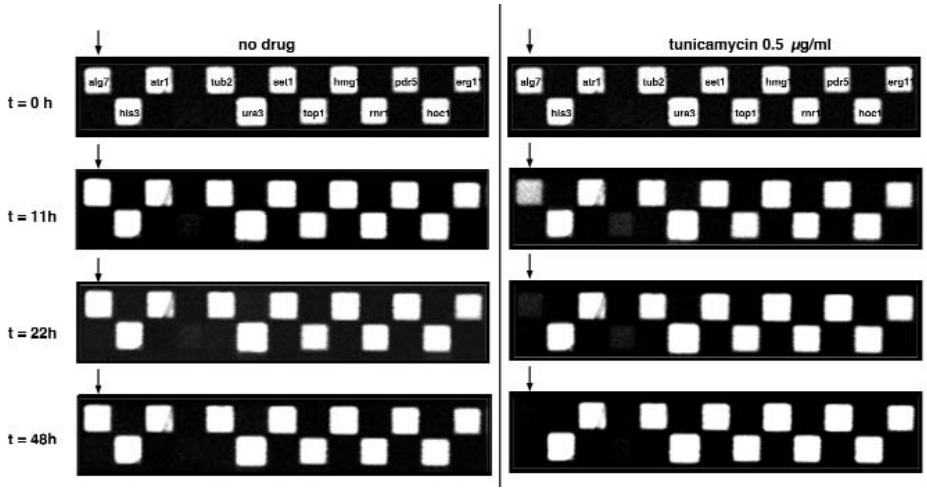

Fig. 4 Growth of 12 heterozygous strains in 0.5 μg/ml tunicamycin validates Alg7p as the drug target in a pool of 12 strains. At t=0, each strain was in equal abundance and was therefore represented as equal signal intensities on the oligonucleotide array. At t=11 h the signal intensity representing the *alg7/ALG7* strain in the tunicamycin pool (arrow) began to decrease. After 48 h of drug exposure, the strain was undetectable. A control tagged wild-type *ho/ho* strain (data not shown) remained at an abundance equal to that of the 11 unaffected heterozygotes throughout the experiment[21].

drug-sensitive, these loci were ruled out as possible drug targets because the proteins they encode are absent in these homozygotes. As *YMR266W* shares homology with genes encoding the MFS family, it may encode a permease or another protein involved in net drug export. Further genetic analysis will allow discrimination of genes conferring sensitivity into categories that are either directly connected to the drug target(s), or involved in drug availability. Those genes directly connected to the drug target will aid in elucidation of the drug target pathway. The unambiguous identification of the known drug target in these experiments encourages future efforts to scale to a genomic level, which would permit screening against all 6,000+ potential drug targets simultaneously.

In addition to identifying drug-sensitive loci, all strains that are haploinsufficient in the absence of drug will be identified. We identified one such strain in the 233-strain pool experiment. This strain carries a deletion in *YMR242C*, which has been classified by sequence homology as a gene that codes for a cytoplasmic ribosomal protein. In the presence of tunicamycin, this strain did not exhibit a slow-growth phenotype. Because the average generation time for most of the strains in the presence of tunicamycin was approximately two times greater than in the absence of drug, the decreased Ymr242cp protein level may no longer be inhibitory for growth under these conditions. In general, strains haploinsufficient in the absence of drug identify gene products (including those that may be essential under defined growth conditions) that may be good candidates for drug targets, because in these strains small changes in protein levels result in a substantial decrease in fitness.

Currently, drug discovery is largely driven by combinatorial chemistry followed by high throughput *in vitro* screening of compounds against a preselected target. This method, though effective, requires that molecular targets be chosen *a priori*. An advantage of our approach to drug-target identification is that no prior knowledge of the target is required, and only those targets that affect the fitness of the organism will be identified. Furthermore, because this is an *in vivo* assay, only drugs that enter the cell and are not significantly metabolized are identified. Finally, novel anti-fungal targets, as well as those targets in critical common pathways that yeast share with higher eukaryotic cells, will be revealed.

This approach will likely identify all targets of any particular drug, toxin, or complex mixture (such as a natural product extract) that result in haploinsufficiency, as all potential targets are individually evaluated for increased sensitivity. This is an advantage over a complementary *in vivo* approach

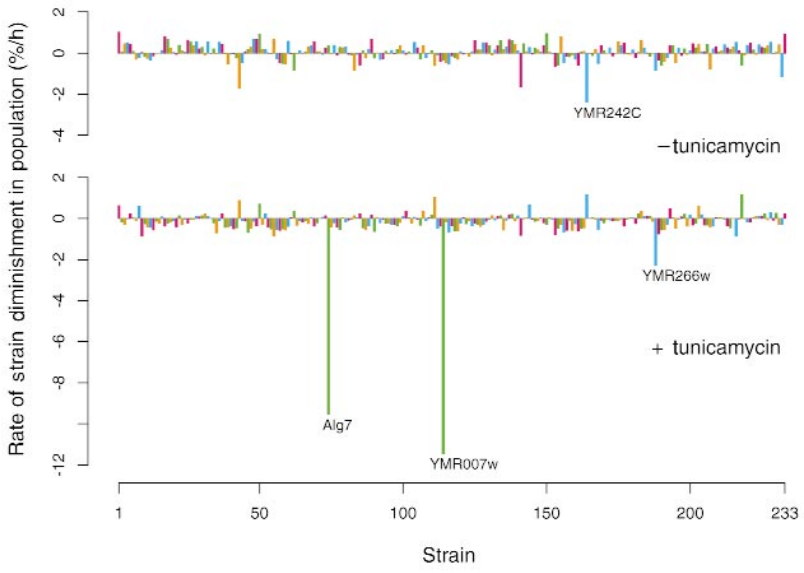

Fig. 5 Tunicamycin sensitivity profiling for 233 heterozygous yeast strains. Estimated differences from overall pool growth rates in the absence (top) and presence (bottom) of tunicamycin are shown. Positive differences indicate estimated growth faster than the overall pool rate; negative differences indicate slower growth. Rates of strain diminishment in the pool were computed as the slope in the regression analysis. Strains identified as possibly haploinsufficient in the statistical analysis were tested separately. In the absence of tunicamycin, strain *ymr242c/YMR242C* was confirmed deficient. In the presence of tunicamycin, strains *ymr007w/YMR007W*, *alg7/ALG7* and *ymr266w/YMR266W* were confirmed deficient. These results identified the Alg7p protein as the known target and the uncharacterized proteins encoded by *YMR266W* and *YMR007W* as hypersensitive to tunicamycin.

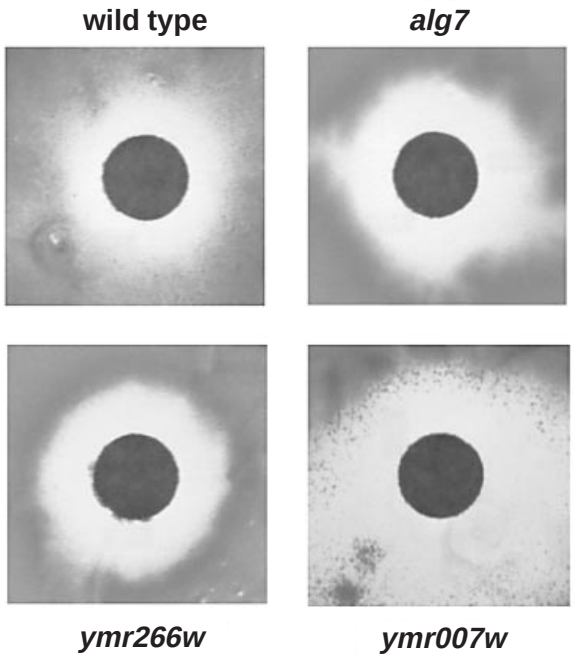

Fig. 6 Halo assays of tunicamycin-sensitive strains. An overnight culture (200 µl) was spread onto YPD plates. Tunicamycin (10 mg/ml) was spotted onto filter paper (~1/4" in diameter) that was placed on a lawn of the four heterozygous strains indicated. Plates were incubated at 30 °C for 3 d.

whereby targets are identified by their ability to confer resistance to a strain when present at high copy[3,4]. In this technique, a more sensitive target present at wild-type levels may mask any resistance conferred by overexpression of an additional target. The less-sensitive target in this case would therefore escape detection.

This approach may also be applied to other organisms. It is not necessary to specifically delete a gene and replace it with a molecular bar code as described in these experiments. It should be possible, in principle, to introduce molecularly bar-coded transposons that would randomly mutagenize genes by insertion throughout the genome, although it is difficult to obtain strains with only single hits following transposition. Location of the insertion may then be accomplished using transposon-specific primers[12,13]. Experimentally, there is also no requirement that the DNA tag used to identify the strain be linked to the mutation.

The identification of heterozygous loci responsible for dominant autosomal disorders is increasing rapidly, suggesting that haploinsufficiency is a more prevalent contributor to disease than previously assumed[14,15]. For example, heterozygosity of a regulatory gene may produce an array of phenotypes, the characteristics of which might indicate the underlying pathway[16]. In addition, natural heterozygotes existing in human populations may exhibit induced haploinsufficiency due to environmental changes or conditions. This would result in counterintuitive inheritancy patterns because a null or low-functioning gene would segregate as a recessive allele for gene function but as a dominant allele for haploinsufficiency under stressed conditions. Furthermore, a common 'toxin' in the environment, or even a natural product in a food supply, may induce haploinsufficiences. The induced haploinsufficiencies described here may help elucidate mechanisms underlying heterozygous disease phenotypes[17,18] as well as observed variable drug toxicities in human populations.

Methods

Reagents. Unless otherwise specified, all reagents were from Sigma. Fluconazole was the gift of J. DeRisi.

Yeast strains. The yeast strain S288c, a wild-type isolate, was used as the parent for mutant construction in the individual growth study as well as in the 12-strain pool experiment. A derivative of S288c, BY4743, was used as the parent in the 233-strain pool experiment (http://sequence-www.stanford.edu/group/yeast_deletion_project/deletions3.html). Culture media and conditions were as described[8].

Individual growth rate analysis. Growth rates of heterozygous deletion strains were measured and compared with the growth rate of wild type at varying drug concentrations. Cells were diluted from an overnight culture to an $O.D._{600}$ of ~0.01 (~$2.2 10^5$ cells/ml) and allowed to grow until the $O.D._{600}$ reached ~0.05 (~10^6 cells/ml; t=0), ensuring that the cells were in logarithmic phase. Drug was then added and growth rate was measured as the optical density of cells ($O.D._{600}$) as a function of time (h) in rich medium[19] (YPD).

Pooled growth studies. Equal numbers of cells (~5×10^5) of each heterozygote strain were pooled and grown in a culture (100 ml) in the presence and absence of drug (starting $O.D._{600}$~0.05). The doubling time in the absence of tunicamycin was ~1.5 h, and in the presence of tunicamycin ~3.0 h. Aliquots of ~2.2×10^7 (~1 $O.D._{600}$) of cells were sampled over time. When the pooled culture reached ~3×10^9 cells (or an $O.D._{600}$ of ~1.3 in 100 ml) the cultures were diluted back to 0.05 $O.D._{600}$ (representing ~5×10^5 cells of each strain) as needed to maintain logarithmic growth. Because the time course of these experiments is within 15 generations of the pooled culture, the possibility of second-site supressor mutations overtaking the culture is minimal. Both the 12-strain pool and the 233-strain pool were performed twice, each time yielding similar results. In addition, any strain appearing deficient in these experiments was verified by growth in individual cultures.

Construction of heterozygous deletion strains. Construction of strains used in the 12-strain pool was as described[8]. An explanation of the construction of deletion strains used in the 233-strain study is available (http://sequence-www.stanford.edu/group/yeast_deletion_project/deletions3.html). A note of caution regarding strain genotypes: it is possible, although rare, that some small fraction of these deletion strains carry second-site mutations resulting from transformation.

Hybridization. Analysis was as described[8].

Data analysis. Analysis of oligonucleotide array fluorescent signal data consisted of two steps: (i) normalization of data to achieve equality of background and maximal signals on each array; and (ii) analysis of the decrease (or increase) of signal intensity for each tag sequence over time. Equalization of signal strength relied on a consensus score based on the fact that for most oligonucleotide array sites, the signal strength did not vary between time points. The slope of a linear regression of the log of the above-background signals from each individual molecular bar code as a function of time identified strains that were either increasing or decreasing in abundance over time.

Acknowledgements

We thank Affymetrix for their help with all aspects of the oligonucleotide array technology used here. Specifically, M. Mittmann and D. Morris for oligonucleotide selection and chip design; E. Gentalen for array synthesis; and D. Lockhart for helpful discussions. We thank C. Nislow and I. Herskowitz for critical reading and helpful comments on the manuscript and all members of the S. cerevisiae Deletion Consortium for their efforts. Supported by a grant from Rhone-Poulenc Rorer and NIH grant H600198.

Received 1 December 1998; accepted 2 February 1999.

1. Fisher, E. & Scambler, P. Human haploinsufficiency—one for sorrow, two for joy. *Nature Genet.* **7**, 5–7 (1994).
2. Lindsley, D.L. *et al.* Segmental aneuploidy and the genetic gross structure of the *Drosophila* genome. *Genetics* **71**, 157–184 (1972).
3. Rine, J. Gene overexpression in studies of *Saccharomyces cerevisiae*. *Methods Enzymol*. **194**, 239–251 (1991).
4. Launhardt, H., Hinnen, A. & Munder, T. Drug-induced phenotypes provide a tool for the functional analysis of yeast genes. *Yeast* **14**, 935–942 (1998).
5. Rine, J., Hansen, W., Hardeman, E. & Davis, R.W. Targeted selection of recombinant clones through gene dosage effects. *Proc. Natl Acad. Sci. USA* **80**, 6750–6754 (1983).
6. Barnes, G., Hansen, W.J., Holcomb, C.L. & Rine, J. Asparagine-linked glycosylation in *Saccharomyces cerevisiae*: genetic analysis of an early step. *Mol. Cell. Biol.* **4**, 2381–2388 (1984).
7. Stearns, T., Hoyt, M.A. & Botstein, D. Yeast mutants sensitive to antimicrotubule drugs define three genes that affect microtubule function. *Genetics* **124**, 251–262 (1990).
8. Shoemaker, D.D., Lashkari, D.A., Morris, D., Mittmann, M. & Davis, R.W. Quantitative phenotypic analysis of yeast deletion mutants using a highly parallel molecular bar-coding strategy. *Nature Genet.* **14**, 450–456 (1996).
9. Kuo, S.C. & Lampen, J.O. Tunicamycin—an inhibitor of yeast glycoprotein synthesis. *Biochem. Biophys. Res. Commun.* **58**, 287–295 (1974).
10. Planta, R.J. & Mager, W.H. The list of cytoplasmic ribosomal proteins of *Saccharomyces cerevisiae*. *Yeast* **14**, 471–477 (1998).
11. Nelissen, B., De Wachter, R. & Goffeau, A. Classification of all putative permeases and other membrane plurispanners of the major facilitator superfamily encoded by the complete genome of *Saccharomyces cerevisiae*. *FEMS Microbiol. Rev.* **21**, 113–134 (1997).
12. Burns, N. *et al.* Large-scale analysis of gene expression, protein localization, and gene disruption in *Saccharomyces cerevisiae*. *Genes Dev.* **8**, 1087–1105 (1994).
13. Smith V., Chou K.N., Lashkari D., Botstein D. & Brown P.O. Functional analysis of the genes of yeast chromosome V by genetic footprinting. *Science* **274**, 2069–2074 (1996).
14. Zinn, A.R. & Ross, J.L. Turner syndrome and haploinsufficiency. *Curr. Opin. Genet. Dev.* **8**, 322–327 (1998).
15. Chen, H. *et al.* Limb and kidney defects in *Lmx1b* mutant mice suggest an involvement of *LMX1B* in human nail patella syndrome. *Nature Genet.* **19**, 51–55 (1998).
16. Karim, F.D. *et al.* A screen for genes that function downstream of Ras1 during *Drosophilia* eye development. *Genetics* **143**, 315–329 (1996).
17. Vogel, F. & Motulsky, A.G. *Human Genetics* 267–299 (Springer-Verlag, Berlin, 1997).
18. Perera, F.P. Environment and cancer: who are susceptible? *Science* **278**, 1068–1073 (1997).
19. Rose, M., Winston, F. & Hieter, P. *Methods in Yeast Genetics: A Laboratory Manual* (Cold Spring Harbor University Press, Cold Spring Harbor, New York, 1990).
20. Wach, A. PCR-synthesis of marker cassettes with long flanking homology regions for gene disruptions in *S. cerevisiae. Yeast* **12**, 259–265 (1996).
21. Baganz, F., Hayes, A., Marren, D., Garner, D.C. & Oliver, S.G. Suitability of replacement markers for functional analysis studies in *Saccharomyces cerevisiae*. *Yeast* **13**, 1563–1573 (1997).
22. Durfee, T. *et al*. The retinoblastoma protein associates with the protein phosphatase type 1 catalytic subunit. *Genes Dev*. **7**, 555–569 (1993).
23. Rittberg, D.A. & Wright, J.A. Relationships between sensitivity to hydroxyurea and 4-methyl-5-amino-1-formylisoquinoline thiosemicarbazone (MAIO) and ribonucleotide reductase *RNR2* mRNA levels in strains of *Saccharomyces cerevisiae*. *Biochem. Cell Biol*. **67**, 352–357 (1989).
24. Turi, T.G. & Loper, J.C. Multiple regulatory elements control expression of the gene encoding the *Saccharomyces cerevisiae* cytochrome P450, lanosterol 14 -demethylase (*ERG11*). *J. Biol. Chem*. **267**, 2046–2056 (1992).