

## Abstract

Aneuploidy is the phenomenon in which an organism contains a number of chromosomes that is not a multiple of the haploid state. Some populations show tolerance for aneuploidy, including wild yeast isolates. Recently there has been much debate as to how these populations maintain aneuploidy. Some hypothesize that there is an innate mechanism of dosage compensation in yeast, while others rebut this argument. In order to determine the rate and effects of aneuploidy in yeast, we analyzed whole transcriptomes from 46 euploid and aneuploid *Saccharomyces cerevisiae* samples. These samples were obtained from two mutation accumulation (MA) experiments: samples from one MA experiment were derived from a highly heterozygous ancestor; the others from a MA experiment with a highly homozygous ancestor. We determined the rate of aneuploidy to be  $1.82 \times 10^{-4}$  events per genome per generation in the heterozygous strain, and  $1.04 \times 10^{-4}$  events per genome per generation in the homozygous strain; suggesting that heterozygosity increases frequency of aneuploid events. Average gene expression across each entire chromosome was determined, and statistical analyses were used to determine if it was as expected with and without dosage compensation. We found no evidence for whole-chromosome dosage compensation in aneuploid yeast. We observed whether or not there was statistically significant dosage compensation on individual genes and found that the majority of genes on aneuploid chromosomes are not compensated, but a subset are partially compensated. We conclude that aneuploidy events are influenced by heterozygosity, and that there is no dosage compensation mechanism in spontaneously-aneuploid samples of *S. cerevisiae*. These findings support the hypothesis that aneuploidy tolerance is not driven by an innate dosage compensation mechanism, but more likely by a transient adaptive response.