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## Erratum

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**Genome Research 10:** 403–409 (2000)

### **Evolution and Variation of the Yeast (*Saccharomyces*) Genome**

Robert K. Mortimer

On page 406, several denotations of Tables 1 and 2 were incorrect. The corrected version is below:

#### **Genome Renewal as a Mechanism of Evolution of Wine Yeast**

Approximately 69% of wine yeast is homothallic and most is diploid (Mortimer et al. 1994; Cavalieri et al. 1998). Many such strains will also sporulate permissively, that is, they will sporulate even on a rich medium. [Table 2](#) describes the heterozygosities seen in 239 strains, of which two-thirds are heterozygous. The traits in wine yeast that are in a heterozygous state cover the spectrum of traits seen in the laboratory studies of this yeast. That natural strains are heterozygous for one or more traits is evidence for mutations occurring during the life of this organism. If an *HO/HO* strain has heterozygosities and sporulates, the haploid spores from such a strain will represent all possible combinations of these heterozygosities. *HO* is a gene that causes mating type to switch (Herskowitz 1992). Because of the *HO* gene, some of the descendants of these haploid spores will change mating type, mate, and form diploids. These diploids will be completely homozygous and will compete with each other and with the original diploid. For  $n$  heterozygosities, there will be  $2n$  new individuals. It is our view that the 35% mostly homozygous diploids presented in [Table 1](#) arose by the process of genome renewal from formerly heterozygous diploids.

Most of these homozygous diploids described in [Table 1](#) are in genotypic classes a and b.