

A chromosomal gene sequence of a species evolves over time as paracentric chromosomal inversion sequences are formed via mutations in individuals and either replace the existing gene sequence in the species or disappear. There have been 102 identified chromosomal inversions in the yeast genus *Lachancea* that entered the genus and survived over the last 100 million years. These inversions help define the differences in ten *Lachancea* species. We present a neutral model of chromosome inversions that fits the observed size distribution of inversions in *Lachancea*. The model relates the inversion record, inversion rate, and population size within a thermodynamic picture.