

A whole genome comparison between lager brewing yeast Weihenstephan 34/70 and its ancestral strains

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Lager brewing yeast (*Saccharomyces pastorianus*) is a natural hybrid of the *S. cerevisiae* and *S. eubayanus*-like strains¹⁾. Reanalysis of its genome sequence using next generation sequencing technology (Illumina) has revealed that the lager brewing yeast genome has a complicated structure, with an uneven distribution of single nucleotide variations (SNVs) in the homologous chromosomes, especially in the *S. cerevisiae*-type chromosomes. In order to understand the origin of its complicated genome structure and uneven distribution of SNVs, we sequenced 2 strains (ale brewing yeast *S. cerevisiae* and *S. eubayanus* CBS12357²⁾) that the *S. pastorianus* may have originated from. First, we assembled each genome and identified SNVs in homologous chromosomes in each strain independently. Then we compared these with Weihenstephan 34/70 and succeeded in distinguishing the event following the natural hybridization of two strains. This analysis will provide better understanding of genome structure variation in the hybrid species and will be a typical model case.

1) Nakao Y et. al. (2009) DNA Res. 16(2):115-29

2) Libkind D et. al. (2011) Proc Natl Acad Sci U S A. 108(35):14539-44