

Whole genome analysis of a lager brewing yeast Weihenstephan 34/70 using next generation sequencing technology

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Lager brewing yeast (*Saccharomyces pastorianus*) is a natural hybrid between *S. cerevisiae* and *S. eubayanus*-like strains¹). Whole genome sequence of lager brewing yeast has been analyzed²), but is still unclear because of its complicated structure.

In order to obtain more precise information about this hybrid nature, we reanalyzed the genome sequence of a lager brewing yeast Weihenstephan 34/70 along with its spore clones, using next generation sequencing technology (Illumina).

As the result, single nucleotide variations (SNVs) between homologous chromosomes within the strain were found more frequently between *S. cerevisiae*-type chromosomes than between the *S. eubayanus*-type ones. Furthermore, the SNVs were concentrated in the proximity of centromere.

The elaborated genome sequences are compared to other industrial yeast genomes and the origin of lager brewing yeast will be discussed.

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

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