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

Miki Okuno¹, Yukiko Kodama², Takehiko Itoh¹

¹Tokyo Institute of Technology, ²Suntory Global Innovation Center Limited

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. eubayasnus 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