ABSTRACT

Wine is produced by fermenting crushed fruits using various types of yeast. Up to present, several studies on yeast have been carried out through biochemical analysis. Recently however, various molecular biological techniques are being preferred. The purpose of this project was to study about microbial diversity in aging wine from Wanjoroen (2006) using the application of Polymerase Chain Reaction (PCR). The four isolated yeast strains that were chosen including sample No.9 (*Saccharomycetaceae)*, sample No.30 *(Brettanomyces*), samples No.15 (unknown) and No.16 (unknown). Confirm tested for their physiological characteristics; such as the temperature affect on growth, the sugar fermentation, sporulation and WL+1% (v/v) Cycloheximide. For molecular analysis, polymerase chain reaction (PCR) was carried out after DNA was extracted from each sample and 26S rDNA region was amplified through PCR using SC primers (SC1/SC2) and NL primers (NL1/NL4). The PCR products were analyzed by 3% agarose gel electrophoresis. Data analysis using NCBI database, blasted primer with 4 specific organisms; *S. cerevisiae S288C, S. cerevisiae* NRRL Y-12632, *S. bayanus* NRRL Y 12624 and *D. Bruxellensis* for estimating the possible fragment. As result from all analysis, the combination of convectional method and PCR could confirmed sample No.9 was *Saccharomycetaceae* and sample No.30 was *Brettanomyces* sp., Moreover, could predicted sample No.15 was *Saccharomycetaceae* which some biochemical test had pointed to *S. cerevisiae, S. kluyver* and *S. paradoxus.* However, still remain one sample, sample No.16 could not be identified.