

ABSTRAK

Henry Cendana (01113180011)

ANALISIS SEQUENCE GENOM SACCHAROMYCES CEREVISIAE PRODUK KOMERSIL

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(viii + 32 halaman; 8 gambar; 2 tabel)

Pada penelitian sebelumnya isolat khamir yang berpotensi mendekolorisasi pewarna telah diidentifikasi sebagai *Saccharomyces cerevisiae* namun terdapat kemungkinan ketidakurutan dari hasil identifikasi yang disebabkan oleh panjang *sequence* yang pendek. Pada penelitian ini dilakukan verifikasi terhadap isolat *Saccharomyces cerevisiae* tersebut dengan metode *whole genome sequencing* (WGS). *Whole genome sequencing* dilakukan dengan *sequencing genome* dengan nanopore *sequencer* dan kemudian hasil *sequencing* dianalisis dengan proses *assembly*, *contigs reordering*, dan *genome comparison*. Pada proses *assembly* dihasilkan *sequence* dengan panjang 12.199.546 basa. Pada *contigs reordering*, *contigs* pada *sequence assembly* disusun ulang sesuai dengan *reference sequence* dan sebagai hasilnya diperoleh 16 kromosom dengan panjang masing-masing kromosom bervariasi sedikit jika dibandingkan dengan kromosom *reference*. Analisis *matrix genome* menunjukkan adanya persamaan sebesar 100% antara *Saccharomyces cerevisiae* GSY2239, *Saccharomyces cerevisiae* BG-1, dan *Saccharomyces cerevisiae* I-328 dengan *sequence assembly*. Analisis dengan *phylogenetic tree* menunjukkan bahwa hasil *sequence Saccharomyces cerevisiae* GSY2239, *Saccharomyces cerevisiae* BG-1, dan *Saccharomyces cerevisiae* I-328 adalah *ingroup* dengan *sequence assembly* yang berarti terdapat kedekatan antara keempat *sequence* tersebut dengan *sequence assembly*. Garis cabang pada *phylogenetic tree* menunjukkan bahwa *Saccharomyces cerevisiae* I-328 lebih dekat dengan *sequence assembly* dibandingkan ketiga *sequence* lainnya. *Saccharomyces cerevisiae* I-328 pada *matrix* terdapat kesamaan sebesar 100% dengan *sequence assembly* dan pada *phylogenetic tree* garis cabang lebih dekat dengan *sequence assembly*. Dari hasil analisis genom di atas dapat disimpulkan bahwa bahwa isolat khamir memiliki kedekatan dengan *Saccharomyces cerevisiae* I-328.

Kata kunci : *Saccharomyces cerevisiae*, *whole genome sequencing*, *sequence*,
genom.

Referensi : 41 (2008-2023)

ABSTRACT

Henry Cendana (01113180011)

GENOME SEQUENCE ANALYSIS *SACCHAROMYCES CEREVISIAE* OF COMMERCIAL PRODUCT

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In previous research, yeast isolates that have the potential to decolorize dyes have been identified as *Saccharomyces cerevisiae*, but there is a possibility of inaccuracies in the identification results caused by the short length of the sequence. In this study, verification of the *Saccharomyces cerevisiae* isolate was carried out using the whole genome sequencing (WGS) method. Whole genome sequencing was performed by genome sequencing with a nanopore sequencer and then the sequenced results were analyzed by assembly, contigs reordering, and genome comparison processes. The assembly process produces a sequence with a length of 12.199.546 bases. In contigs reordering, the contigs in the sequence assembly are rearranged according to the reference sequence and as a result 16 chromosomes are obtained with the length of each chromosome varying slightly when compared to the reference chromosome. Matrix genome analysis showed a 100% similarity between *Saccharomyces cerevisiae* GSY2239, *Saccharomyces cerevisiae* BG-1, and *Saccharomyces cerevisiae* I-328 with sequence from assembly. Analysis using a phylogenetic tree shows that the sequence results of *Saccharomyces cerevisiae* GSY2239, *Saccharomyces cerevisiae* BG-1, dan *Saccharomyces cerevisiae* I-328 are ingroup with the sequence from assembly, which means that there is a closely related between the four sequences and the sequence assembly. The branch lines on the phylogenetic tree show that *Saccharomyces cerevisiae* I-328 is closer to the sequence assembly than the other three sequences. *Saccharomyces cerevisiae* I-328 in the matrix has a 100% similarity with the sequence assembly and in the phylogenetic tree the branch lines are closer to the sequence assembly. From the results of the genome analysis above, it can be concluded that yeast isolates have a closely related with *Saccharomyces cerevisiae* I-328.

Keywords: *Saccharomyces cerevisiae*, whole genome sequencing, sequence, genome

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