

ABSTRACT

Iqvan Nur Cahyo. 24020122130076. Exploration of Whole-Genome Sequencing (WGS) to Reveal Genomic Structure and Mating-Type Proteins in *Morchella rinjaniensis*, a Novel Tropical Species from Indonesia. Supervised by Nurhayati and Rini Riffiani.

Morels (Morchella spp.) are high-value edible fungi widely recognized for their distinctive flavor and increasing market demand. Successful fruiting body formation and cultivation development are influenced by the sexual reproductive mating system, which is controlled by mating-type genes. Although homothallic and heterothallic traits have been reported in various Morchella species, the organization of mating-type (MAT) genes in M. rinjaniensis remains unknown. Therefore, this study was conducted to investigate the genomic and protein structure of the mating-type locus in M. rinjaniensis using Whole-Genome Sequencing (WGS). GenomeScope analysis indicated that the genomic characteristics were consistent with a haploid genome pattern. The assembly results showed a genome size of 58 Mb with an N50 scaffold value of 40 kb, and genome completeness based on BUSCO reached 95.3%. Further protein structure analysis showed a conserved functional domain level of MAT proteins with other species in the Morchella genus, indicating conservation of biological functions related to sexual reproduction. Overall, this study provides new information on the genomic structure of the mating-type locus in M. rinjaniensis and expands the understanding of reproductive biology and evolution. These findings may contribute to the development of breeding and cultivation strategies for tropical morel mushrooms in Indonesia.

Keywords: *Morchella rinjaniensis*; mating-type; WGS; AlphaFold3; morel