

TURBOCHARGED ODOR THAT ATTRACTS ANIMALS: STRUCTURAL ANALYSIS OF MGL PROTEINS IN *DURIO ZIBETHINUS* (DURIAN)

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Durian (*Durio zibethinus*) is a Southeast Asian tropical plant well-known for its notorious, sulfury, pungent smell. Studies have shown that ripe durian fruits from the trees can be detected by seed-dispersing animals up to a half mile away due to the strong odor. Methionine gamma lyases (MGL) are the genes that are particularly responsible for the regulation of odor compounds which are known as volatile sulfur compounds (VSC). VSCs are the chemicals which release the pungent, sulfury aroma in durian. Interestingly, the durian genome has four MGL copies unlike other plants which typically have just two MGL copies. The extra MGL copies explain the turbocharged pungent odor which relate to the high production of VSC in durian. This study analyzed the secondary and tertiary structure of MGL proteins in durian using computational modeling and comparative structural approach. Our results showed that all 4 MGL genes in durian have 89% to 93% similar amino acids sequence identity. Sequence analysis showed that one of the MGL genes, MGLb_1 (accession number XP_022773569) contained more residue substitutions compared to other MGL genes. Phylogenetic analysis demonstrated that the MGL genes in durian are evolutionary-related with high genetic diversity which separates MGLb_1 into different clades. The active sites in MGL protein sequences are highly conserved. However, the regions proximal to the active sites in MGLb_1 showed more residue substitutions than others. Our tertiary analysis suggested some possible residue substitutions in MGLb_1 that may affect the activity of MGL in the recognition and elimination of methionine which contributes to the strong odor. This study opens a platform for genetic engineering to further investigate the impacts of these residue substitutions in MGLb_1 on the function of durian MGL gene products.

Keywords: durian, *Durio zibethinus*, L-methionine gamma-lyase, Musang King, durian genome, Helicteroideae, Malvales, volatile sulfur compounds