

Isolation, subcellular localization and phylogenetic of Transaldolase genes from *Zea mays* cv sweet corn bi-color

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The Pentose Phosphate Pathway (PPP) also is known as 6-phosphogluconate pathway which occurs in the cytosol of the plant cell. There are two main arms in PPP; the oxidative and non-oxidative arms. The main functions of this pathway is to generate reducing equivalents in the form of NADPH, for reductive biosynthesis reactions within cells in the biosynthesis of fatty acids and steroid. This pathway also provide the cell with ribose-5-phosphate (R5P) for the synthesis of the nucleotides and nucleic acids. Transaldolase (TAL) is an enzyme which plays an important role in the non-oxidative portion of the pentose phosphate pathway. The actual reaction is between glyceraldehydes 3-phosphate and sedoheptulose 7-phosphate, resulting the formation of C₄ product erythrose 4-phosphate and fructose 6-phosphate. In this study, transaldolase (TAL) has been successfully isolated and identified from *Zea mays* cv Sweet corn bi-color. The objectives of the study were achieved where the specific primer designed has function effectively in isolated TAL with 773 bp of nucleotide sequences. Analysis of homology through multiple sequence alignment revealed that TAL from *Z. mays* cv Sweet corn bi-color is highly similar with the plant species compared to animal and bacteria. ClustalW analysis found that TAL from *Z. mays* hit the score of 85.0 as they are close related in terms of taxonomy level which they are from the family of Poaceae. Other plants such as *Solanum lycopersicum* and *Solanum tuberosum* are from family Solanaceae, *Dimorcarpus longan* is from family Sapindaceae whereas *Hyacinthus orientalis* is from Hyacinthus family. However, it is discovered that TAL from *Z. mays* cv Sweet corn bi-color with TAL in *Oryza sativa* subsp. *Indica* only possess score of 64.0.

Keywords: Transaldolase, pentose phosphate pathway, subcellular localisation, phylogenetic.