

Phanatchakorn Bantaothit 2011: Characterization of Gene in Drought-Tolerant Maize (*Zea mays* L.) under Drought Stress. Master of Science (Botany), Major Field: Botany, Department of Botany. Thesis Advisor: Associate Professor Niran Juntawong, Dr.nat.tech. 98 pages.

Plants have various defensive mechanisms against drought in order to reduce water use. Molecular response of plant to drought implicated in up-regulation of gene expression. Almost 2000 drought-responsive genes were identified under progressive drought stress. In this study, an expression of gene in two maize lines; KSX 4605 (drought-sensitive) and SW 2301 (drought-tolerant) was reported. Under water deficit by 15% PEG in half Hoagland solution, the 2-week-old seedling of SW 2301 is more tolerant to drought than that of KSX 4605. There is a difference in the PCR product of amplified shoot cDNA by using VP14 primers with extra one band in 729 bp in SW 2301 but not in KSX 4605.

The 792-bp-fragment was subjected to RACE-PCR for the full length identification. The 1607-bp-fragment was obtained with Open Reading Frame (ORF) from 56 to 1345bp. The sequence showed high similarity with mRNAs of an unknown protein in *Zea mays*, *Sorghum bicolor* and *Oryza sativa* var. Japonica. The protein was highly similar to the conserved domain (KU70) of Ku protein in NCBI database. In the cluster analysis, this full length sequence showed close similarity to monocot groups. This protein required further study for its expression, function and its connection to drought tolerance in the future.

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