

Pattama Srinamngoen 2014: cDNA-AFLP of Flowering Stage in Sugarcane and Colinearity with Sorghum [*Sorghum bicolor* (L.) Moench]. Doctor of Philosophy (Agricultural Biotechnology), Major Field: Agricultural Biotechnology, Interdisciplinary Graduate Program. Thesis Advisor: Associate Professor Sontichai Chanprame, Ph.D 124 pages.

Sugarcane (*Saccharum* spp.) and Sorghum (*Sorghum* spp.) have become an increasingly important crop for bioenergy such as biofuel. Sugarcane has an autopolyploid complex genome whereas sorghum has a diploid simple genome. Flowering is one of sugar-related agronomic traits in both species. Here, we obtained cDNA of 0–15 cm long inflorescence of *S. spontaneum* using cDNA-amplified restriction fragment length polymorphism (cDNA-AFLP) to develop flower transcriptome profiling with 26 primer combinations. A total of 183 transcript-derived fragments (TDFs) were screened and 96 TDFs were sequenced. Out of 96, 26 TDFs were selected as flowering putative genes to study colinearity with sorghum genome. For colinearity of flowering putative genes, a genetic map with 169 SSR co-dominant SSR markers and 9 TDFs marker loci were conducted on 14 linkage groups collectively spanning 1077.8 cM that corresponding the 10 sorghum chromosomes. Interestingly, nine TDFs marker loci can be mapped into 5 linkage groups. In this study, we successfully identify the homologous location of sugarcane flowering TDFs in sorghum genome. Moreover, sfw4DS.1X TDF could be a part of gene that related to flowering and showed codominant expression in sorghum RILs population. This means it carries genotypic value of both parents and can be served as a candidate specific marker for breeding selection, while sfw2DS.3E showed dominant expression that good enough for breeding program as well.

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Thesis Advisor's signature

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