

Functional analysis of *Cis* Regulatory Elements (CREs) in pollen specific/preferential genes

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Abstract:

Promoter is a region of DNA located in 5' upstream region from the transcription start site (TSS) of gene that has been known as play a critical role in regulating gene expression and widely used as an ideal tools for crop improvement and analysis of gene functions. Recently, based on microarray data we have identified 20 pollen specific or preferred promoters from rice (*Oryza sativa* L.), including 9 early microspore (*RMP1* through 9) and 11 late pollen specific promoters (*OsLPS1* through 11) (Nguyen et al. 2015, 2016a,b). Moreover, detailed analysis promoter sequencens revealing several *cis*-regulatory elements (CREs) involved in tissues, organs-specific or preferential expression such as GTGANTG10, POLLEN1LeLAT52. However, not only CREs but also novel motifs or enhancer elements involved in specific expression also need to be concerned. In order to better understand the function of CREs, these promoters are being studied in detail using the method of deletion analysis in transgenic plants, rice and *Arabidopsis*. Our study will be useful for understading the roles of CREs in regulating specific expression of gene in pollen grains, and also provide new set of pollen specific promoters for plant breeders in Vietnam.

Keywords: CREs rice, pollen, promoter