

Selection of optimized candidate reference genes for qRT-PCR normalization in rice (*Oryza sativa* L.) during *Magnaporthe oryzae* infection and drought

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ABSTRACT. Drought and rice blast disease caused by *Magnaporthe oryzae* are two of the most serious threats to global rice production. To explore the mechanisms underlying gene expression induced in rice by stresses, studies involving transcriptome analyses have been conducted over the past few years. Thus, it is crucial to have a reliable set of reference genes to normalize the expression levels of rice genes affected by different stresses. To identify potential reference genes for studies of the differential expression of target genes in rice under *M. oryzae* infection and drought conditions, the present study evaluated five housekeeping genes for the normalization of gene expression. The stability of the expression of these genes was assessed using the analytical software packages geNorm and NormFinder. For all samples analyzed, the stability rank was *UBQ5*

> *GAPDH* > *eIF-4α* > β-TUB > 18S rRNA. The data showed that the *UBQ5*, *GAPDH*, and *eIF-4α* genes are appropriate, high-performing reference genes and will be highly useful in future expression studies of fungal infections and drought in rice.

Key words: Housekeeping genes; Gene expression; Stable expression; Real-time quantitative reverse transcription polymerase chain reaction; Normalization