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In-depth analysis of internal control genes for quantitative real-time PCR in *Brassica oleracea* var. *botrytis*

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ABSTRACT. Quantitative reverse-transcription PCR (qRT-PCR) is a versatile technique for the analysis of gene expression. The selection of stable reference genes is essential for the application of this technique. Cauliflower (*Brassica oleracea* L. var. *botrytis*) is a commonly consumed vegetable that is rich in vitamin, calcium, and iron. Thus far, to our knowledge, there have been no reports on the validation of suitable reference genes for the data normalization of qRT-PCR in cauliflower. In the present study, we analyzed 12 candidate housekeeping genes in cauliflower subjected to different abiotic stresses, hormone treatment conditions, and accessions. geNorm and NormFinder algorithms were used to assess the expression stability of these genes. *ACT2* and *TIP41* were selected as suitable reference genes across all experimental samples in this study. When different accessions were compared, *ACT2* and *UNK3* were found to be the most

suitable reference genes. In the hormone and abiotic stress treatments, *ACT2*, *TIP41*, and *UNK2* were the most stably expressed. Our study also provided guidelines for selecting the best reference genes under various experimental conditions.

Key words: Cauliflower; Reference genes; geNorm; NormFinder