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Evaluation of reference genes for quantitative RT-qPCR in rice, weed rice and barnyardgrass subjected to drought

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Stress for drought is largely responsible for lost in world grain production specially in tropical regions. Plants respond to stress such drought modifying expression of specific genes. Use the quantitative technique PCR in real time allows analyze gene expression in different experimental conditions. However, the precise analyze of the result of RT-qPCR is directly related to normalizing gene used, which must present constitutive expression similar to different sample/ treatment evaluated in experiment. The study was aimed to select normalizing gene with stable expression in rice, weed rice and (barnyardgrass) when subjected to drought. The experiment was conducted in factorial design, where factor A was plants (rice (*Oryza sativa*), weed rice (*Oryza* spp.) and barnyardgrass (*Echinochloa* spp.) and factor B was hydric condition (without drought and with drought). The collect of shoot in plants was carried out five days after stress. Likely candidate genes were selected (UBC-E2, UBQ10 Tubulina, 18S and Elf-4a) and they had patterns of expression measured by real-time PCR. The data generated were analyzed statistically and was also calculated and compared to average expression stability (M) and pairwise variations (V) using the algorithm of the program GeNorm. Analyses show that more stable genes were UBC-E2 and UBQ10 (M=0,89 and 0,93, respectively) and less stable gene was Elf-4a (M=1,79). It was also observed through the pairwise variations that the use of two normalizing genes are sufficient to ensure quality of RT-qPCR (V=0,13). In conclusion, this study indicates that two normalizing genes (UBC-E2 and UBQ10) are sufficient for proper quantitative RT-qPCR analysis in rice, weed rice and barnyardgrass when subjected to drought.

Palavras-chave: Oryza spp., Echinochloa spp, Abiotic stress, gene expression