Identification and validation of reference genes for normalization of transcripts levels in roots of potatoes infected by nematodes

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Potato cyst nematodes induce changes in gene expression after infecting the roots. For studying gene expression, reverse transcription quantitative real-time PCR (RT-qPCR) is now a standard method. However, for accurate quantification of transcripts, a set of internal control genes, stable under different experimental conditions, is necessary for transcript normalization. Very few experimental data on suitable reference genes are available for plant-nematode interactions. In this study, we tested eight potential candidate reference genes identified through a microarray study performed on the pathosystem Arabidopsis/Meloigodygne for normalizing levels of potato gene transcripts, after invasion by nematodes. The transcription profiles of these genes were assessed by RT-qPCR. Samples used in these experiments were RNAs, issued from roots of infected and uninfected potato plants, carrying resistant or susceptible alleles against Globodera pallida, following a kinetic of four days. Analyses were performed using the geNorm and NormFinder softwares. Our results showed that the eight candidate reference genes were stably expressed in our conditions. For accurate normalization in RT-qPCR studies, RPN7 (26S proteasome regulatory subunit, involved in protein synthesis) and MST2 (mercaptopyruvate sulfurtransferase) were the top ranked genes and, therefore, are reliable reference genes in compatible and incompatible potato-nematode interactions.

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