


Erratum

Erratum To: Physiological Role of Aerobic Fermentation Constitutively Expressed in an Aluminum-Tolerant Cell Line of Tobacco (*Nicotiana Tabacum*)

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In the originally published version of this manuscript, the ethylene signaling pathway in Arabidopsis shown in the Figure 3 was incorrectly referred. The correct pathway is as follows: Ethylene -| ETR1 -> CTR1 -| EIN2 -> EIN3/EIL1 -> ERFs. In addition, information was missing from the Figure 3 caption. An explanation of the subgroups of the ERF family shown in the figure (Group IX, VIII, VI, VII) has been added to the caption, which also necessitated two new references in the paper.

The corrected caption is:

Expression of the genes encoding transcription factors (EIL, ERFs) and chitinases (CHNs) associated with ethylene signaling pathway in SL and ALT301 under normal growth condition. Gene expression analysis was performed by real-time RT-PCR. Values are the mean \pm SE ($n = 3-5$ from three to five independent experiments, respectively). Significant differences between SL and ALT301 are indicated with asterisks ($*P < 0.05$, $**P < 0.01$, Welch's t -test). Ethylene signaling pathway in Arabidopsis (Kazan 2015) is shown (top). Group names of the ERF genes are indicated, which is based on Rushton et al. (2008) and Nakano et al. (2006). Note that some of the ERF genes have several synonyms (see the National Center for Biotechnology Information [NCBI] database using the gene accessions listed in Supplementary Table S6). Abbreviations: ETR1, Ethylene Response1; CTR1, Constitutive Triple Response1; EIN2, Ethylene Insensitive2; EIN3, Ethylene Insensitive3; EIL1, Ethylene Insensitive-Like Protein1; ERF, Ethylene Response Factor. The gene Tsi1 encodes Tobacco stress-induced gene1.

The two new references are:

Nakano, T., Suzuki, K., Fujimura, T. and Shinshi, H. (2006) Genome-wide analysis of the ERF gene family in Arabidopsis and rice. *Plant Physiol.* 140: 411–432.

Rushton, P.J., Bokowiec, M.T., Han, S., Zhang, H., Brannock, J.F., Chen, X., et al. (2008) Tobacco transcription factors: novel insights into transcriptional regulation in the Solanaceae. *Plant Physiol.* 147: 280–295.

These errors have been corrected.