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scientific reports

Published online: 27 July 2021

OPEN Author Correction: Elucidation of the core betalain biosynthesis pathway in Amaranthus tricolor

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Correction to: Scientific Reports https://doi.org/10.1038/s41598-021-85486-x, published online 17 March 2021

The original version of this Article contained errors.

A Data Availability section was omitted. It is now included and reads:

Sequencing data generated for this study are deposited at Short Read Archive with the accession code SRR15044103.

Additionally, one of the images in Figure 1D was missing an axis label. This figure has been updated. The original Figure 1 and accompanying legend appear below.

The original Article has now been corrected.



∢Figure 1. Identification of *AmCYP76AD1* as a key element required for betalain pigment production in Amaranthus tricolor. (a) The leaf-color phenotypes of the red-leaf cultivar (AMR) and green-leaf cultivar (AMG) of three-week-old A. tricolor. (b) Extraction of chlorophyll pigments (hydrophobic layer) and betalain pigments (hydrophilic layer) from three-week-old leaves of AMR and AMG (left panel). Absorbance spectra of the extracted betalain pigments from AMR and AMG (right panel). The absorbance at 538 nm for betacyanins is indicated with a red dashed line, and the absorbance at 476 nm for betaxanthins is indicated with a yellow dashed line. (c) Liquid chromatography-tandem mass spectrometry (LC-MS/MS) analysis of three-weekold leaves of AMR and AMG. Shown are extracted ion chromatograms (XICs) of masses corresponding to tyrosine (m/z = 182), L-DOPA (m/z = 198), betalamic acid (m/z = 212), betanidin (m/z = 389), and betanin (m/z=551). Time, retention time (min). (d) Expression levels of genes related to the betalain biosynthesis pathway in AMR and AMG analyzed by qRT-PCR. Statistically significant differences were determined using Student's t-test (*P < 0.01 for AMR vs. AMG). (e) Putative core betalain biosynthesis pathway in A. tricolor. Am, Amaranthus tricolor, CYP76AD1, cytochrome P450 76AD1; DODA, DOPA-4,5-dioxygenase; cDOPA5GT, cyclo-DOPA 5-O-glucosyltransferase; B5GT, betanidin-5-O-glucosyltransferase; UGT79B30-like 4, UDP-glucose glucosyltransferase 79B30-like 4; ADH, arogenate dehydrogenase; PPO, polyphenol oxidase; CATPO, catalasephenol oxidase; TyDC, tyrosine decarboxylase.

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