CORRECTION

Correction: *Arabidopsis* ERF1 Mediates Cross-Talk between Ethylene and Auxin Biosynthesis during Primary Root Elongation by Regulating *ASA1* Expression

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Fig 1, Fig 4A and 4C, Fig 8C and 8D, S2 Fig and S8 Fig are incorrectly labeled. Please see the complete, correct figure captions here.



Citation: Mao J-L, Miao Z-Q, Wang Z, Yu L-H, Cai X-T, Xiang C-B (2016) Correction: *Arabidopsis* ERF1 Mediates Cross-Talk between Ethylene and Auxin Biosynthesis during Primary Root Elongation by Regulating *ASA1* Expression. PLoS Genet 12(5): e1006076. doi:10.1371/journal.pgen.1006076

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Fig 1. *ERF1* expression is responsive to ethylene. (a) Ethylene-induced *ERF1* expression in wildtype. Seeds of Col-0 were germinated on MS medium for 5 d then treated with 10 μM ACC for 0, 0.5, 1, 3, 6, and 12 h. The transcriptional level of *ERF1* was detected by quantitative RT-PCR (qRT-PCR). Values are mean ± SD of three replicates. ACC, 1-aminocyclopropane-1-carboxylic acid (precursor of ethylene biosynthesis). (b) Ethylene-induced expression of *ERF1* pro:*GUS*. Five-day-old seedlings of transgenic lines were treated with 10 μM ACC for 0, 3, and 6 h before GUS staining. Upper DZ and lower DZ represent different primary root regions. Scale bar, 0.5 cm. (c) Ethylene-induced expression of *ERF1* in wildtype. Seeds of Col-0 were germinated on MS medium with 0 or 0.8 μM ACC for 5 d, and relative *ERF1* transcription levels were measured by qRT-PCR. Values are mean ± SD of three replicates (***P<0.001). Asterisks indicate Student's t-test significant differences. (d) Ethylene-activated expression in *ERF1* pro:*GUS* lines. Transgenic plants were grown on MS medium with either 0 or 0.8 μM ACC for 5 d before GUS staining assay. Scale bar, 0.5 cm. (e) The relative *ERF1* expression level was determined in ethylene signaling related mutants *ein2-5*, *ein3-1*, *ein3-1eil1* and compared to wildtype (Col-0) seedlings. Seedlings of constitutive (*ctr1-1*) and *β*-estradiol inducible *EIN3-FLAG (iE/qm) (EIN3ox*) expression were also examined. Seeds (*ein2-5*, *ein3-1*, *ein3-1eil1*, *ctr1-1* and Col-0) were germinated on MS medium with either 0 or 0.8 μM ACC for 5 d. Seeds of *EIN3ox* were grown on medium containing 1 μM β-estradiol and 0 or 0.8 μM ACC for 5 d. Roots of seedlings were used for qRT-PCR analysis. Values are mean ± SD of three replicas (***P<0.001). Asterisks indicate Student's t-test significant differences.

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Fig 4. ERF1 directly binds to *ASA1* **promoter region** *in vitro* **and** *in vivo.* **(a)** EMSA assay for binding to GCC-box sequence in the promoter of *ASA1* byERF1 protein *in vitro*. Dig-labeled probes were incubated with ERF1-MBP protein. As indicated, unlabelled probes were used as competitors, unlabelled probes with mutated GCC-box sequence were used as non-competitors, and the ERF1-MBP protein bound probes were separated from free probes by an acrylamide gel. (b) Yeast-one-hybrid assay. pGADT7/ERF1 (AD-ERF1) and pHIS2/ASA1pro (BD-ASA1pro) constructs were co-transformed into yeast strain Y187. AD-empty and BD-empty, AD-empty and BD-ASA1pro, AD-ERF1 and BD-empty, AD-empty and BD-3*GCC-box were used as negative controls while AD-ERF1 and BD-3*GCC-box were used as a positive control. (c). Chromatin immunoprecipitation-PCR for *ASA1* promoter. Roots of 5-day-old *35S:HA:ERF1* and Col-0 seedlings were used. Anti-HA antibodies were used as negative control (NC). (d) Quantitative real-time PCR was performed using the same ChIP products and PCR primers flanking GCC-boxes in *ASA1* promoter as in c. The region of *ASA1* that do not contain GCC-box was used as negative control. Values are mean ± SD of three replicas (***P<0.001). Asterisks indicate Student's t-test significant differences.

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Fig 8. ASA1 acts downstream of ERF1. (a) The primary root phenotypes of Col-0, *asa1-1*, *ERF1ox* and *ERF1ox asa1-1* seedlings grown on MS medium with either 0 or 0.1 μ M estradiol for 5 d. *ERF1ox* is the transgenic plants expressing ERF1 protein under control of the estradiol-inducible promoter in Col-0 background. Scale bar, 1 cm. (b) qRT–PCR analysis of transcriptions of *ERF1*. The roots of 5-day-old Col-0, *asa1-1*, *ERF1ox* and *ERF1ox asa1-1* seedlings grown on MS medium with either 0 or 0.1 μ M estradiol were used. Values are mean ± SD of three replicas (***P<0.001. Asterisks indicate Student's t-test significant differences). (c-d). Primary root length of Col-0, *asa1-1*, *ERF1ox* and *ERF1ox asa1-1* seedlings grown on MS medium with either 0 or 0.1 μ M estradiol were measured. Data shown are average and SD (Values are mean ± SD, n = 20).

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Supporting Information

S2 Fig. Primary root phenotype and the relative *ERF1* expression level in *ERF1* knockdown and overexpression lines compared to wildtype. (a) Seeds of the transgenic lines and wildtype were germinated vertically on MS medium for 5 days, and the representative seedlings were photographed. Scale bar, 1 cm. (b) The primary root length of the 5-d-old transgenic lines and wildtype was measured. Data shown are average and SD (n = 20, **P*<0.05, ***P*<0.01, ****P*<0.001. Asterisks indicate Student's t-test significant differences). (c) The expression level of *ERF1* in these materials was tested by qRT-PCR. Values are mean ± SD of three replicates (**P*<0.05, ****P*<0.001. Asterisks indicate Student's t-test significant differences). (DOC)

S8 Fig. Primary root elongation of *asa1-1* **mutant in response to ACC. (a)** The primary root phenotypes of Col-0, *asa1-1*, *ERF10x* and *ERF10x asa1-1* seedlings grown on MS medium with either 0 or 1 μ M ACC for 5 d. Scale bar, 1 cm. **(b-c)** Primary root length of Col-0, *asa1-1*, *ERF10x* and *ERF10x asa1-1* seedlings grown on MS medium with either 0 or 1 μ M ACC were

measured. Data shown are average and SD (Values are mean \pm SD, n = 20). (DOC)

Reference

 Mao J-L, Miao Z-Q, Wang Z, Yu L-H, Cai X-T, Xiang C-B (2016) Arabidopsis ERF1 Mediates Cross-Talk between Ethylene and Auxin Biosynthesis during Primary Root Elongation by Regulating ASA1 Expression. PLoS Genet 12(1): e1005760. doi:10.1371/journal.pgen.1005760 PMID: 26745809