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CORRECTION

Correction to: Identification and functional validation of a unique set of drought induced genes preferentially expressed in response to gradual water stress in peanut

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The original version of this article contains the following duplicate figures, namely blots showing expression data of clones:

- Figure 6 *AhWSI 153* (gene encoding NAC domain-containing protein) and Fig. 7 *AhWSI 350* (gene encoding HSP 70)
- Figure 6 *AhWSI 36* (gene encoding BRI1) and Fig. 7 *AhWSI 84* (gene encoding Aldehyde reductase)
- Figure 7 *AhWSI 90* (gene encoding Transcinnamate 4 monooxygenase) and Fig. 7 *AhWSI77* (gene encoding Nitrite reductase).

Since the authors could no longer provide pictures of the original figure files, it was agreed to conduct *denovo* experiments to generate expression data by qRT-PCR for *AhWSI 153, AhWSI 350,AhWSI 84* and *AhWSI 90*.

In order to generate the transcript expression data by using RT-qPCR, peanut plants were grown and subjected to stress as described in the Material and methods section of the original article. cDNA was synthesized from RNA extracted from the leaves of control plants (100% field capacity; FC) and stress plants (60, 40 and 20% FC) and was then subjected to qRT-PCR analysis. PCR reactions were performed in a BioRad CFX96 Real-Time PCR Detection System (Bio-Rad, USA) using SYBR Green to monitor dsDNA synthesis. Reactions contained 5 µl of 2X SYBR® Green Mastermix reagent (BioRad), 1 µl cDNA, and 200 nm of both forward and reverse gene-specific primer in a final volume of 10 µl. The expression level of each gene was calculated as fold change with regards to expression levels of the reference gene: actin ($2^{-\mathrm{dtCT}}$; dtCT = GOI-Ref Gene). Gene-specific primers were designed using the Primer 3 Software (http://primer3.ut.ee/; Untergasser et al. 2012; Koressaar and Remm 2007) with the following criteria: $T_m = 60 \pm 1$ °C, 18–25 bp length, close to the 3′-end if possible, GC content 40–60%, and PCR products between 60 and 150 bp.

The following gene-specific primers were used:

AhWSI 153: NAC-For-acgagatggaacagcaaggg,
NAC-Rev-cacgacccaaatcaatgggc;
AhWSI 350: HSP70-For-gttggctgaggtggatgaat,
HSP70-Rev-atctgcaccacctcccatag;
AhWSI 90: Transcinnamate-4-monooxygenase-For-gtttaggcccgagaggttcc,
Transcinnamate-4-monooxygenase-Rev-gccccaaagtgattccgaga;
AhWSI 84: Aldehyde reductase-For-aactctgggatggcgaacag,
Aldehyde reductase-Rev-agcagcactaccctgaaacc, and
Actin-For-atgctagtggtcgtacaactgg,
Actin-Rev-ctagacgaaggatagcatgtgg.

The four re-examined genes, *AhWSI 153* (NAC domain-containing protein), *AhWSI 350* (HSP 70), *AhWSI 90*

The original article can be found online at https://doi.org/10.1007/s00438-009-0432-z.

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(Transcinnamate 4 monooxygenase) and *AhWSI 84* (Aldehyde reductase), are highly expressed in plants subjected to the severe stress of 20% FC compared to control plants maintained at 100% FC (Figure S1, a–d).

The results indicate that the clones have significant expression under drought stress, which confirms the findings described in the original article.

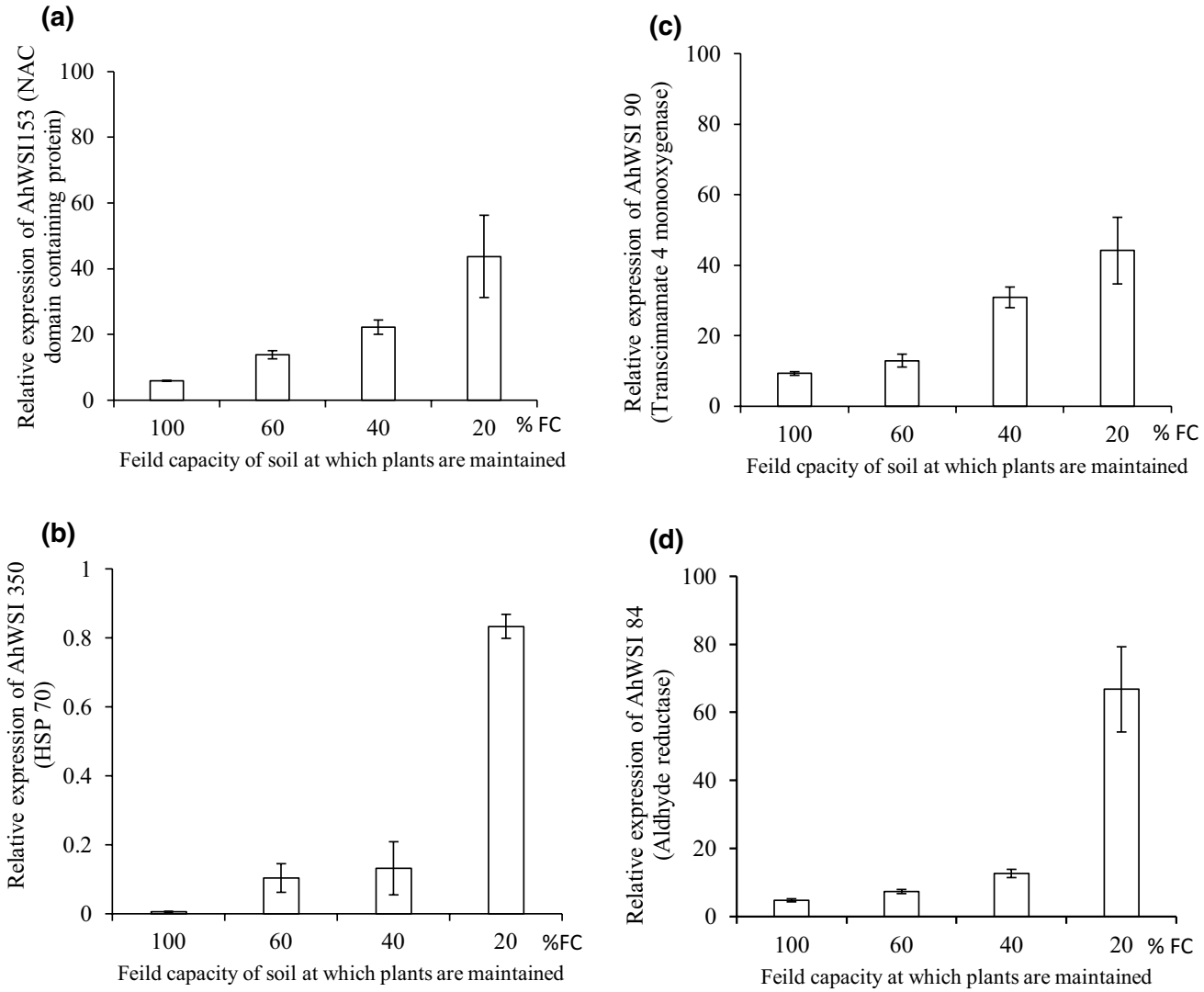

Figure S1: Stress responsive expression pattern as analyzed by qRT-PCR of (a)*AhWSI 153* (NAC domain-containing protein), (b) *AhWSI 350* (HSP 70), (c) *AhWSI 90* (Transcinnamate 4 monooxygenase) and (d) *AhWSI 84* (Aldehyde reductase).

References

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