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Correction: Comparative transcriptome and metabolome profiling unveil genotype-specific strategies for drought tolerance in cotton

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A Correction on

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In the published article, **Figure 2A** contains an error. Upon our verification, it was identified that the labels “A3” and “64-22-3” in **Figure 2A** were reversed: specifically, the image on the left should be labeled “64-22-3”, while the image on the right should be labeled “A3”. The corrected **Figure 2** is provided below.

The original version of this article has been updated.

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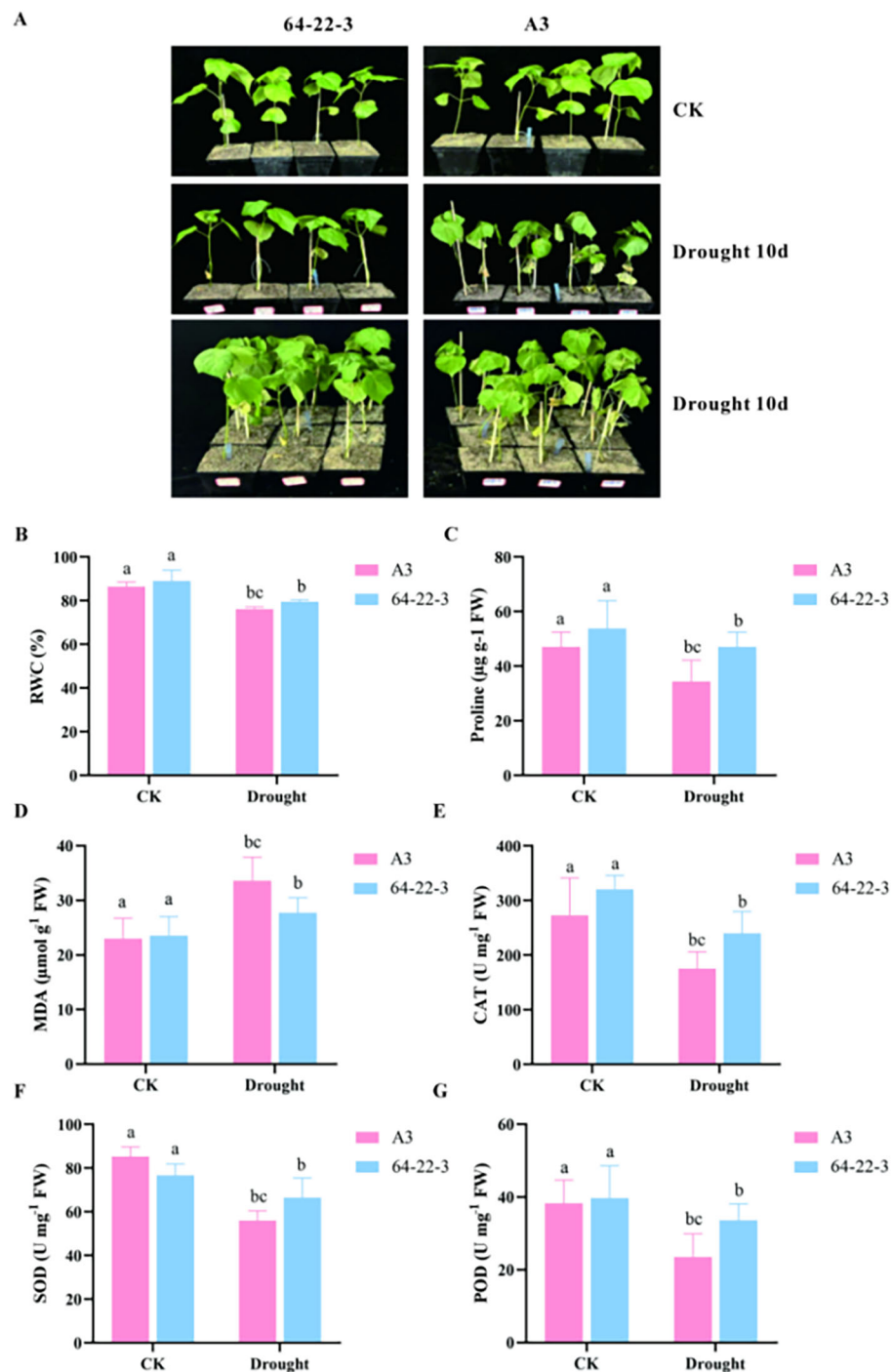


FIGURE 2

Phenotypic and physiological characterization of cotton under normal irrigation and drought conditions. Different lowercase letters indicate significant differences among treatment groups at $p < 0.05$ level. (A) Phenotypic comparison between normally irrigated and drought-stressed cotton plants; (B) Leaf relative water content (RWC, %) in control and drought-treated groups; (C) Proline content (Pro) under normal irrigation and drought stress; (D) Malondialdehyde content (MDA) in control and drought-exposed plants; (E) Catalase (CAT) activity in cotton under well-watered and drought-stress conditions. (F) Superoxide dismutase (SOD) content in cotton under well-watered and drought-stress conditions. (G) Peroxidase (POD) activity in cotton under well-watered and drought stress conditions.