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# Corrigendum: Comparative transcriptomic analysis and functional characterization reveals that the class III peroxidase gene *TaPRX-2A* regulates drought stress tolerance in transgenic wheat

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## KEYWORDS

transcriptomics, drought tolerance, class III peroxidase, *TaPRX-2A*, ROS

## A Corrigendum on

Comparative transcriptomic analysis and functional characterization reveals that the class III peroxidase gene *TaPRX-2A* regulates drought stress tolerance in transgenic wheat

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In the published article, there was an error in **Figure 6A**, **Figure 7C** as published. In **Figure 6A**, the representative photo of TaOE2 was duplicated and used as TaOE3 at 0 day. In **Figure 7C**, the representative photo of TaOE2 was duplicated and used as TaOE3. The corrected **Figure 6A** and its caption “**Figure 6** *TaPRX-2A* overexpression increased the drought tolerance. (A) Phenotype of *TaPRX-2A*-overexpressing transgenic and WT wheat (the cultivar “KN199”) with drought treatment. (B) Survival rates of *TaPRX-2A*-overexpressing transgenic lines and WT wheat. (C) shoot length of *TaPRX-2A*-overexpressing transgenic lines and WT wheat. (D) Relative water content (RWC), and (E) root length. (F) MDA content of *TaPRX-2A*-overexpressing transgenic lines and WT wheat. (G) soluble sugar content of *TaPRX-2A*-overexpressing transgenic lines and WT

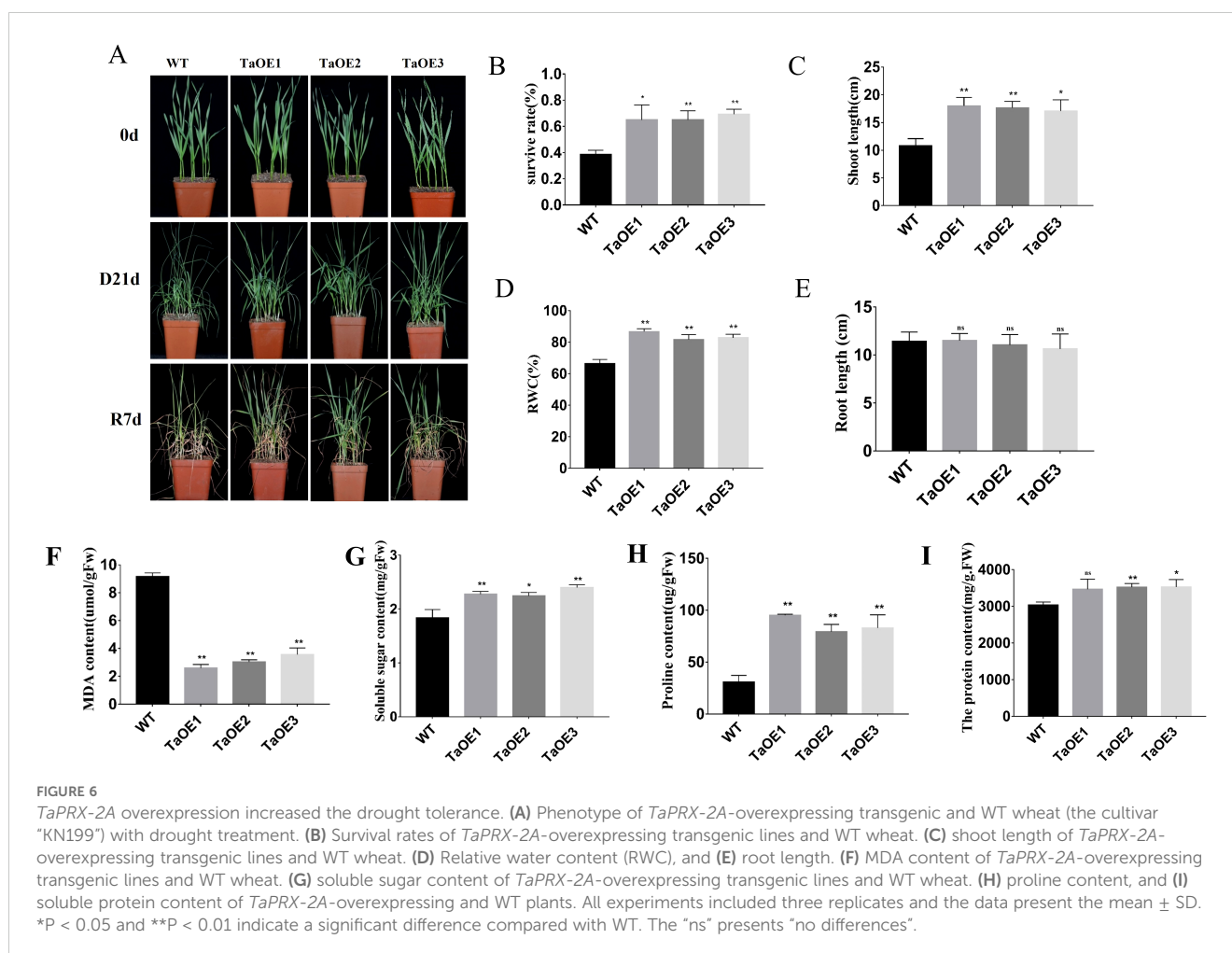
wheat. (H) proline content, and (I) soluble protein content of *TaPRX-2A*-overexpressing and WT plants. All experiments included three replicates and the data present the mean  $\pm$  SD. \* $P < 0.05$  and \*\* $P < 0.01$  indicate a significant difference compared with WT.” and the corrected **Figure 7C** along with its caption “**Figure 7** Analysis of ROS scavenging capacity and antioxidant enzymes activity in transgenic wheat lines. (A) Detection of  $O_2^-$  generation by NBT staining and  $O_2^-$  content (B). (C) Detection of  $H_2O_2$  accumulation by DAB staining and  $H_2O_2$  content (D). (E) Detection of SOD activity in *TaPRX-2A*-overexpressing transgenic lines and WT wheat. (F) Detection of CAT activity in *TaPRX-2A*-overexpressing transgenic lines and WT wheat. (G) Detection of POD activity in *TaPRX-2A*-overexpressing transgenic lines and WT wheat. All experiments included three replicates and the data present

the mean  $\pm$  SD. \* $P < 0.05$  and \*\* $P < 0.01$  indicate a significant difference compared with WT.” appear below.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

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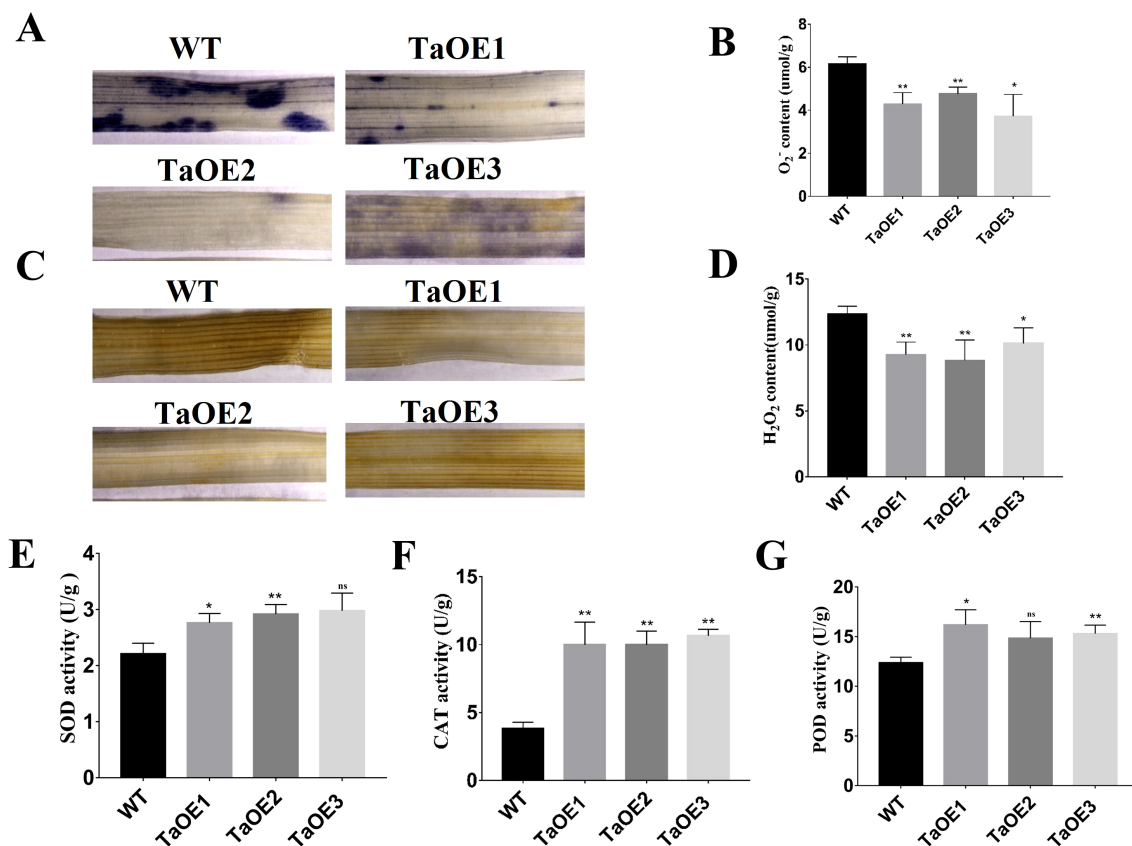


FIGURE 7

Analysis of ROS scavenging capacity and antioxidant enzymes activity in transgenic wheat lines. (A) Detection of O<sub>2</sub><sup>-</sup> generation by NBT staining and O<sub>2</sub><sup>-</sup> content (B). (C) Detection of H<sub>2</sub>O<sub>2</sub> accumulation by DAB staining and H<sub>2</sub>O<sub>2</sub> content (D). (E) Detection of SOD activity in *TaPRX-2A*-overexpressing transgenic lines and WT wheat. (F) Detection of CAT activity in *TaPRX-2A*-overexpressing transgenic lines and WT wheat. (G) Detection of POD activity in *TaPRX-2A*-overexpressing transgenic lines and WT wheat. All experiments included three replicates and the data present the mean ± SD. \*P < 0.05 and \*\*P < 0.01 indicate a significant difference compared with WT. The "ns" presents "no differences".