

Supplementary Materials

Aluminum Stress Induces Irreversible Proteomic Changes in the Roots of the Sensitive but Not the Tolerant Genotype of Triticale Seedlings

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Content:

Figure S1 The stages of the experiment: (A) triticale seeds germinating on the polyethylene grid tray; (B) 5th days old triticale seedlings; (C) the growth chamber view.

Figure S2 Protein separation by 2-DE on gels stained in Coomassie Brilliant Blue (A-F). Proteome of L17 Al-sensitive line control (A) and 48h after Al stress treated (B); proteome of L444 Al-sensitive line control (C) and 48h after Al stress treated (D); proteome of L198 Al-tolerant line control (E) and 48h after Al stress treated (F). The differential protein spots, which were common for both studied Al-sensitive lines, are marked in red on gel pictures of L17 and L444 line (control vs. Al-treated). The differential protein spots, which were characteristic only for one studied Al-sensitive lines, are marked in green on gel pictures of L17 and L444 line (control vs. Al-treated). The Image Master 2D Platinum 7.0 software was used for differential spots identification.

Figure S3 Comparison in: A) number of up/down-regulated and silenced/induced proteins and B) number of common protein spots according to established criterions ($p \leq 0.01$ and difference in spot intensity ≥ 2 -fold or 0.2 relative intensity of silenced/induced proteins).

When the criterion of probability has been weakened from 99% to 95% and twofold difference was not considered, more than 80% of differential proteins were common between control and stress-treated roots tips proteomes of Al-sensitive seedlings.



Figure S1. The stages of the experiment:
(A) triticale seeds germinating on the polyethylene grid tray;
(B) 5th days old triticale seedlings;
(C) the growth chamber view.

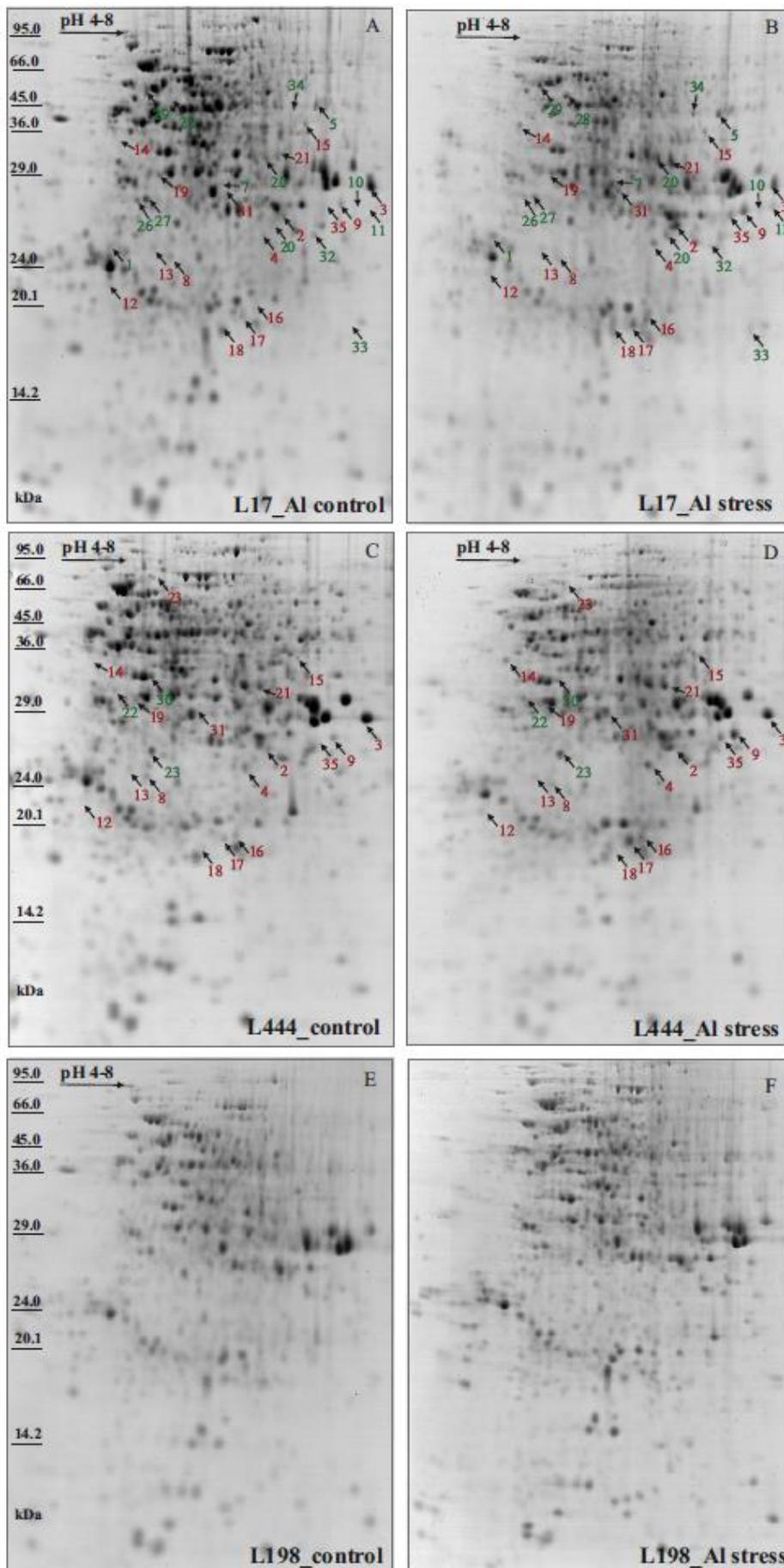


Figure S2. Protein separation by 2-DE on gels stained in Coomassie Brilliant Blue (A-F). Proteome of L17 Al-sensitive line control (A) and 48h after Al stress treated (B); proteome of L444 Al-sensitive line control (C) and 48h after Al stress treated (D); proteome of L198 Al-tolerant line control (E) and 48h after Al stress treated (F). The differential protein spots, which were common for both studied Al-sensitive lines, are marked in red on gel pictures of L17 and L444 line (control vs. Al-treated). The differential protein spots, which were characteristic only for one studied Al-sensitive lines, are marked in green on gel pictures of L17 and L444 line (control vs. Al-treated). The Image Master 2D Platinum 7.0 software was used for differential spots identification.

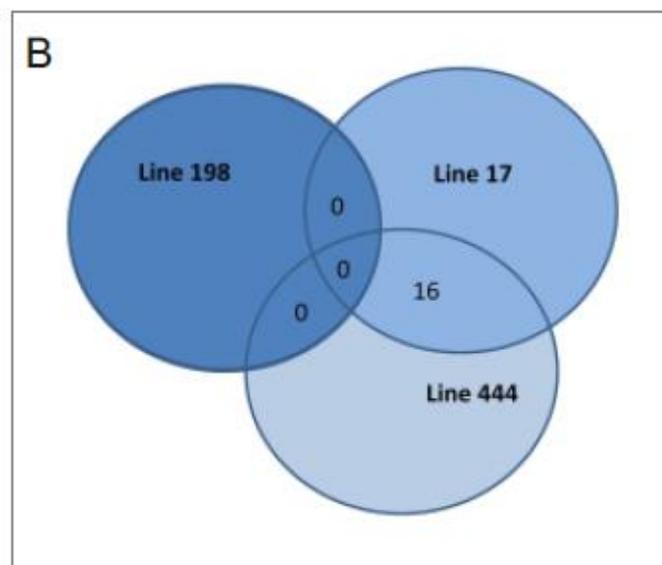
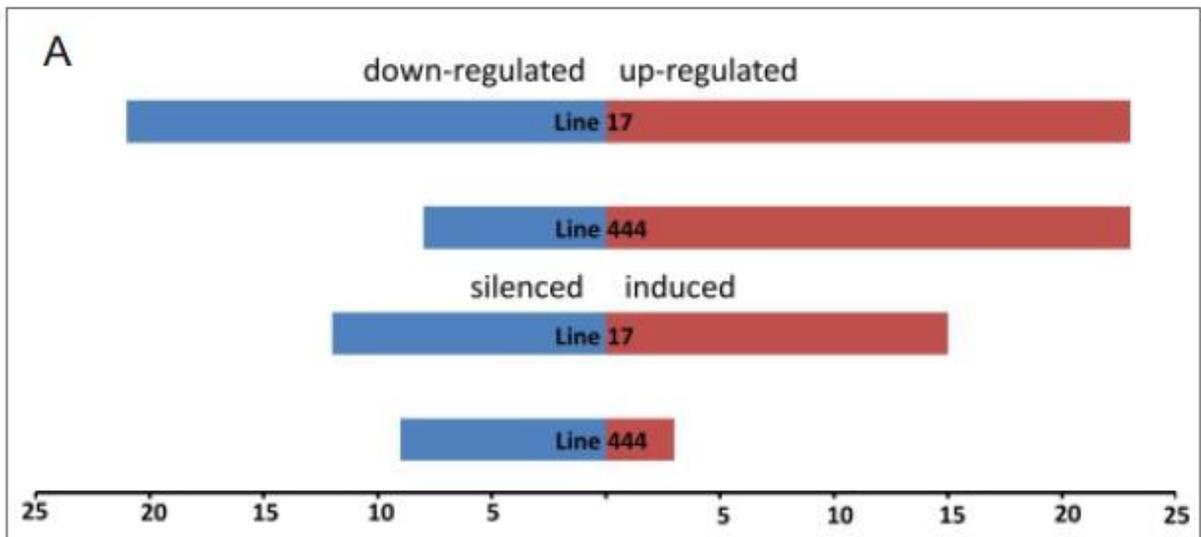


Figure S3. Comparison in: (A) number of up/down-regulated and silenced/induced proteins and (B) number of common protein spots according to established criteria ($p \leq 0.01$ and difference in spot intensity ≥ 2 -fold or 0.2 relative intensity of silenced/induced proteins). When the criterion of probability has been weakened from 99% to 95% and twofold difference was not considered, more than 80% of differential proteins were common between control and stress-treated roots tips proteomes of Al-sensitive seedlings.