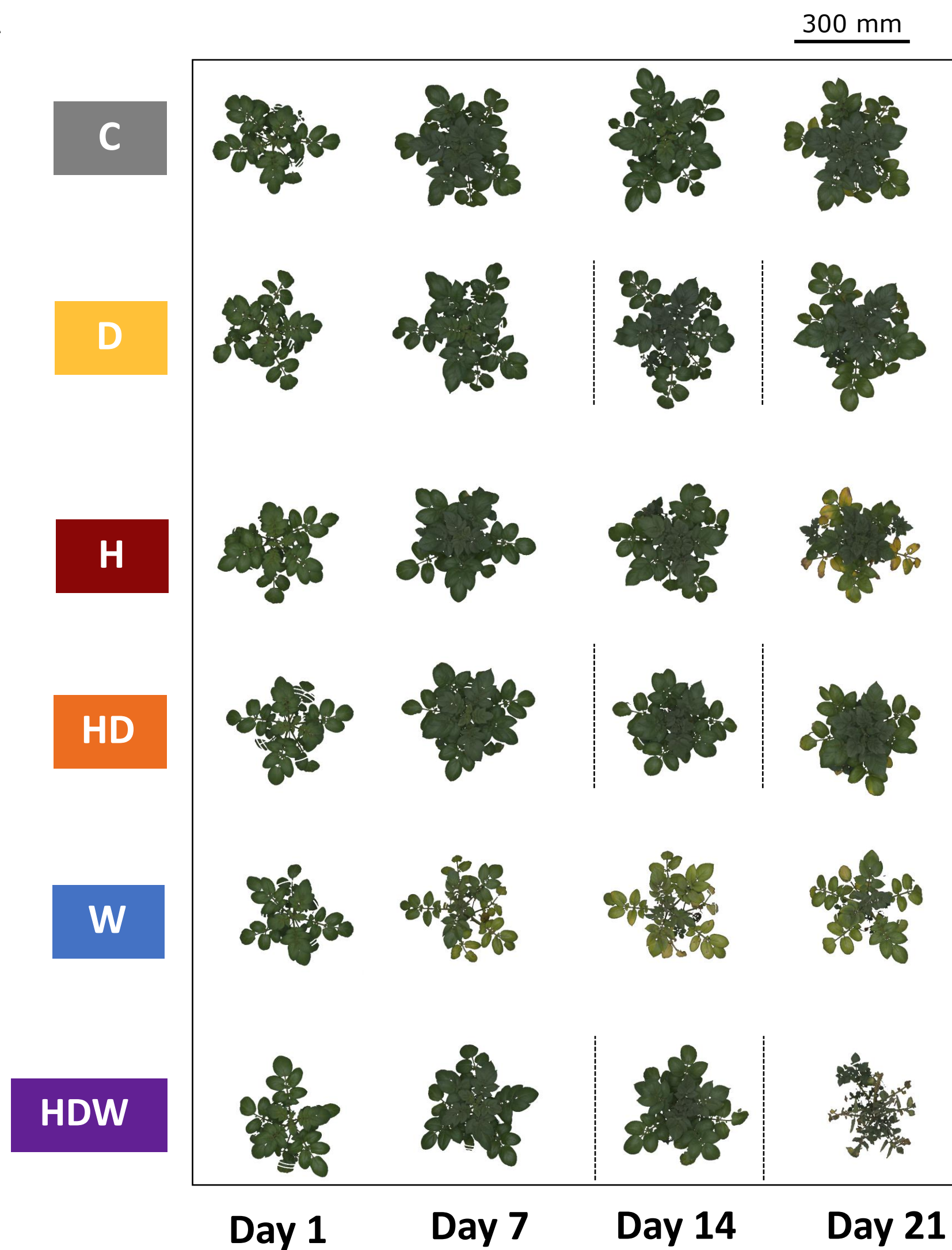
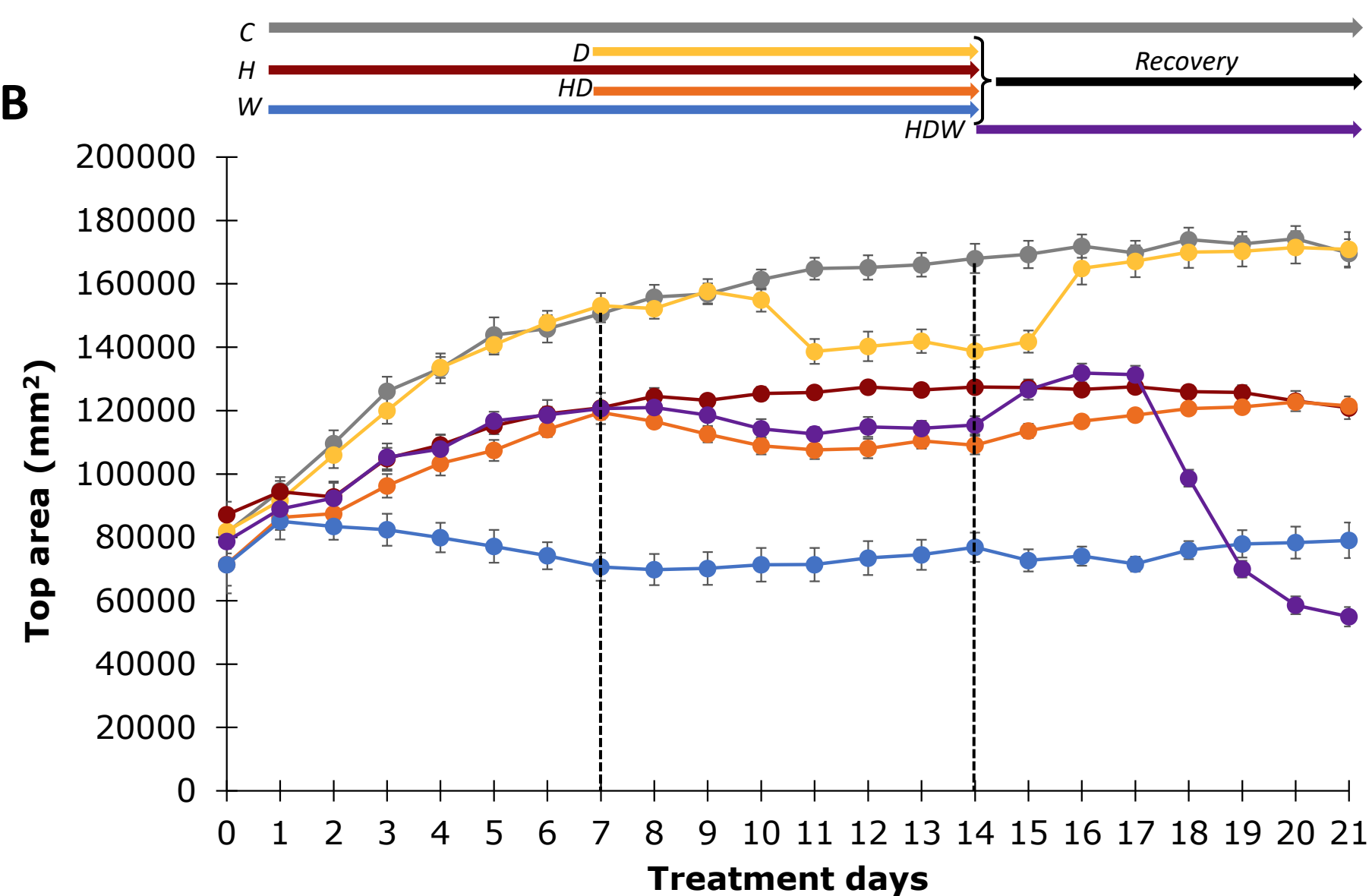


—●— Control —●— Drought —●— Heat —●— Heat + Drought —●— Waterlogging —●— Heat + Drought + Waterlogging

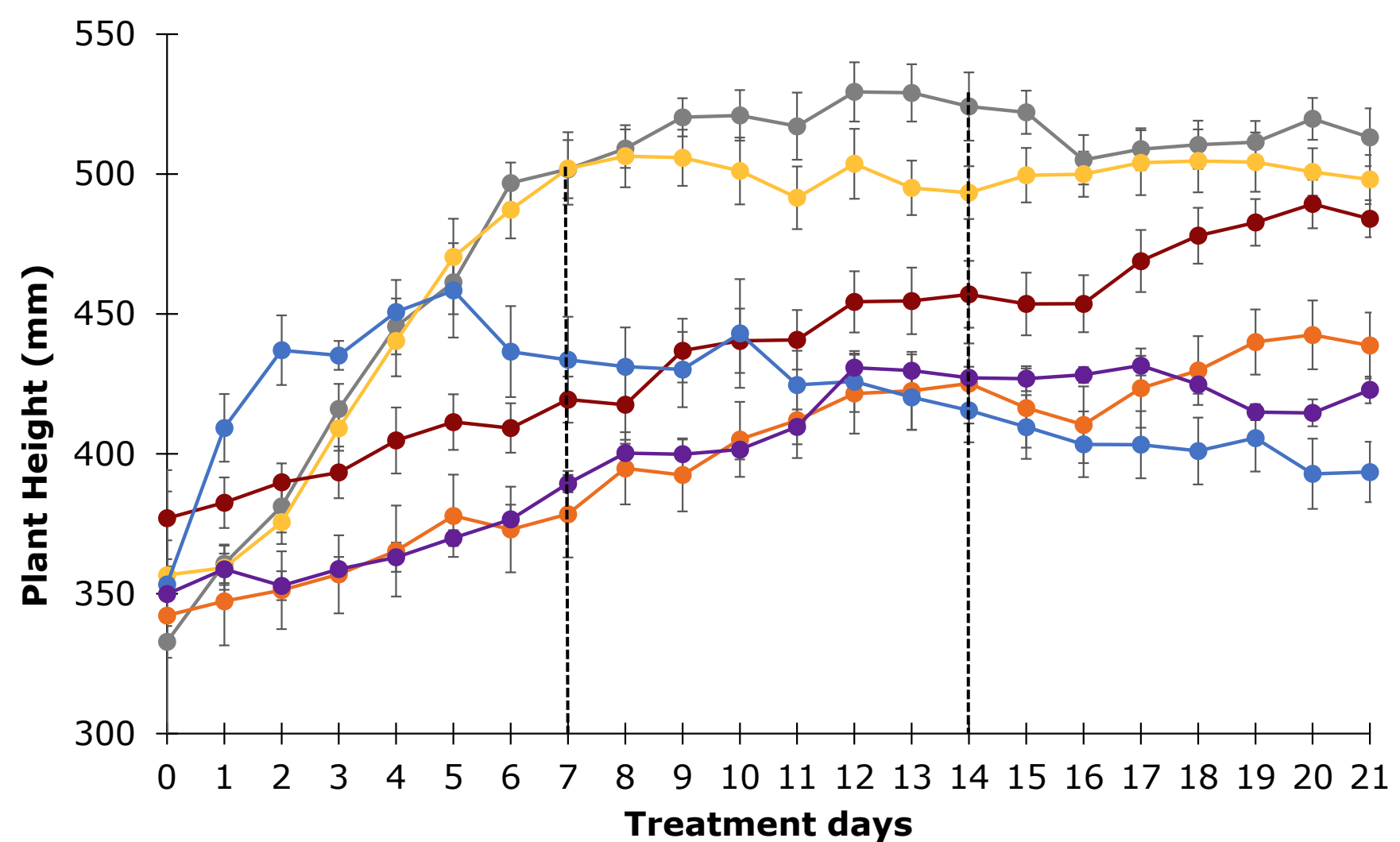
A



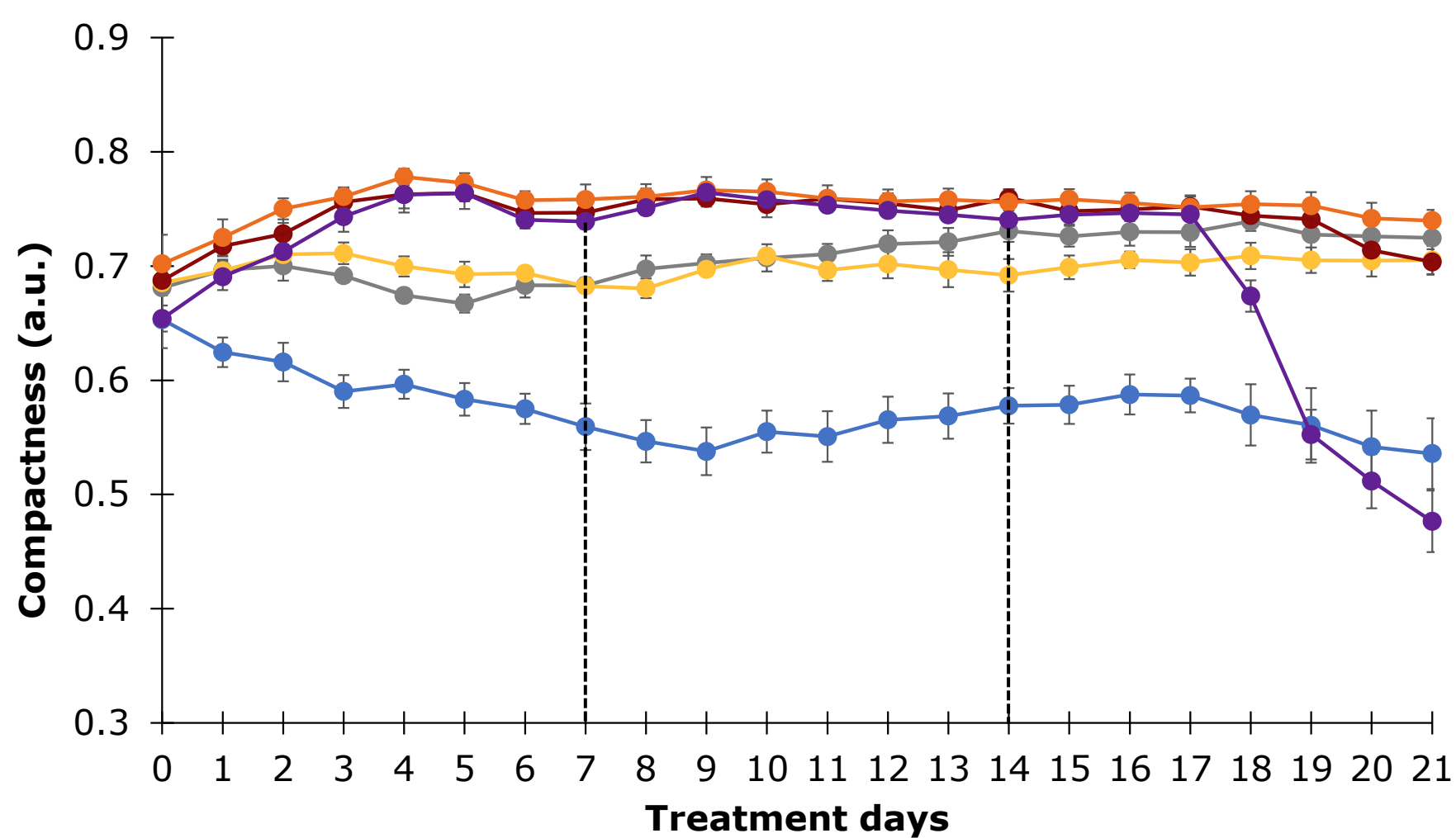
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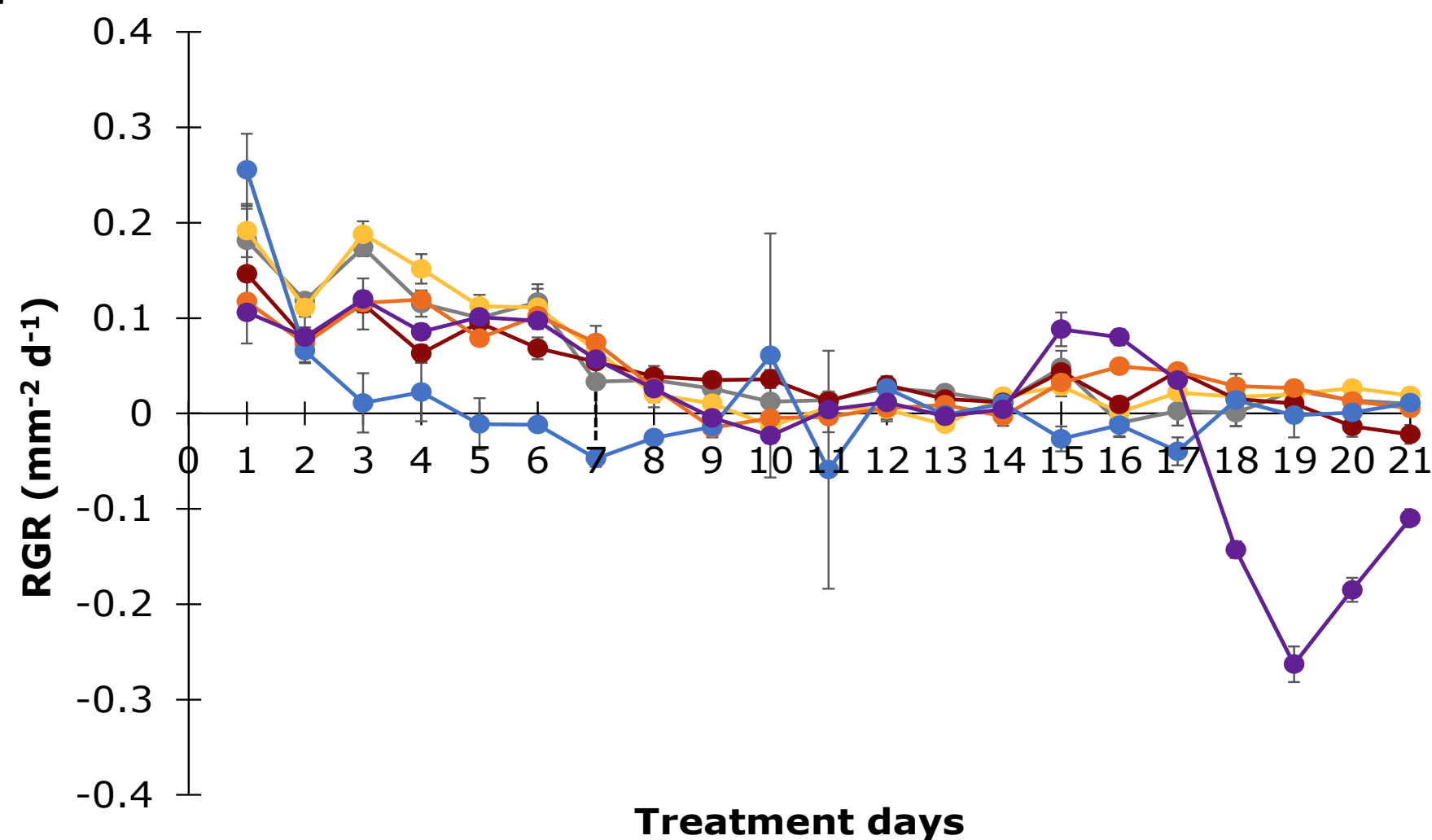
C



D



E

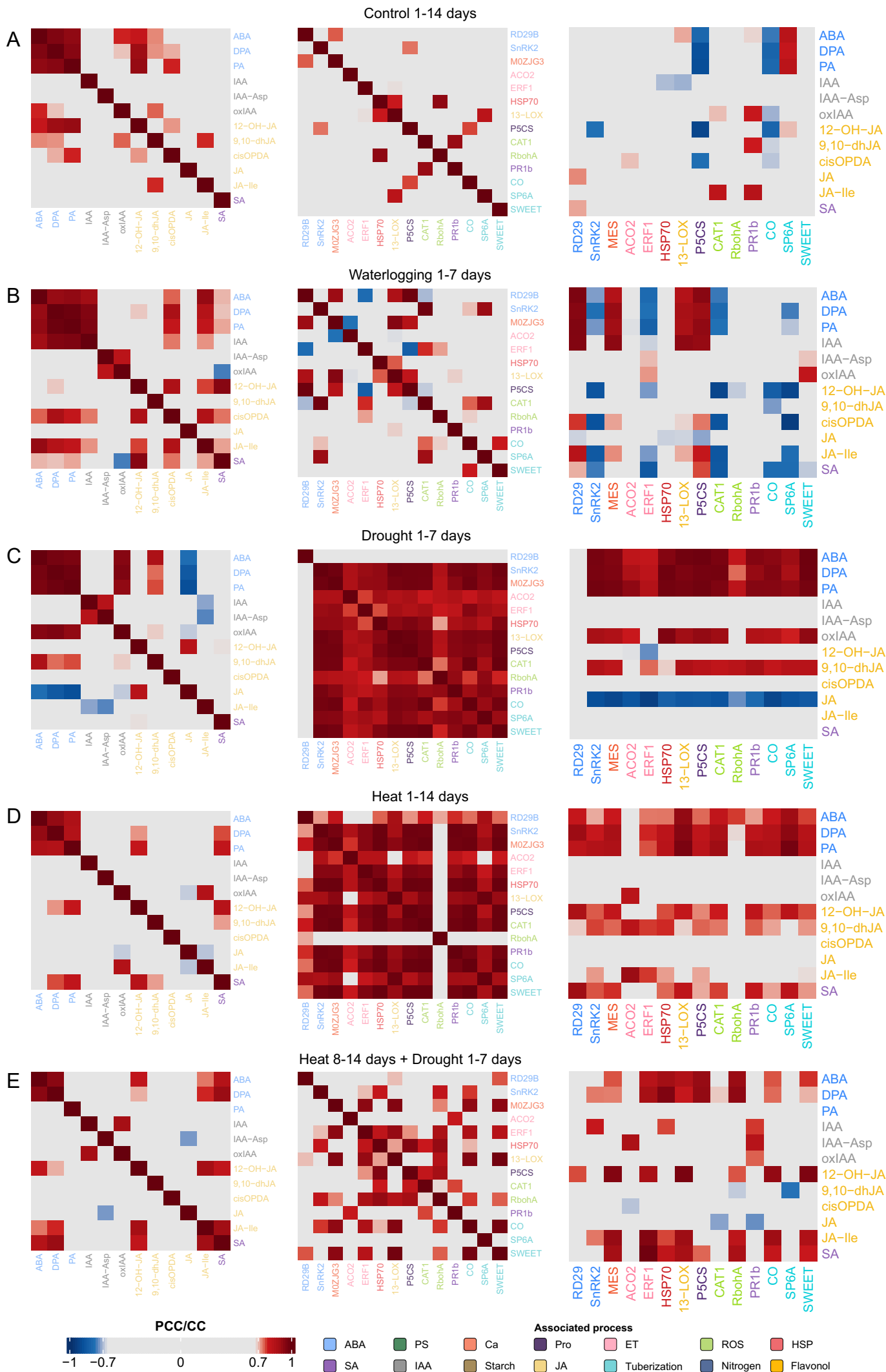


Supplementary Figure S1: Plant morphological responses of control and stress-exposed plants. (A) Top view RGB images at selected time points of tissue sampling starting from day 1 where i) in the first week heat stress was induced for H, HD, HDW marked rows, then ii) in the second week drought was induced for D, HD, HDW up to day 14, and finally iii) in the third week waterlogging was induced for HDW up to day 21, while the other treatments were recovered. Images were digitally extracted for comparison. (B-E) Parameters based on analyzed RGB images; Top area, plant height, compactness, and relative growth rate (RGR). The data represent mean values \pm standard error of mean (n = 6). C: control, D: individual drought stress, H: individual heat stress, HD: combined drought with heat stress, W: individual waterlogging stress, HDW: triple-stress condition.

	D28	H28	HD28	W28
Glucose	-0.520	0.886	1.026	-0.363
Fructose	0.185	-0.362	0.497	0.708
Sucrose	0.014	0.019	0.480	2.050
Starch	0.115	-0.419	-0.289	-0.563
Ala	-0.137	-0.731	-0.437	0.919
Arg	-0.291	-0.710	-0.262	1.588
Asn	-0.124	-0.508	-0.187	2.802
Asp	-0.107	-0.038	0.164	1.230
Gln	-0.056	-0.562	-0.098	2.611
Glu	-0.225	-0.404	-0.299	0.091
Gly	-0.300	-0.846	-0.568	1.045
His	-0.428	-0.664	-0.322	1.546
Ile	-0.250	-0.542	-0.323	1.001
Leu	-0.298	-0.295	-0.075	1.017
Lys	-0.477	-0.876	-0.753	0.434
Met	-0.239	-0.817	-0.485	0.408
Phe	-0.389	-1.437	-1.090	-1.158
Pro	-0.241	-0.131	0.028	2.850
Ser	-0.146	-0.595	-0.374	1.447
Thr	-0.083	-0.775	-0.365	1.189
Tyr	-0.361	-0.824	-0.742	-0.059
Val	-0.141	-0.640	-0.301	0.963

	D28	H28	HD28	W28
Number oftubers	+26%	+32%	+16%	-82%
Totaltubersweight	-4.6%	-48%	-48%	-97%

Supplementary Figure S2: Log2FC of a tuber metabolite's relative abundance between stress and control. Numbers in bold correspond to comparisons with p-value < 0.05. Additionally, log2FC for number of tubers and total tuber weight is shown.



Supplementary Figure S3: Correlation analysis within and between omics levels. A) Two weeks of control condition, B) one week of waterlogging, C) one week of drought, D) two weeks of heat, E) one week of heat combined with one week of drought. For correlation analysis within omics levels (left panel: hormones, middle panel: transcripts) heatmaps display Pearson correlation coefficient (PCC). For analysis between components of different molecular levels (right panel: hormones vs transcripts) heatmaps display canonical correlation analysis (CCA) results. Variable prioritisation for CCA was conducted using multiblock sPLS-DA (Singh et al., 2019).