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Functional Plant Biology

Supplementary Material

Short daily ultraviolet exposure enhances intrinsic water-use efficiency and delays senescence in Micro-Tom tomato plants

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Figure S1. UV spectral emission measured with JAZ EL-XR1 spectroradiometer.

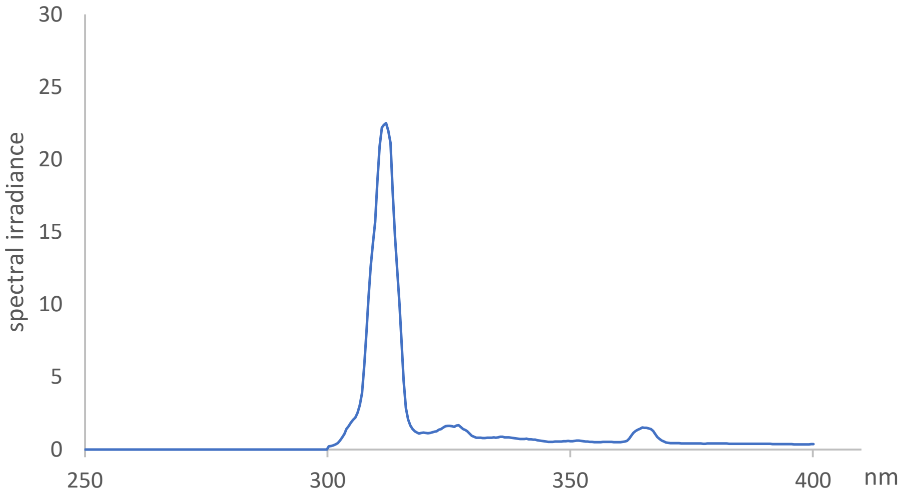


Figure S2. Time course of the leaf gas exchange parameters measured after 60 min from the end of the treatment at the 8th and 11th day of UV radiation and after 3 days of recovery (rec). Data represent the mean of 5 replicates ± SE. For each day, different letters correspond to significant differences between CTR and UV group according to two-way ANOVA (treatment × time) followed by Tukey's test.

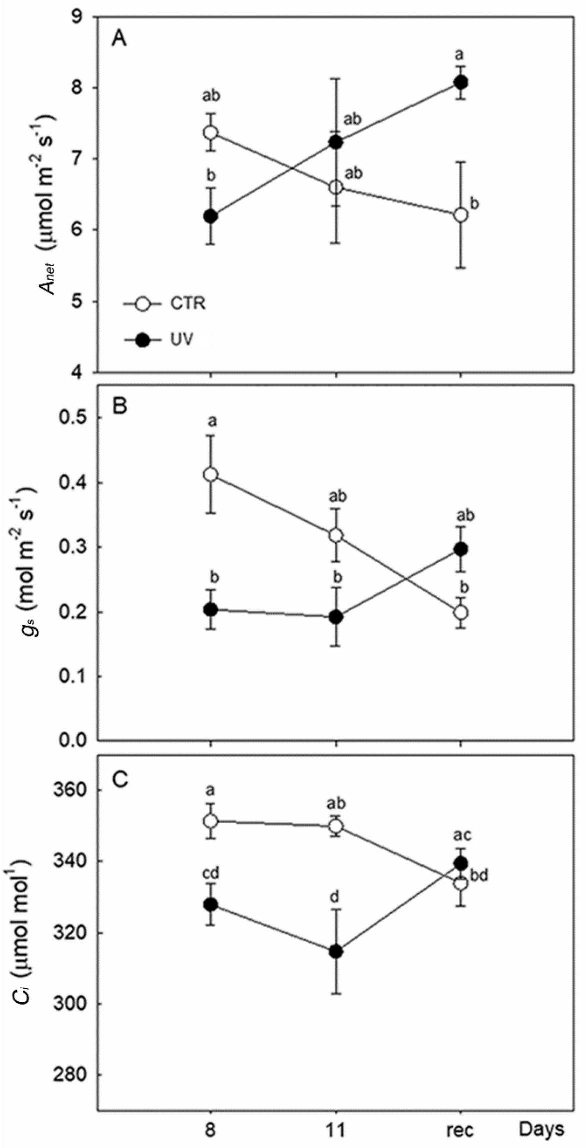


Figure S3. Time course of total chlorophylls and total carotenoids concentrations (μg g^{-1} FW) in Micro-Tom tomato (*S.lycopersicum*) at the 8th and 11th day of UV radiation and after 3 days of recovery (rec). Data represent the mean of 3 replicates ± SE. For each day, different letters correspond to significant differences between CTR and UV group according to two-way ANOVA (treatment × time) followed by Tukey's test.

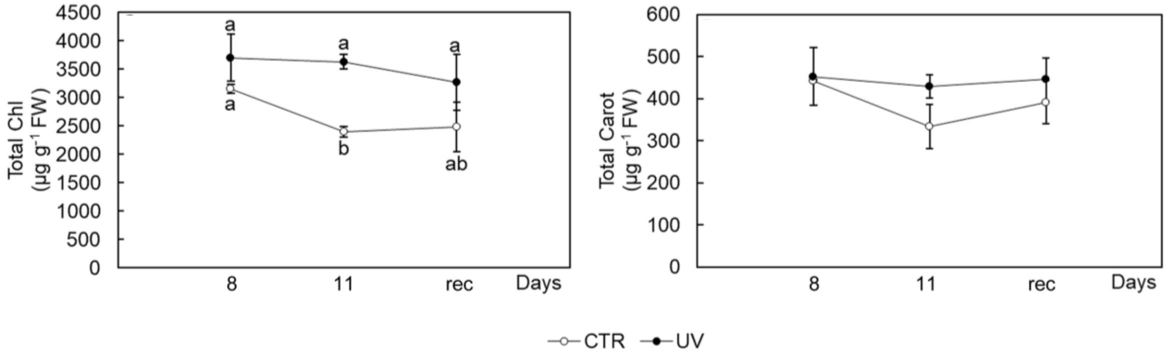
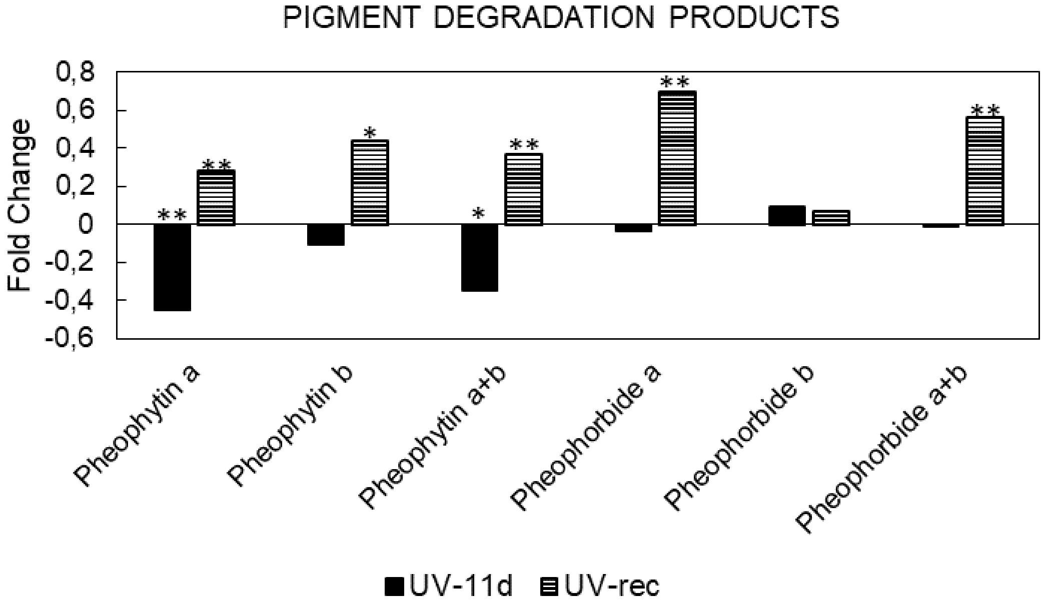


Figure S4. Pigment degradation products by untargeted metabolomic analysis using UHPLC-ESI-QTOF-MS. Data are expressed as Fold change between UV treated plants and the respective controls at each time point investigated (11 days of UV-B and 3 days of recovery). For each day, asterisks (*) indicate significant difference between CTR and UV group (*P ≤ 0.05. **P<0.01. *** P<0.001) according to t-Student.

Metabolites were analysed as reported by Senizza et al. (2020), by using an Agilent 6550 iFunnel quadrupole-time-of-flight mass spectrometer and an Agilent 1200 series ultra-high-pressure liquid chromatographic system (UHPLC-ESI/QTOF-MS). The mass spectrometer worked in SCAN mode with a range from 100 to 1200 m/z, positive and negative polarity and extended dynamic range mode (nominal mass resolution = 30,000 FWHM). Metabolite annotation was performed by the Profinder B.07 software tool (Agilent Technologies, USA) by their monoisotopic accurate mass and isotopes patterns (accurate spacing and isotopes ratio) according to Senizza et al. (2020), using the database exported from Plantcyc 9.6 (Plant Metabolic Network, http://www.plantcyc.org). Identification was carried out in compliance with Level 2 (putatively annotated compounds) as set out by the COSMOS Metabolomics Standards Initiative (http://cosmos-fp7.eu/msi).



Reference

Senizza, B., Zhang, L., Miras-Moreno, B., Righetti, L., Zengin, G., Ak, G., ... & Rouphael, Y. (2020). The strength of the nutrient solution modulates the functional profile of hydroponically grown lettuce in a genotype-dependent manner. Foods, 9(9), 1156.

Fig. S5 Aerial biomass (g FW).

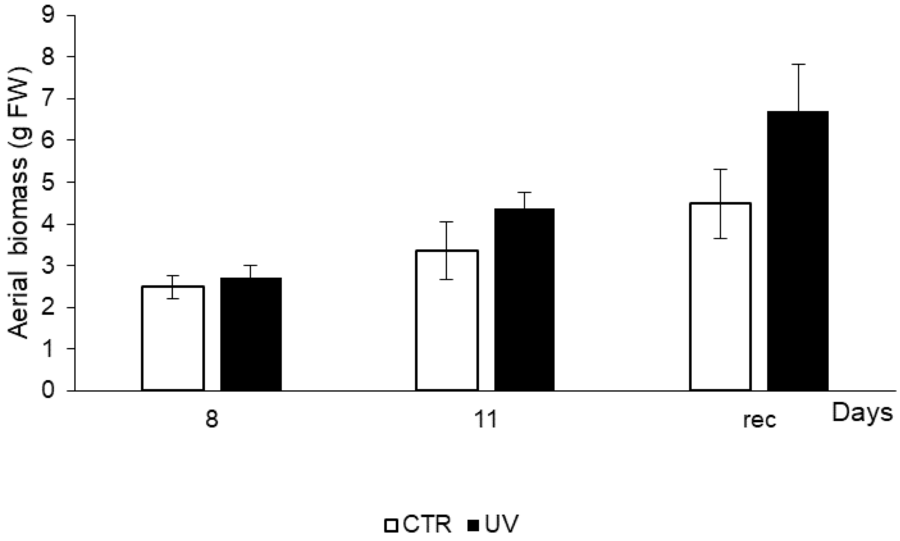


Table S1. Primer list for quantitative RT-PCR (*Solanum lycopersicum*). EF1, elongation factor 1; OST1, OPEN STOMATA 1; SLAC1, SLOW ANION CHANNEL-ASSIOCIATED 1; RBOH1, RESPIRATORY BURST OXIDASE 1; SAG113, SENESCENCE-ASSOCIATED GENE113; DFR, DIHYDROFLAVONOL 4-reductase; SGR1, STAY GREEN 1; ERF13, Ethylene responsive factor 13.

Target gene	**Forward primer (5′-3′)**	**Reverse primer (5′-3′)**
SlEF1A	GCTGCTGTAACAAGATGGATGC	GGGGATTTTGTCAGGGTTGTAA
SlOST1	CAGTTTGAGGAGCCAGATCA	GTCATCGTCAATGTCCAAGC
SlSLAC1	CGCTGATGAATTTGATG GCTTGG	TGCGGCGCACTCTTTGTCTCC
SlRBOH1	GCACCACCTTCTCATCA TTG	GAGTTCTTTCCCCTGCGTAA
SlSAG113	AAATGATATTACGGTGA CCGGC	CTCAAATCCACCACAACAACAC
SlDFR	TCCGAAGACGACAACGGTTT	TGACAAGCCAAGAGCCGATAA
SlSGR1	CCAGTGAGTGTTATGCC TTGG	TCAACTTTGCTGCTCTTGCAAG
SlERF13	ACCAAGCCGCTTACAAG ATTCGG	TAGGTACGTCCGAGCCAATCAG