

Supplementary Information for

Changes in resource partitioning between and within organs support growth adaptation to neighbour proximity in *Brassicaceae* seedlings

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This PDF file includes:

Figs. S1 to S5

Other supplementary materials for this manuscript include the following:

Dataset S1

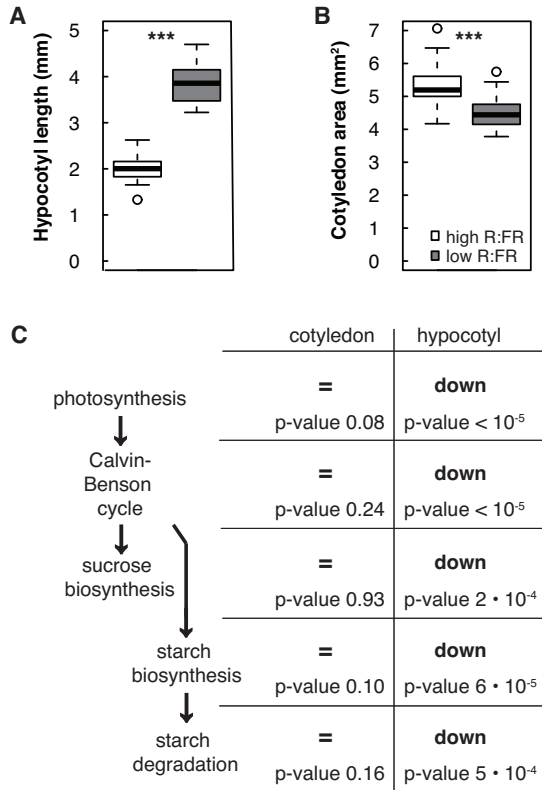


Fig. S1. Shade avoidance response in *Arabidopsis thaliana* seedlings. Hypocotyl length (A) and cotyledon area (B) in high and low R:FR. Col-0 seedlings were grown on horizontal plates in high R:FR for the first 3 d and subsequently divided over high and low R:FR for another 4 d of growth. Data are represented as standard boxplot representing median and interquartile (IQR) range between the 25th and 75th percentiles. Whiskers extend to 1.5-fold the IQR, dots represent data points outside 1.5-fold IQR. Hypocotyls and cotyledons were dissected and scanned for measurements after 7 d of growth. Asterisks indicate significant difference, n = 30. Significance codes: ‘*’ 0.05 > p > 0.01, ‘**’ 0.01 > p > 0.001, ‘***’ p < 0.001. (C) Metabolic pathway enrichment analysis on genes differentially regulated in cotyledons and hypocotyls of 5-d-old *Arabidopsis* seedlings after 3 h of low R:FR, using the PlantCyc tool. =, no significant enrichment; down, pathway significantly downregulated.

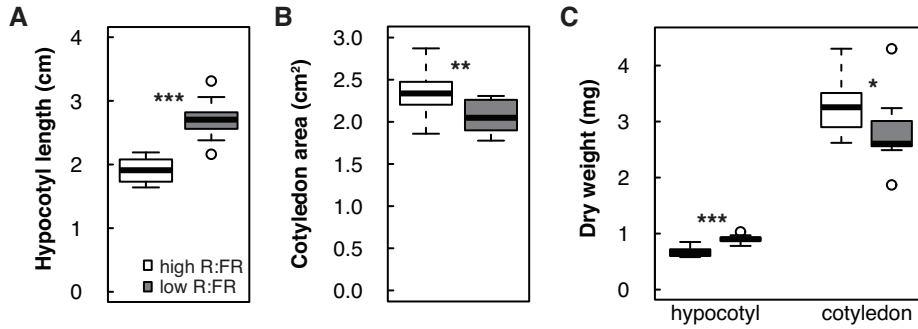


Fig. S2. Shade avoidance response in *Brassica rapa* seedlings. Five-day old *B. rapa* seedlings were divided over high or low R:FR treatment for another 2 d of growth. Hypocotyls and cotyledons were dissected after 2 d of treatment, and hypocotyl length (A), cotyledon area (B) and biomass (C) were subsequently determined. Data are represented as standard boxplot representing median and interquartile (IQR) range between the 25th and 75th percentiles. Whiskers extend to 1.5-fold the IQR, dots represent data points outside 1.5-fold IQR. n=30. Significance codes: ‘*’ $0.05 > p > 0.01$, ‘**’ $0.01 > p > 0.001$, ‘***’ $p < 0.001$.

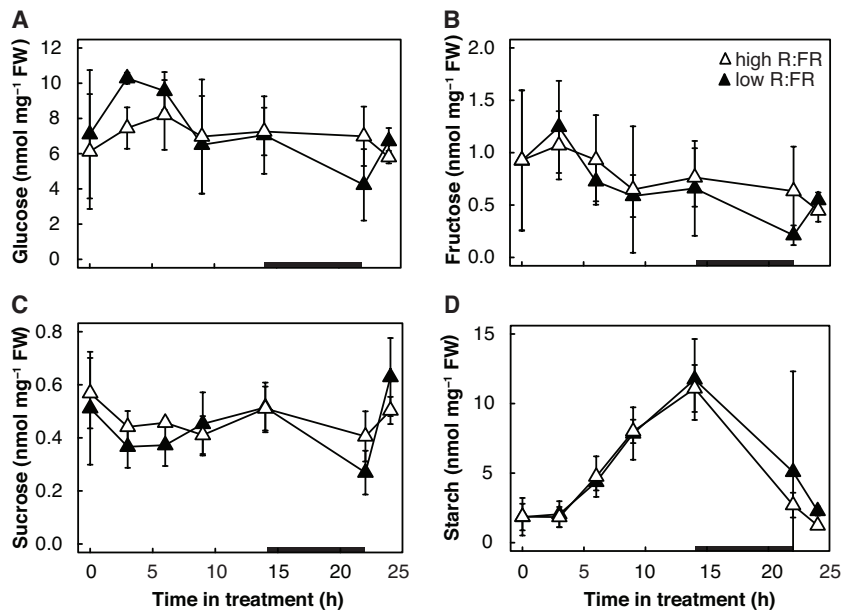


Fig. S3. Metabolite levels in *Brassica rapa* cotyledons during the first 24 h of the shade avoidance response. Five-day-old *B. rapa* seedlings were subjected to high or low R:FR at ZT2 ($t = 0$). Cotyledons were analysed for glucose (A), fructose (B), sucrose (C) and starch (D) levels at the indicated time points after the start of low R:FR, including just before dark and immediately after dawn. Black bar in the x-axis represents the dark period. Data represent means $\pm 2\text{SE}$, $n = 4$ replicates of four pooled seedlings. Corresponding hypocotyl data is shown in Fig. 3.

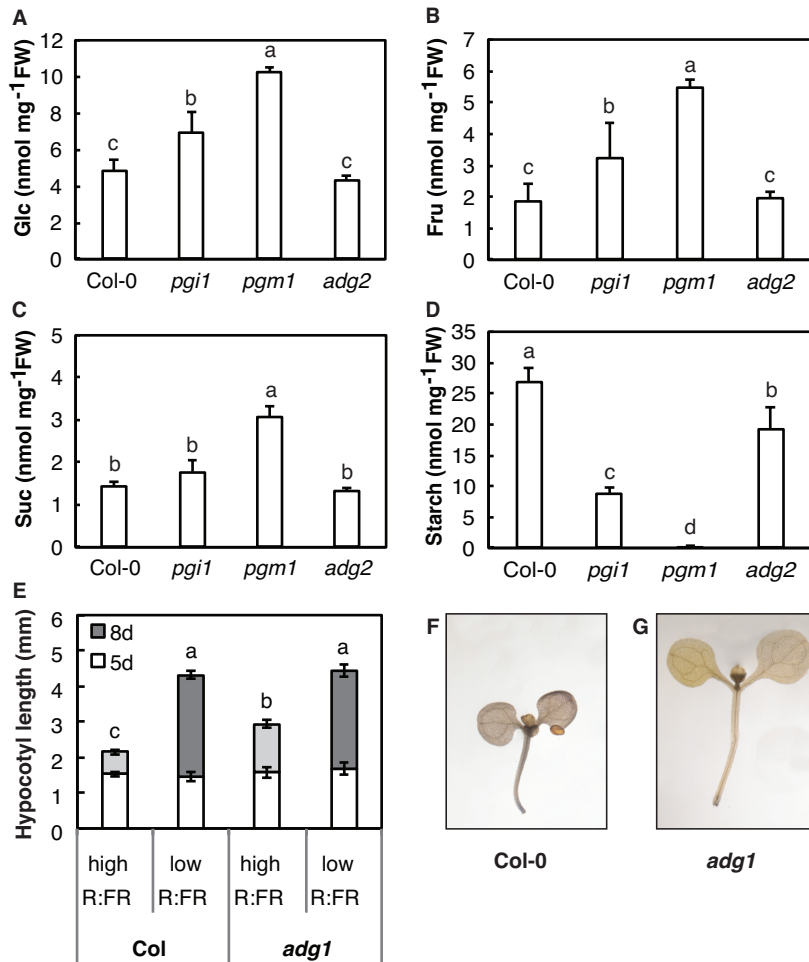


Fig. S4. Metabolite levels in Arabidopsis starch mutant cotyledons. Cotyledons from 8-d-old Arabidopsis seedlings were collected at midday and analysed for glucose (A), fructose (B), sucrose (C) and starch (D) levels. Data represent means \pm 2SE, $n = 4$ replicates of 5 pooled seedlings. Letters indicate significant differences ($p < 0.05$). The *pgi1-1* mutant lacks the plastidial isoform of phosphoglucose isomerase, which interconverts fructose 6-phosphate and glucose 6-phosphate. The *pgm1-1* mutant lacks the plastidial isoform of phosphoglucomutase which interconverts glucose 6-phosphate and glucose 1-phosphate. The *adg2-1* mutant lacks the large, non-catalytic subunit of ADPglucose pyrophosphorylase, which interconverts ATP and glucose 1-phosphate with ADPglucose and inorganic pyrophosphate. (E) Hypocotyl length of the starch mutant *adg1-1* and wild type (Col) grown in long days after 5 d of growth in high R:FR and a subsequent 3 d in high (light grey) or low (dark grey) R:FR. Data represent means \pm 2SE, $n > 20$, Two-Way ANOVA, $p < 0.05$. Starch staining of representative seedlings of Col-0 (F), *adg1-1* (G) seedlings after 7 d in high R:FR harvested at ZT12.

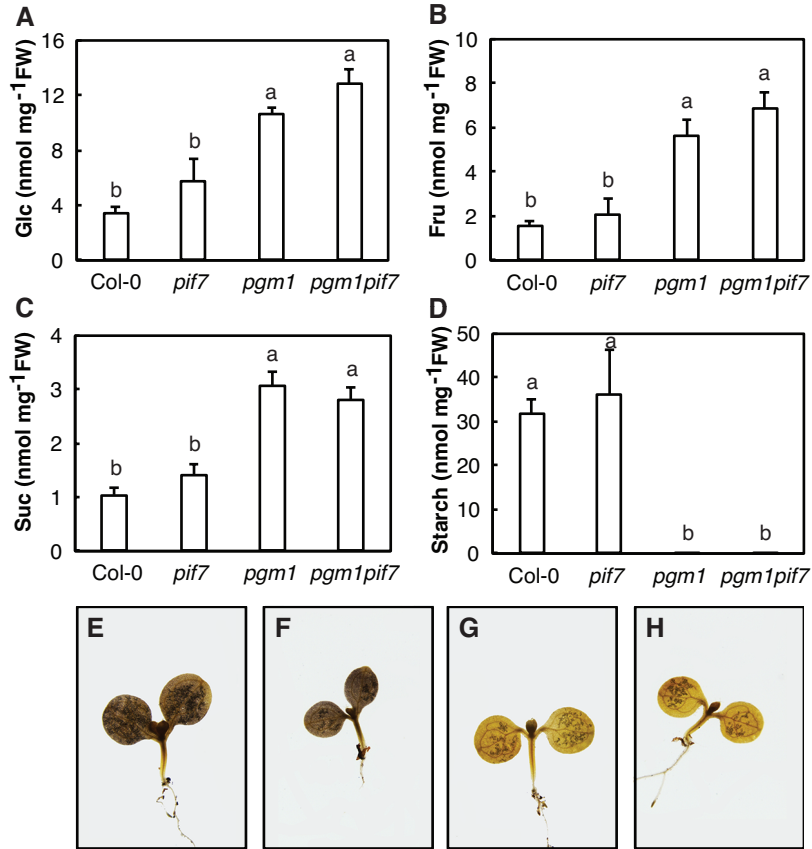


Fig. S5. Metabolite levels in Arabidopsis *pif7* mutant cotyledons. Cotyledons from 8-d-old Arabidopsis seedlings were collected at midday and analysed for glucose (A), fructose (B), sucrose (C) and starch (D) levels. Representative picture of iodine-stained Col-0 (E), *pif7* (F), *pgm1-1* (G) and *pgmpif7* (H) seedlings after 7 d in high R:FR harvested in the middle of the photoperiod. Data represent means \pm 2SE, n = 4 replicates of 5 pooled seedlings. Letters indicate significant differences ($p < 0.05$).

Additional data (separate file)

Dataset S1: Differential gene expression in the hypocotyl between white light and white light with additional far-red (FR) light for genes involved in carbon metabolism pathways.