

Supplementary Material: Unraveling Massive Crocins Transport and Accumulation through Proteome and Microscopy Tools during the Development of Saffron Stigma

Lourdes Gómez-Gómez, Verónica Parra-Vega, Alba Rivas-Sendra, Jose Maria Seguí-Simarro, Rosa Victoria Molina, Claudia Pallotti, Ángela Rubio-Moraga, Gianfranco Diretto, Alicia Prieto and Oussama Ahrazem



Figure S1. Heatmap of chromoplast genes/metabolites involved in saffron apocarotenoid synthesis. Green and red squares represent the values of log₂-transformed relative data with respect to the white stage according to the color scale shown.

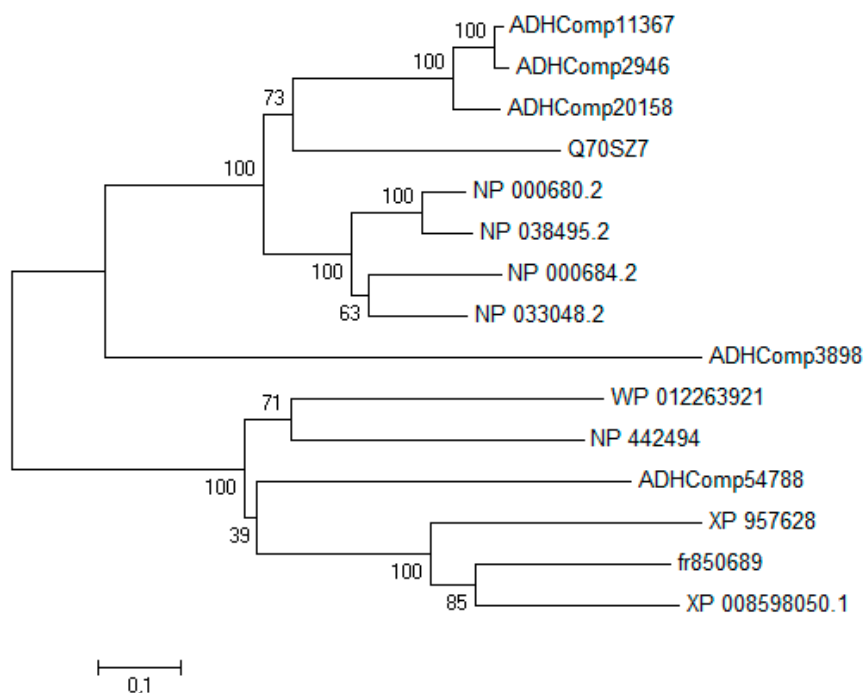


Figure S2. Dendrogram of several ADHs, obtained by using the Neighbor-Joining method. The sequences used were: huADH1A2, NP_000684.2 (*Homo sapiens*); huADH1A1, NP_000680 (*Homo sapiens*); huADH1A3, NP_033048.2 (*Homo sapiens*); ADH1, NP_038495.2 (*Mus musculus*); CsADH, Q70SZ7 (*Crocus sativus*); ADH, WP_010873792 (*Synechocystis sp.*); MaADH, WP_012263921 (*Microcystis aeruginosa*); CarD, fr850689 (*Gibberella fujikuroi*); BbADH3B1 (*Beauveria bassiana*); NcADH (*Neurospora crassa*); ADHComp2946, ADHComp20158, ADHComp3898, ADHComp54788 and ADHComp11367 (*Crocus sativus*).

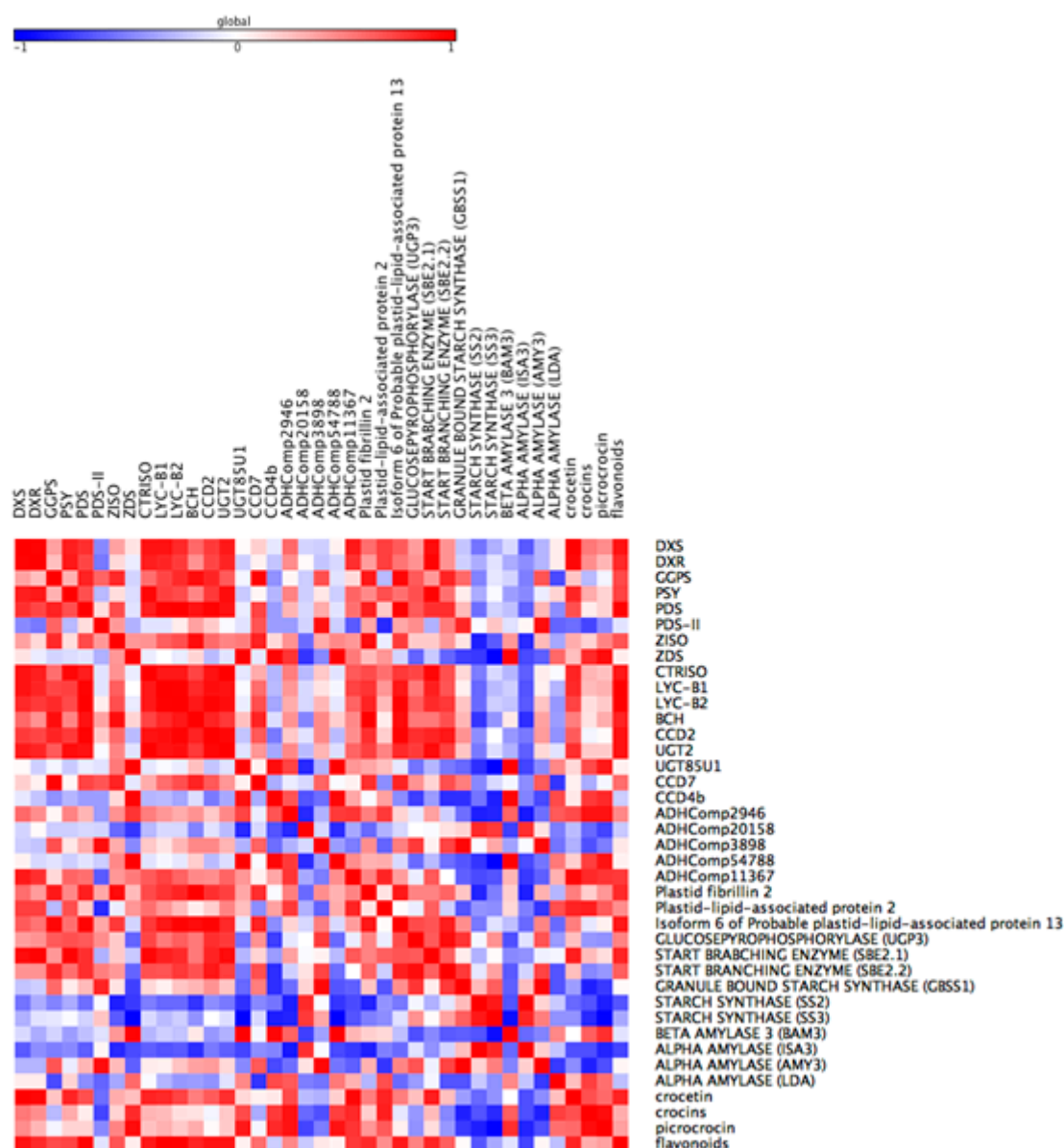


Figure S3. Correlation matrix of chromoplast-related transcripts and metabolites in the saffron stigma. Squares represent the correlation between the gene/metabolite heading the column and the gene/metabolite heading the row. Correlation analysis was carried out by calculating the Pearson correlation coefficient for each data pair and visualized using the GENE-E software. Pearson ($|r|$) values are shown and highlighted with different shades of red (positive correlations) or blue (negative correlations).

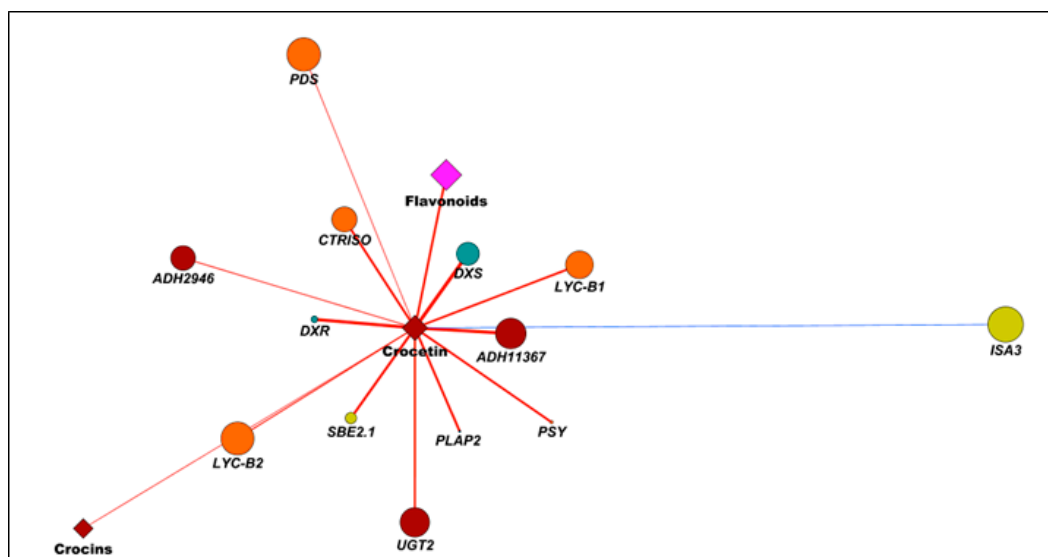


Figure S4. Correlation network of saffron chromoplast-related genes/metabolites using crocetin as central hub. Genes and metabolites are represented as rounds and diamonds. Different colors identify genes/metabolites involved in MEP (turquoise), carotenoid (orange), apocarotenoid (burgundy), plastid development (green), and starch (yellow) biosynthesis. Blue and red edges refer, respectively, to negative and positive correlations; only correlations $>|0.65|$ are shown. Edge width and node size were drawn according, respectively, the Pearson correlation coefficient ($|p|$) and the node strength (ns). Edge length was inversely proportional to $|p|$.

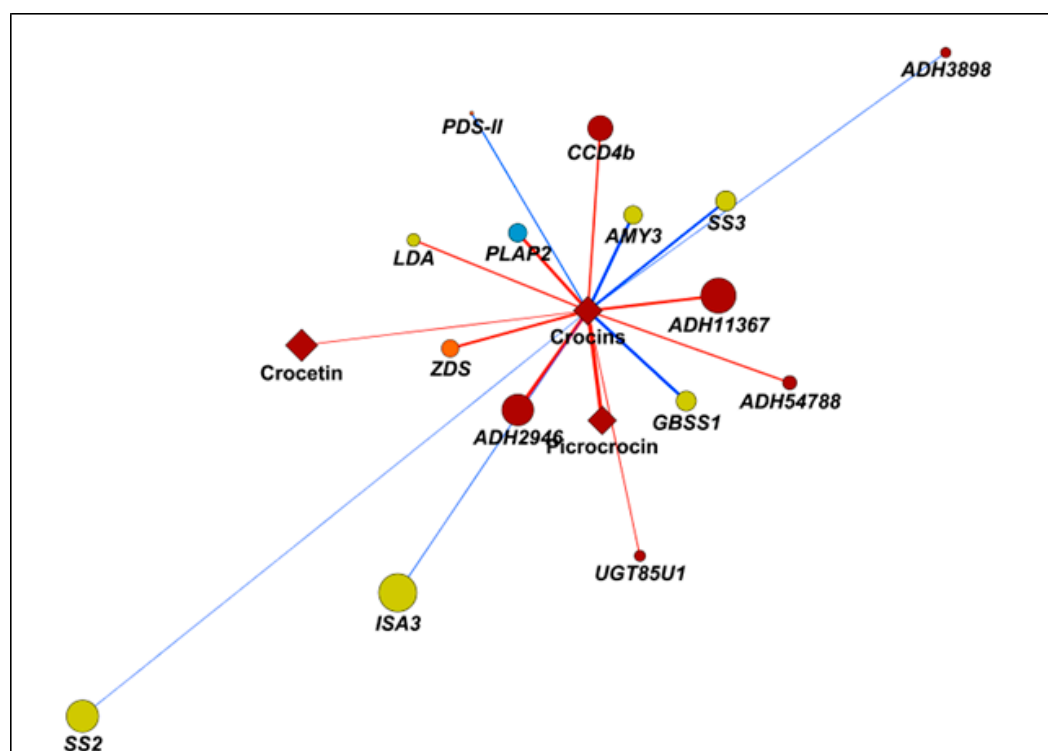


Figure S5. Correlation network of saffron chromoplast-related genes/metabolites using crocins as central hub. Genes and metabolites are represented as rounds and diamonds. Different colors identify genes/metabolites involved in MEP (turquoise), carotenoid (orange), apocarotenoid (burgundy), plastid development (green), and starch (yellow) biosynthesis. Blue and red edges refer, respectively, to negative and positive correlations; only correlations $>|0.65|$ are shown. Edge width and node size were drawn according, respectively, the Pearson correlation coefficient ($|p|$) and the node strength (ns). Edge length was inversely proportional to $|p|$.