

# Supplementary Materials: Proteomic Analysis of *Hylocereus polyrhizus* Reveals Metabolic Pathway Changes

Qingzhu Hua, Qianjun Zhou, Susheng Gan, Jingyu Wu, Canbin Chen, Jiaqiang Li, Yaoxiong Ye, Jietang Zhao, Guibing Hu and Yonghua Qin

**Table S1.** Differentially expressed on genes but not on proteins ( $p$ -value < 0.05, fold change (pro) < 1.3, fold change (RNA) > 2).

Gene Ontology (GO) Classification	Number (No.) Protein
<b>Biological Process (BP)</b>	
GO:0055114//oxidation-reduction process	18
GO:0006184//GTP catabolic process	4
GO:0015937//coenzyme A biosynthetic process	2
GO:0006526//arginine biosynthetic process	2
GO:0006032//chitin catabolic process	1
GO:0016998//cell wall macromolecule catabolic process	1
GO:0006839//mitochondrial transport	1
GO:0009156//ribonucleoside monophosphate biosynthetic process	1
<b>Molecular Function (MF)</b>	
GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	9
GO:0005506//iron ion binding	9
GO:0020037//heme binding	9
GO:0045735//nutrient reservoir activity	3
GO:0004055//argininosuccinate synthase activity	2
GO:0004594//pantothenate kinase activity	2
GO:0008184//glycogen phosphorylase activity	2
GO:0016811//hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	2
GO:0043531//ADP binding	2
GO:0003868//4-hydroxyphenylpyruvate dioxygenase activity	1
GO:0004314//[acyl-carrier-protein] S-malonyltransferase activity	1
GO:0004556//alpha-amylase activity	1
GO:0004568//chitinase activity	1
GO:0008061//chitin binding	1
GO:0030674//protein binding, bridging	1
GO:0051015//actin filament binding	1
GO:0003840//gamma-glutamyltransferase activity	1
GO:0008113//peptide-methionine (S)-S-oxide reductase activity	1
GO:0016701//oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	1
GO:0016790//thiolester hydrolase activity	1
<b>Cellular Component (CC)</b>	
GO:0043234//protein complex	2
GO:0005874//microtubule	2
GO:0009538//photosystem I reaction center	1
GO:0031966//mitochondrial membrane	1
GO:0009522//photosystem I	1
GO:0042555//MCM complex	1

**Table S2.** Differentially expressed on genes but on proteins ( $p$ -value < 0.05, fold change (pro) < 1.3, fold change (RNA) > 2).

KEGG Pathway	No. Protein
ko00330 Arginine metabolism	5
ko00250 Alanine aspartate glutamate metabolism	4
ko00620 Pyruvate metabolism	4
ko00710 Carbon fixation in photosynthetic organisms	4
ko00061 Fatty acid biosynthesis	3
ko00910 Nitrogen metabolism	3
ko01004 Lipid biosynthesis proteins	3
ko00199 Cytochrome P450	2
ko00130 Ubiquinone terpenoid-quinone biosynthesis	2
ko00770 Pantothenate biosynthesis	2
ko04540 Gap junction	2
ko00905 Brassinosteroid biosynthesis	1

**Table S3.** Negative correlation ( $p$ -value < 0.05, FC (pro) > 1.5, FC (RNA) > 2).

GO Classification	No. Protein
<b>Biological Process (BP)</b>	
GO:0042549//photosystem stabilization	1
GO:0006090//pyruvate process	1
GO:0006231//dTTP biosynthetic process	1
GO:0006545//glycine process	1
GO:0006869//lipid transport	1
GO:0009165//nucleotide biosynthetic process	1
<b>Molecular Function (MF)</b>	
GO:0003677//DNA binding	4
GO:0008234//cysteine-type peptidase activity	2
GO:0009055//electron carrier activity	2
GO:0003756//protein disulfide activity	1
GO:0005337//nucleoside transmembrane transporter activity	1
GO:0008146//sulfotransferase activity	1
GO:0050242//pyruvate, phosphate dikinase activity	1
GO:0004146//dihydrofolate activity	1
GO:0004799//thymidylate activity	1
GO:0004866//endopeptidase inhibitor activity	1
GO:0004869//cysteine-type endopeptidase inhibitor activity	1
GO:0016671//oxidoreductase activity	1
<b>Cellular Component (CC)</b>	
GO:0009279//cell outer membrane	1
GO:0009654//oxygen evolving complex	1
GO:0019898//extrinsic to membrane	1
GO:0009523//photosystem II	1

**Table S4.** Negative correlation ( $p$ -value < 0.05, FC (pro) > 1.5, FC (RNA) > 2).

KEGG Pathway	No. Protein
ko04142 Lysosome	4
ko04145 Phagosome	2
ko04210 Apoptosis	1
ko04115 p53 signaling pathway	1
ko04712 Circadian plant	1

Table S5. Gradient used for grading of polypeptides.

Time (min)	0	2	17	29	30	31	36	37	57
Buffer A (%)	96	92	80	65	55	5	5	96	96
Buffer B (%)	4	8	20	35	45	95	95	4	4

Table S6. Gradient used for LC-MS/MS.

Time (min)	0	5	6	48	62	65	70	70.5	90
Buffer A (%)	97	97	94	83	70	20	20	97	97
Buffer B (%)	3	3	6	17	30	80	80	3	3

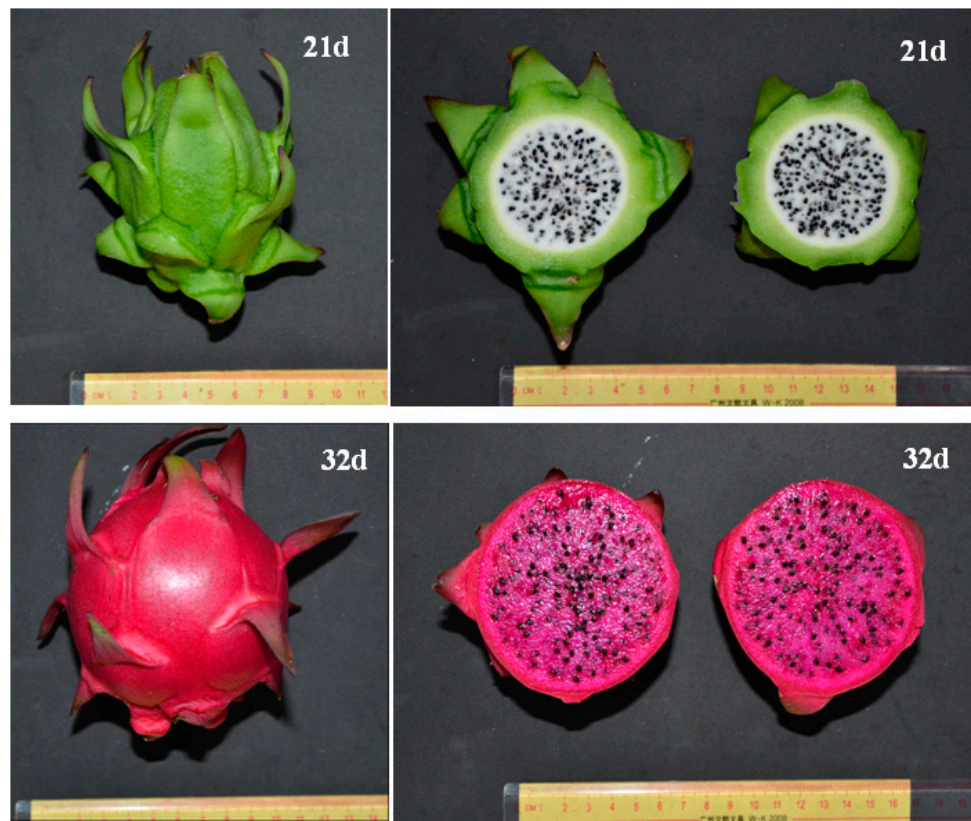


Figure S1. Pictures of pitaya fruits (entire and cut in to observe internal color) collected on the 21st day (white pulp) and 32rd day (red white).