

Characterization of starch in *Cucurbita moschata* germplasms throughout fruit development

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Table S1. List of primers used for qRT-PCR.

Gene	Primer sequence (5'-3')
<i>Actin-F</i>	CGGCCATTGAGAAAAGCTACGAAC
<i>Actin-R</i>	CCCACCACTGAGGACGATGTTACCA
<i>PGM-F</i>	GCTGGAGCAACTGTAAGAA
<i>PGM-R</i>	GGACAAACATAATGCCAAA
<i>AGPase-F</i>	ATCACTGTAGCTGCATTACCC
<i>AGPase-R</i>	TCAACCTTCATCGCTTCA
<i>SS-F</i>	GGAATGGCAGGTAGGTT
<i>SS-R</i>	ATCGTCCGCAGAGTTAT
<i>GBSS-F</i>	TTGCAGGACTGCCAGTAGGA
<i>GBSS-R</i>	AGAACATCACCAAGCCCAC
<i>SBE-F</i>	TGTTGAAAGAGGGATTGCG
<i>SBE-R</i>	TCATAACTCCACCCGTTGC
<i>DBE-F</i>	GACTCGCACATCACCACATC
<i>DBE-R</i>	TTTCATTGTATGGCGGCTG

<i>SP</i> -F	GGGCCACTACAGTTGGTTG
<i>SP</i> -R	TCTCCACATTGCCCATCT

Table S2. Genes involved in starch metabolism.

Gene abbreviation	Unigene ID
<i>PGM</i>	Unigene0002629, Unigene0037284
<i>AGPase</i>	Unigene0047165, Unigene0040458, Unigene0040454, Unigene0039030, Unigene0031387, Unigene0016505, Unigene0003314
<i>GBSS</i>	Unigene0046257, Unigene0043814, Unigene0035250, Unigene0035248, Unigene0029421
<i>SBE</i>	Unigene0023284, Unigene0038340, Unigene0038341, Unigene0052676, Unigene0004574, Unigene0038339, Unigene0001527, Unigene0022306
<i>SS</i>	Unigene0001083, Unigene0007832, Unigene0021341, Unigene0021342, Unigene0040073, Unigene0040074, Unigene0040075
<i>DBE</i>	Unigene0053977, Unigene0027020, Unigene0032724, Unigene0032725
<i>SP</i>	Unigene0008725, Unigene0008726, Unigene0011332, Unigene0011333, Unigene0012033, Unigene0012034, Unigene0014537, Unigene0015199, Unigene0024594, Unigene0043760, Unigene0043761, Unigene0008725

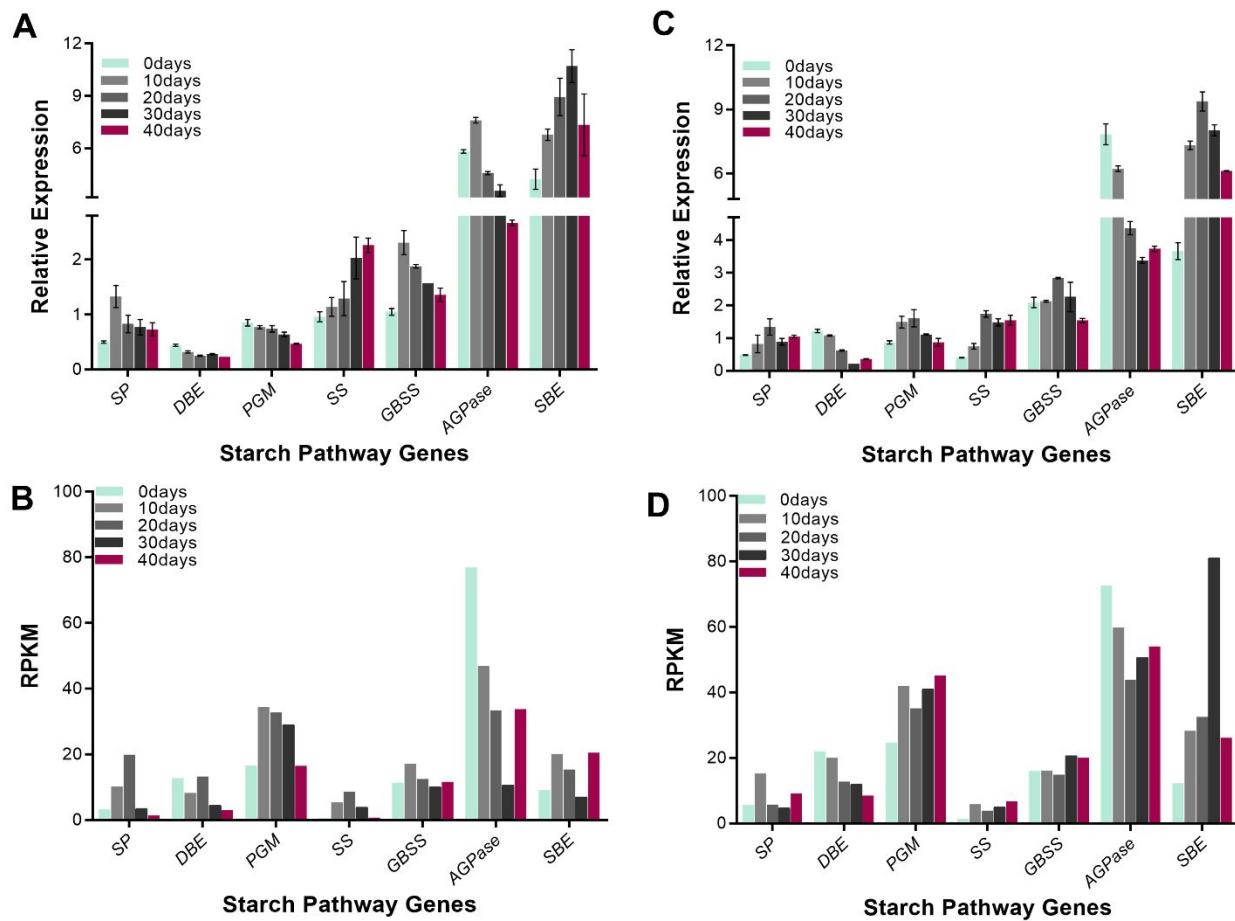


Figure S1. Relative expression and RPKM of different genes from starch pathway.

Samples were collected at different stages of fruit development. RNA was extracted and cDNA was synthesized for qRT-PCR. Actin was used as internal control. **(A)** Relative expression of genes from starch pathways in CMO-E, **(B)** RPKM values of genes from starch pathways in CMO-E, **(C)** Relative expression of genes from starch pathways in CMO-X and **(D)** RPKM values of genes from starch pathways in CMO-X. Results are the mean values from three independent experiments. Vertical bars represent SD.

Table S3. Sugar contents during different developmental stages of *C. moschata* fruit.

Days	Fructose (mg/g DW)		Glucose (mg/g DW)		Sucrose (mg/g DW)	
	CMO-E	CMO-X	CMO-E	CMO-X	CMO-E	CMO-X
0	49.88±1.76	51.06±1.64	89.86±3.15	57.48±2.90	10.88±1.86	7.9±0.36
5	93.04±2.88	85.8±4.19	108.39±3.01	60.58±7.06	11.75±1.32	8.77±0.03
10	105.9±4.13	84.89±5.26	139.97±7.23	70.35±5.91	19.13±1.05	14.04±0.01
20	107.4±8.81	103.72±11.43	154.77±7.50	75.53±6.19	38.28±2.14	29.73±0.24
30	102.6±6.08	38.44±6.03	153.94±6.52	29.51±4.09	115.46±10.96	165.65±11.12
40	75.59±4.49	31.52±3.00	133.92±5.26	27.5±4.20	165.2±9.59	208.59±11.41