Supplementary materials



Figure S1. Trait for flesh color and cream-colored spots on the pericarp. Flesh color of mature fruits at harvest (ca. three months after transplanting) in the parental lines, **(A)** 'Bí Hồ Lô TN 6 (TN 6)' and **(B)** 'Shishigatani'-K. **(C)** Presence/absence of cream-colored spots on the pericarp of immature fruits. A single F2 individual is shown as a representative of fruit with (left) or without spots (right). Scale bar, 5 cm.



Figure S2. Schematic representation of the measurement of fruit-size related traits. Up: largest circumference on the upper part; Mid: smallest circumference on the middle part; and Low: largest circumference on the lower part.



0.5 1 1.5 2 2.5 3 3.5 4

12 14 16 18 20 22 24 26













Figure S3. Frequency distributions of the traits scored for the F_2 population of 'TN 6' × 'Shishigatani'-K. Trait code names are shown on the top of each histogram (A–Q). The xand y-axes indicate trait value and individual number, respectively. The black bars represent data of the F_2 population. Filled, gray, and open arrows indicate average values of 'TN 6', F_1 , and 'Shishigatani'-K, respectively.



10a	11	12	13a	14a	15a
0.0 0.55701Chr10 11.9 055701Chr10 13.1 055930Chr10 13.4 055930Chr10 21.4 055903Chr10 25.5 056559Chr10 25.5 056590Chr10 32.7 056872Chr10 39.3 057230Chr10 51.2 057230Chr10 51.2 057230Chr10 61.6 057296Chr10 67.8 057502Chr10 055565Chr10 055565Chr10 055565Chr10 055565Chr10 055565Chr10 055565Chr10 055565Chr10 055656Chr10 055656Chr10 055656Chr10 055656Chr10 055656Chr10 055656Chr10 054644Chr10 055665Chr10 00306Chr10 20.9 00306Chr10 05507Chr10 05807	0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.0 065438Chr12 14.5 065438Chr12 18.7 065382Chr12 19.0 069328Chr12 41.8 069328Chr12 41.8 069328Chr12 53.6 067582Chr12 55.2 067592Chr12 56.1 06747Chr12 58.7 067313Chr12 58.7 067313Chr12 58.4 067313Chr12 58.4 067313Chr12 58.4 067313Chr12 58.7 0687312Chr12 98.5 069767Chr12 93.5 069708Chr12 93.5 069718Chr12 99.7 06592Chr12 113.5 069322Chr12	0.0 11.9 12.5 12.5 12.7 12.7 12.7 12.7 12.7 12.7 12.7 12.7 12.7 13.5 10.70085Chr13 13.5 10.70085Chr13 13.5 10.70085Chr13 13.5 10.70085Chr13 13.5 10.70085Chr13 13.5 10.70085Chr13 13.5 10.70085Chr13 13.5 10.72085Chr13 13.5 10.72085Chr13 13.5 10.72085Chr13 13.5 10.72085Chr13 13.5 10.72085Chr13 13.5 10.72085Chr13 13.5 10.72085Chr13 13.5 10.72085Chr13 13.5 10.72085Chr13 13.5 10.7286SChr13 13.5 10.5	0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
16	17	18	19a		
0.0 085059Chr16 10.4 085224Chr16 11.1 085213Chr16 23.1 085492Chr16 29.4 085881Chr16 40.4 085995Chr16 47.9 086128Chr16 49.8 08612Chr16 55.8 086817Chr16 55.3 086618Chr16 69.9 086974Chr16 73.3 087083Chr16 74.4 087141Chr16 74.4 087357Chr16	0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.0 0.0 093884Chr18 15.9 093548Chr18 20.8 093293Chr18 35.4 092887Chr18 38.7 092829Chr18 38.7 092829Chr18 48.5 097377Chr18 67.1 096900Chr18 67.8 096900Chr18 67.8 096900Chr18 67.8 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 0965280Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 096900Chr18 69.1 09690Chr18 69.1 09690Chr18 69.1 096900Chr18 69.1 09690Chr18 69.1 096900Chr18 69.1 09690Chr18 69.1 09690Chr18 69.1 09690Chr18 69.1 095280Chr18 69.1 095280Chr18 69.1 095280Chr18 69.1 095280Chr18 69.1 0951367078	0.0 1006982chr19 8.5 1000300chr19 13.0 1000480chr19 13.0 27.8 0980840chr19 34.1 0984780chr19 34.4 0994020chr19 34.4 0994020chr19 35.2 0998410chr19 57.8 1000400chr19 57.8 0998410chr19 57.5 CMTm170 19b	40.8 42.1 078094Chr14 47.2 077810Chr14 47.7 078219Chr14 47.7 078219Chr14 078219Chr14 47.7 078219Chr14 078219Chr14 1025370 12.8 1025370 14.1 1025380 21.9 1027860 43.0 1034080 45.6 1034080 60.1 1040850	Chr20 Chr20 Chr20 Chr20 Chr20 Chr20 Chr20-CAPS
93.4 087691Chr16 97.3 087772Chr16		86.77 095135Chr18 87.1 095129Chr18 87.8 095083Chr18	0.0 099929Chr19 2.0 099931Chr19	60.1 1040880 60.7 1044080	onr20
111.5 112.9 088235 088235		91.7 91.7 904895 cm 18 101.3 108.5 094896 cm 18 108.5 094224 cm 18 127.5 093016 cm 18 138.8 097211 cm 18 143.4 095261 cm 18 144.0 094557 cm 18 146.4 096556 cm 18	19c 0.0 100815Chr19 7.2 100819Chr19 28.3 CMTm144	80.0 80.0 1044460 80.0 1044460 1044460 1044460 1044460 1044460 1044460 1044460 1044460 1044460 1044460 1044460 1044460 1044460 1044460 1044460 1044460 1044460 104677 84.2 1048377 88.0 1046377 1022000 1023410 1023410	Chr20 Chr20 Chr20 Chr20 Chr20

Figure S4. A linkage map of the F₂ population ('TN 6' × 'Shishigatani'-K). The number of each linkage group (LG) refers to that of the *C. moschata* pseudochromosome [4]. Marker names and genetic distance (cM) are indicated on the right and left of each LG, respectively. SSR, CAPS, and dCAPS markers are indicated by bold type. The phenotype trait marker (*Mottled skin*) on LG 3 is italicized. Other markers are RAD markers, in which the number of pseudochromosomes assigned to the *C. moschata* genome [4] is presented as Chrxx. The positions of the QTLs detected in this study are indicated by colored boxes. Scale bar, 10 cM.

Trait	Abbreviation	Scale	Range in F2	Mean ± SD in F2	Mean ± SD in F1	Mean ± SD in 'TN 6'	Mean ± SD in
			$(n = 88)^4$	$(n = 88)^4$	$(n = 3)^4$	$(n = 4)^4$	'Shishigatani'-K $(n = 4)^4$
Flowering trait							
Flowering time of male flower	M flwr	Days after transplant to the opening of the first male flower	36-63	51.9 ± 4.3	53.0 ± 0.0	55.0 ± 3.1	48.3 ± 0.8
Flowering time of female flower	F flwr	Days after transplant to the opening of the first female flower	42-67	53.2 ± 5.5	57.0 ± 5.6	55.0 ± 2.8	52.8 ± 2.0
Fruit trait							
Degree of rib on the surface	Rib	0–3 (no rib = 0, intermediate = 1–2, deep rib = 3)	0.00-3.00	0.823 ± 0.535	0.750 ± 0.000	0.286 ± 0.247	0.800 ± 0.245
Degree of wartiness on the surface	Wart	0–3 (no wart = 0, intermediate = 1–2, heavy wart = 3)	0.00 - 2.50	0.794 ± 0.630	1.042 ± 0.059	0.071 ± 0.175	1.200 ± 0.678
Fresh weight	Fw	kg	0.66-3.66	1.696 ± 0.662	1.826 ± 0.844	0.910 ± 0.252	1.311 ± 0.536
Height	Н	cm	13.63-24.60	18.477 ± 2.591	18.356 ± 2.885	14.750 ± 0.726	19.043 ± 1.900
Circumference on upper part	Up	Largest circumference on the upper part (cm) ³	22.10-54.50	36.623 ± 7.650	36.406± 13.689	29.238 ± 4.147	29.943 ± 7.275
Circumference on middle part	Mid	Smallest circumference on the middle part (cm) ³	20.40-52.60	32.985 ± 6.263	32.506± 10.199	28.4000 ± 4.155	27.386 ± 6.152
Circumference on lower part	Low	Largest circumference on the lower part (cm) ³	30.13-65.00	42.859 ± 6.356	46.317 ± 4.266	35.775±5.353	43.457 ± 5.352
Ratio of circumferences on upper/middle parts	Up/Mid	-	0.879 - 1.512	1.1179 ± 0.1329	1.102 ± 0.130	1.0197 ± 0.0277	1.0938 ± 0.0213
Ratio of circumferences on lower/middle parts	Low/Mid	-	0.784 - 1.752	1.3190 ± 0.1703	1.510 ± 0.409	1.1624 ± 0.0509	1.6757 ± 0.3234
Lightness or darkness of flesh color	L*		57.753-79.693	66.8586 ± 4.0928	62.5939 ± 1.6696	63.0429 ± 1.5209	73.0713 ± 3.5161
Red/green coordinate of flesh color	a∗	-	7.230-28.937	18.9036 ± 5.3388	23.4222± 4.4406	27.4225 ± 1.8181	12.2292 ± 7.0320
Yellow/blue coordinate of flesh color	b *	-	48.650-76.982	68.5265 ± 4.8773	72.3617 ± 1.3993	70.2913 ± 1.9495	57.4887 ± 8.0470
Chroma (color saturation or intensity) of flesh color	С*	-	55.617-80.141	71.4670 ± 5.0668	76.1053 ± 2.6971	75.4123 ± 0.9686	58.6977 ± 10.0104
¹ Hue angle (relative amounts of redness and	hue	0°–90°	68.340 - 84.404	74.7676 ± 3.7759	72.1148 ± 2.8586	68.4326 ± 0.9433	78.9385 ± 4.6124
yellowness) of flesh color ²							
Brix	Brix	%	9.39-20.73	14.508 ± 2.221	14.243 ± 21.221	18.940 ± 2.226	14.000 ± 3.006

Table S1. List of traits analyzed, and the phenotypic values of the F2 population and the parental lines.

 $\sqrt{(a^*)^2 + (b^*)^2}$. As chromaticity increases, a color becomes more vivid. As it decreases, a color becomes more dull

² tan⁻¹(b */a *). An angular measurement, in which 0° = red and 90° = yellow.

³ See Figure S2 for representative phenotype of each scale

⁴ *n*: number of plants investigated.

SSR locus	Primer sequence (5'-to-3')	LG ¹	Chr ²
CMTm7	Forward: AACCAAACTCCGGCAAGA	p8	10
	Reverse: GTTCTCTCCGTTCAGGATGG		
CMTm48	Forward: AAGCCTTTGGGGGACCTTTAC	p2	4
	Reverse: TTGAAACCTTCAAACAAGAAATTG		
CMTm77	Forward: AACACTCGGCCACAACATC	p8	10
	Reverse: CTCCTTGTAAAACGGGTTGC		
CMTm144	Forward: ACATGGGCATACCTCGAATC	p7	19
	Reverse: CACCTGGCTGTTTTGTCTGA		
CMTm170	Forward: TCAGACCCACTCCCATGAAC	p7	19
	Reverse: AGCGAACACGTGAAAACGTC		
CMTm187	Forward: ATCGGTGAGTCCCAAAAATG	p18	9
	Reverse: ATCACAAAGCGGGAAAACAC		
CMTm214	Forward: TGCTTTGATCAGTGAGCAGT	p18	9
	Reverse: GGATGTACTCTCCGGACTTTC		
CMTm232b	Forward: AGAAAGAAATAAGGAACCCACAG	p10a	1
	Reverse: CGTCTCGCAATTCTTCAACT		
CMTmC61	Forward: TTATTGTCGTCGCTCTGCAC	p20	14
	Reverse: TCCGGAACTATTATAACAACGACA		
CMTp88	Forward: ACCTACCGTCACACCCACAT	p5	4
	Reverse: CCACCTGAAAACAGGGCTAA		
CMTp125	Forward: CTTGTTCCGCAGCATCAG	p16	11
	Reverse: AGTGAGAGGGAGACGCAAAG		
CMTp216b	Forward: CGTTGGCCATGGAAGTCT	p5	No hit
	Reverse: CCCTATATGAGACCGCGAGA		

Table S2. List of *Cucurbita* simple sequence repeat (SSR) markers localized on the linkage map in this study

¹Linkage group (LG), on which each SSR locus was localized in the previous report [8].

 2 Pseudochromosome (chr), from which each SSR locus was found in the *C. moschata* whole genome [4].



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