G3 · Genes | Genomes | Genetics

Title: **The mosaic (MSC) mutants of cucumber: a method to produce knock-downs of mitochondrial transcripts**

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Sequence reads have been deposited into Genbank Sequence Read Archive SRP051771 (release date June 1, 2015). IRB number for recombinant DNA research at the University of Wisconsin is SC12-008R.

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Table S1 Low-coverage regions in the mt DNA of the mitochondrial mutant MSC3, 12, and 16 as compared to the progenitor, wild-type inbred B.

Mutant Line	Region (bp) Start	End	Size (bp)	Chromosome*	Annotation
MSC3	392,242	441,105	48,863	MC	*nad5ex4* (NADH dehydrogenase subunit 5 C-terminus); trnW-CCA (tRNA-Trp); *atp4* (ATPase subunit 4) and chloroplast-like DNA
	585,075	636,619	51,544	MC	
	1	31,162	31,161	83.8 kb	
		Tota	131,568	7.8%	
MSC12	149,606	161,705	12,099	MC	
	195,676	267,406	71,730	MC	*rps7* (ribosomal protein S7)
	347,550	362,669	15,119	MC	JLV5-Del (Lilly *et al.* 2001) was identified in MSC16)
	567,690	568,518	828	MC	
	572,554	622,942	50,388	MC	
	911,926	917,574	5,648	MC	
	22,564	25,406	2,842	44.8 kb	
	1	83,817	83,816	83.8 kb	
		Total	242,470	14.4%	
MSC16	149,606	161,706	12,100	MC	
	195,676	283,618	87,942	MC	*rps7* (ribosomal protein S7)
	347,550	362,669	15,119	MC	JLV5-Del (Lilly *et al.* 2001)
	567,711	568,451	740	MC	
	572,554	622,942	50,388	MC	
	911,926	917,574	5,648	MC	
	22,564	25,270	2,706	44.8 kb	
	1	83,817	83,816	83.8 kb	
		Total	258,459	15.3%	

MC = Master chromosome of 1.6 megabases (Mb).

44.8 kb = Extra-chromosome of 44.8 kb

83.8 kb = Extra-chromosome of 83.8 kb

*All locations are based on the mitochondrial sequence of Alverson *et al.* (2011).

Table S2 Fold change of copy number of mitochondrial and nuclear genes in wild-type inbred B and mitochondrial mutants MSC3, 12 and 16.

Gene	Line	Average Fold-change	S.E.	t-test
gadph ^{n}	Line B	0.89	0.06	CONTROL
gadph ^{n}	MSC3	0.86	0.10	0.4059
gadph ^{n}	MSC12	0.79	0.05	0.1267
gadph ^{n}	MSC16	0.83	0.05	0.2371
actin3 ^{n}	Line B	1.00	0.06	CONTROL
actin3 ^{n}	MSC3	1.21	0.08	0.0574
actin3 ^{n}	MSC12	1.05	0.04	0.2899
actin3 ^{n}	MSC16	1.08	0.08	0.2600
nad9	Line B	1.00	0.02	CONTROL
nad9	MSC3	1.38	0.22	0.0782
nad9	MSC12	2.60	0.25	0.0016*
nad9	MSC16	1.88	0.16	0.0031*
cob	Line B	1.00	0.02	CONTROL
cob	MSC3	1.29	0.05	0.0034*
cob	MSC12	1.47	0.20	0.0400*
cob	MSC16	1.32	0.08	0.0096*
rps7	Line B	1.02	0.15	CONTROL
rps7	MSC3	0.92	0.16	0.3371
rps7	MSC12	0.12	0.04	0.0021*
rps7	MSC16	0.12	0.05	0.0023*
ccmFc	Line B	1.00	0.04	CONTROL
ccmFc	MSC3	1.31	0.16	0.0715
ccmFc	MSC12	2.09	0.32	0.0143*

ccmFc	MSC16	2.38	0.75	0.0716
nad7	Line B	1.00	0.07	CONTROL
nad7	MSC3	1.04	0.12	0.4124
nad7	MSC12	1.23	0.18	0.1535
nad7	MSC16	1.08	0.12	0.2998
ccmB	Line B	1.05	0.23	CONTROL
ccmB	MSC3	1.30	0.21	0.2366
ccmB	MSC12	1.68	0.17	0.0482*
ccmB	MSC16	1.59	0.28	0.1039
atp1	Line B	1.03	0.16	CONTROL
atp1	MSC3	1.16	0.14	0.2794
atp1	MSC12	2.22	0.26	0.0089*
atp1	MSC16	2.42	0.24	0.0042*
cox1	Line B	1.01	0.10	CONTROL
cox1	MSC3	1.20	0.25	0.2568
cox1	MSC12	1.71	0.17	0.0116*
cox1	MSC16	2.04	0.28	0.0127*
nad6	Line B	1.01	0.10	CONTROL
nad6	MSC3	1.27	0.14	0.0985
nad6	MSC12	2.15	0.17	0.0023*
nad6	MSC16	2.38	0.25	0.0039*
ubqc ^{n}	Line B	1.00	0.00	CONTROL
ubqc ^{n}	MSC3	1.11	0.12	0.2041
ubqc ^{n}	MSC12	1.05	0.09	0.2886
ubqc ^{n}	MSC16	1.03	0.10	0.3820
sdh3	Line B	1.04	0.25	CONTROL

sdh3	MSC3	1.23	0.07	0.2100
sdh3	MSC12	2.09	0.09	0.0048*
sdh3	MSC16	2.16	0.36	0.0265*
nad3	Line B	1.02	0.16	CONTROL
nad3	MSC3	1.43	0.16	0.0741
nad3	MSC12	2.00	0.08	0.0029*
nad3	MSC16	1.88	0.33	0.0402*
rrn5	Line B	1.01	0.12	CONTROL
rrn5	MSC3	1.05	0.10	0.4057
rrn5	MSC12	1.17	0.00	0.1311
rrn5	MSC16	1.26	0.05	0.0683
rpl2	Line B	1.00	0.04	CONTROL
rpl2	MSC3	1.00	0.08	0.4799
rpl2	MSC12	1.86	0.07	0.0003*
rpl2	MSC16	2.10	0.12	0.0006*
rps3	Line B	1.01	0.12	CONTROL
rps3	MSC3	1.40	0.16	0.0660
rps3	MSC12	2.31	0.20	0.0025*
rps3	MSC16	2.53	0.20	0.0015*
rpl5	Line B	1.00	0.07	CONTROL
rpl5	MSC3	1.38	0.19	0.0710
rpl5	MSC12	2.05	0.32	0.0171*
rpl5	MSC16	2.86	0.34	0.0030*
nad5	Line B	1.03	0.19	CONTROL
nad5	MSC3	0.36	0.11	0.0194*
nad5	MSC12	1.85	0.39	0.0661

nad5	MSC16	1.47	0.20	0.0931
atp4	Line B	1.03	0.19	CONTROL
atp4	MSC3	0.43	0.04	0.0182*
atp4	MSC12	1.69	0.31	0.0724
atp4	MSC16	1.88	0.19	0.0170*
rrnS	Line B	1.01	0.12	CONTROL
rrnS	MSC3	1.06	0.11	0.4046
rrnS	MSC12	1.29	0.06	0.0556
rrnS	MSC16	1.39	0.11	0.0432*
aox ^{nm}	Line B	1.00	0.07	CONTROL
aox ^{nm}	MSC3	1.21	0.22	0.2082
aox ^{nm}	MSC12	1.00	0.07	0.4992
aox ^{nm}	MSC16	1.24	0.10	0.0640
porin ^{nm}	Line B	1.16	0.47	CONTROL
porin ^{nm}	MSC3	34.74	33.31	0.1853
porin ^{nm}	MSC12	0.80	0.20	0.2589
porin ^{nm}	MSC16	2.34	1.03	0.1788
cox2	Line B	1.00	0.07	CONTROL
cox2	MSC3	1.12	0.30	0.3596
cox2	MSC12	1.79	0.14	0.0040*
cox2	MSC16	1.95	0.04	0.0002*
rps13	Line B	1.04	0.21	CONTROL
rps13	MSC3	1.33	0.23	0.1968
rps13	MSC12	2.19	0.00	0.0025*
rps13	MSC16	2.05	0.30	0.0253*
mttb	Line B	1.06	0.26	CONTROL

mttb	MSC3	1.42	0.11	0.1383
mttb	MSC12	2.46	0.06	0.0033*
mttb	MSC16	2.26	0.23	0.0130*
rps10	Line B	1.00	0.08	CONTROL
rps10	MSC3	1.12	0.05	0.1431
rps10	MSC12	2.02	0.24	0.0080*
rps10	MSC16	2.25	0.13	0.0007*
atp8	Line B	1.00	0.04	CONTROL
atp8	MSC3	1.15	0.09	0.0998
atp8	MSC12	1.55	0.04	0.0003*
atp8	MSC16	1.82	0.04	0.0001*
rrnL	Line B	1.00	0.04	CONTROL
rrnL	MSC3	1.25	0.15	0.0952
rrnL	MSC12	3.03	0.68	0.0207*
rrnL	MSC16	2.25	0.53	0.0400*

* Significant difference between an MSC mutant for a given mitochondrial or nuclear gene compared to wild-type B at $\alpha = 0.05$, Student's t-test.

[n] Nuclear-encoded gene with no function in the mitochondria.

[nm] Nuclear-encoded mitochondrially targeted gene.

Table S3 Fold change in transcript levels of mitochondrial and nuclear genes from wild-type inbred B and mitochondrial mutants MSC3, 12 and 16.

Gene	Line	Average Fold-change	S.E.	t-test
rps7	Line B	1.12	0.18	CONTROL
rps7	MSC3	2.32	0.34	0.0044*
rps7	MSC12	0.21	0.07	0.0005*
rps7	MSC16	0.36	0.08	0.0016*
rrn5	Line B	1.05	0.12	CONTROL
rrn5	MSC3	1.67	0.49	0.1246
rrn5	MSC12	1.15	0.19	0.3181
rrn5	MSC16	1.16	0.16	0.2837
rpl2	Line B	1.09	0.37	CONTROL
rpl2	MSC3	1.76	0.47	0.0148*
rpl2	MSC12	2.00	0.29	0.0087*
rpl2	MSC16	2.00	0.31	0.0118*
nad3	Line B	1.31	0.32	CONTROL
nad3	MSC3	2.06	0.46	0.1028
nad3	MSC12	2.92	0.46	0.0041*
nad3	MSC16	4.75	1.14	0.0087*
sdh3	Line B	1.08	0.16	CONTROL
sdh3	MSC3	2.08	0.48	0.0395*
sdh3	MSC12	2.05	0.43	0.0256*
sdh3	MSC16	1.85	0.42	0.0583
nad6	Line B	1.23	0.28	CONTROL
nad6	MSC3	1.55	0.31	0.2295
nad6	MSC12	2.54	0.64	0.0379*

nad6	MSC16	2.57	0.66	0.0435*
ubqc [n]	Line B	1.09	0.35	CONTROL
ubqc [n]	MSC3	1.51	0.80	0.1613
ubqc [n]	MSC12	1.11	0.21	0.4583
ubqc [n]	MSC16	1.36	0.25	0.1873
nad9	Line B	1.43	0.48	CONTROL
nad9	MSC3	2.13	0.40	0.1391
nad9	MSC12	4.40	1.11	0.0122*
nad9	MSC16	5.21	1.71	0.0309*
cob	Line B	1.19	0.25	CONTROL
cob	MSC3	1.92	0.26	0.0301*
cob	MSC12	2.13	0.34	0.0156*
cob	MSC16	3.13	0.71	0.0142*
actin3 [n]	Line B	3.46	2.54	CONTROL
actin3 [n]	MSC3	3.15	0.86	0.4545
actin3 [n]	MSC12	2.88	1.41	0.4222
actin3 [n]	MSC16	3.99	0.87	0.4244
rps10	Line B	1.19	0.50	CONTROL
rps10	MSC3	1.90	1.32	0.1541
rps10	MSC12	1.89	0.41	0.0790
rps10	MSC16	2.64	0.53	0.0143*
rps3	Line B	1.09	0.17	CONTROL
rps3	MSC3	1.21	0.20	0.3276
rps3	MSC12	2.04	0.34	0.0097*
rps3	MSC16	1.93	0.37	0.0328*
mttb	Line B	1.07	0.16	CONTROL

mttb	MSC3	1.57	0.34	0.1084
mttb	MSC12	2.01	0.32	0.0067*
mttb	MSC16	1.82	0.24	0.0113*
atp4	Line B	1.03	0.09	CONTROL
atp4	MSC3	0.47	0.07	0.0001*
atp4	MSC12	1.12	0.19	0.3112
atp4	MSC16	1.01	0.14	0.4523
cox2	Line B	1.03	0.18	CONTROL
cox2	MSC3	1.12	0.24	0.2669
cox2	MSC12	1.25	0.15	0.1114
cox2	MSC16	1.32	0.18	0.0917
aox ^{nm}	Line B	1.03	0.10	CONTROL
aox ^{nm}	MSC3	1.94	0.22	0.0017*
aox ^{nm}	MSC12	2.33	0.27	0.0003*
aox ^{nm}	MSC16	2.66	0.35	0.0007*
rrnS	Line B	1.06	0.13	CONTROL
rrnS	MSC3	1.35	0.18	0.1090
rrnS	MSC12	0.73	0.12	0.0383*
rrnS	MSC16	0.82	0.11	0.0905
rps13	Line B	1.10	0.17	CONTROL
rps13	MSC3	1.35	0.11	0.1150
rps13	MSC12	2.85	0.39	0.0003*
rps13	MSC16	2.82	0.71	0.0213*
rpl5	Line B	1.09	0.39	CONTROL
rpl5	MSC3	1.81	0.45	0.0112*
rpl5	MSC12	2.27	0.57	0.0396*

rpl5	MSC16	2.05	0.23	0.0026*
atp8	Line B	1.02	0.08	CONTROL
atp8	MSC3	1.09	0.23	0.3999
atp8	MSC12	1.33	0.23	0.0916
atp8	MSC16	1.45	0.22	0.0504
nad5	Line B	1.13	0.22	CONTROL
nad5	MSC3	0.14	0.02	0.0011*
nad5	MSC12	1.28	0.34	0.3535
nad5	MSC16	1.16	0.27	0.4686
rrnL	Line B	1.06	0.12	CONTROL
rrnL	MSC3	1.15	0.21	0.3519
rrnL	MSC12	1.19	0.30	0.3461
rrnL	MSC16	1.51	0.28	0.0843
cox1	Line B	1.13	0.41	CONTROL
cox1	MSC3	1.58	0.68	0.1262
cox1	MSC12	1.85	0.58	0.1347
cox1	MSC16	3.07	1.03	0.0500*
atp1	Line B	1.11	0.19	CONTROL
atp1	MSC3	2.05	0.24	0.0039*
atp1	MSC12	1.77	0.57	0.1510
atp1	MSC16	1.91	0.50	0.0849
nad1	Line B	1.03	0.08	CONTROL
nad1	MSC3	0.95	0.14	0.3251
nad1	MSC12	1.08	0.32	0.4367
nad1	MSC16	1.18	0.31	0.3286
nad7	Line B	1.05	0.11	CONTROL

nad7	MSC3	1.16	0.16	0.2910
nad7	MSC12	1.06	0.25	0.4889
nad7	MSC16	1.19	0.25	0.3109
ccmB	Line B	1.10	0.31	CONTROL
ccmB	MSC3	2.15	1.41	0.0784
ccmB	MSC12	1.55	0.19	0.0400*
ccmB	MSC16	2.30	0.40	0.0090*
porin [n]	Line B	1.08	0.15	CONTROL
porin [n]	MSC3	1.01	0.19	0.3941
porin [n]	MSC12	0.80	0.23	0.1624
porin [n]	MSC16	0.87	0.16	0.1690
ccmFc	Line B	1.08	0.15	CONTROL
ccmFc	MSC3	1.34	0.22	0.1781
ccmFc	MSC12	2.81	0.71	0.0176*
ccmFc	MSC16	2.34	0.47	0.0145*
gadph [n]	Line B	1.03	0.08	CONTROL
gadph [n]	MSC3	1.32	0.17	0.0829
gadph [n]	MSC12	1.17	0.17	0.2137
gadph [n]	MSC16	1.14	0.26	0.3495

* Significant difference between an MSC mutant for a given mitochondrial or nuclear gene compared to wild-type B at $\alpha = 0.05$, Student's t-test.

[n] Nuclear-encoded gene with no function in the mitochondria.

[nm] Nuclear-encoded mitochondrially targeted gene.

Table S4 Primer sequences that were used for quantitative-PCR.

Location	Gene	Forward Primer	Reverse Primer
Nuclear	*gadph*	AGGAAGAGTCCGAGGGAAAA	ACGAGGATGTGAAGCCAAAC
	aox2	GCACCATCAGCCCAAAAC	AGCATCCCTCCAACCATTC
	ubqc	CACAGCTCGATATTGGACAGA	AATTTTCATCCCAACCCACA
	actin3	CCAAGGCGAATAGAGAGAAAA	GCAACATACATAGCGGGAGTG
Complex I	*nad9*	ACAAACCAGTGCAGACGAAG	CCGGATGATTGATGGAAGAA
	nad7	GCAGCACCTTACGATGTTCA	TGTCGCATCTCTTCGATACG
	nad6	TCCGTCTGGTTTTTGCTTTC	GTGGTTCTGTCGTCCTCCTC
	nad3	CACTCGGTCTTCCTTTTCCA	AACGACTTCTGGCATCACC
	nad5 ex4	AGGATATTAGGGGAAGCAGTGAG	CCAAGAAGATAGAGAGTCCCACA
Complex II	*sdh3*	TGGGTTTGATTTGCTTCACC	CGACGGATATTAGGATGAGCTTT
Complex III	*cob*	CTTGGTGAATAGGGCGAAAA	TGACAAAGCGGGAGGTGTAG
Complex IV	*cox1*	TTCCCATGCATTTCTTAGGG	AACGACGAATCCCAACTACG
	cox2	GATCTCAAGACGCAGCAACA	CATAAAGCGCGAACCAAGA
	ccmFc	GCCTCATTTCCTTTCCTTCC	TCACGCTTCGCTGAACTATG
	ccmB	CGGAATGGATCGGTTAAACA	AAGAGCCGAACGAGAATGAA
Complex V	*atp1*	TGAAACACAAGCTGGAGACG	ACACGACTGACGGATAAGCC
	atp4	GCAGCAATTTCCCAATCCT	TGCACTGTCTTTTCGCACTT
	atp8	TGCCTTTTCTTCTTGACTTTCT	TCCTTGCTCCGTATGTTCTTC
Ribosome LU	*rpl2*	AGCCAAGAGGGGAGAGCA	CCGAGAAGAACGATTAGGG
	rpl5	GCCCGGAGAATTTAAGAAAGA	TGACCTAGCACGAGAAAGCA
	rrnL	GTCAGCGAGAAAATGGGAAC	CGGGTCAAATAGGAAGAACGA
Ribosome SU	*rrn5*	AGCGATCGACGTGAAAACAC	TCCTTCATTACTAGCCGC
	rrnS	TGCGCTTTAGTTTGATTGCT	AGTCTGAGGACCCGTTTTGG
	rps7	TGACGATCCCTGGCTACAA	ATGGTTGAGGCCGTAGAGAA
	rps13	GTCTGCTCGTTCTCCCCTCT	AAAAAGCCATTCAGGTTCGTT
	rps10	GGAAGATTGGATTGCCTGAA	ATGCCTTTCTGTTTTTATGACC
	rps3	GGAGCGAATACACAGGGAAG	CGAAGAAAGGAAAGAGCGAGA