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Genome-wide identification and analysis of the *MLO* gene families in three *Cucurbita* species

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Electronic Supplementary Material (ESM)

The authors are fully responsible for both the content and the formal aspects of the electronic supplementary material. No editorial adjustments were made.

Table S1. Features of the *MLO* family genes in the *Cucurbita* genus

Gene	Gene ID	Chr	LMD (aa)	TM	ORF (bp)	AA (aa)	MW (KDa)	PI
<i>CmoMLO01</i>	CmoCh20G005110.1	Chr20	487	7	1464	488	69.56	9.24
<i>CmoMLO02</i>	CmoCh13G001880.1	Chr13	489	7	1470	490	66.77	9.23
<i>CmoMLO03</i>	CmoCh02G008830.1	Chr02	487	7	1464	488	67.35	8.84
<i>CmoMLO04</i>	CmoCh04G014330.1	Chr04	482	7	1449	483	65.58	9.16
<i>CmoMLO05</i>	CmoCh18G008900.1	Chr18	478	7	1437	479	69.51	9.29
<i>CmoMLO06</i>	CmoCh01G005680.1	Chr01	517	8	1524	518	140.27	9.09
<i>CmoMLO07</i>	CmoCh13G001900.1	Chr13	483	7	1452	484	63.58	9.08
<i>CmoMLO08^a</i>	CmoCh05G009880.1	Chr05	158/173	4	999	333	49.90	8.28
<i>CmoMLO09^a</i>	CmoCh06G001580.1	Chr06	457	7	1374	458	62.92	8.96
<i>CmoMLO10^a</i>	CmoCh07G003740.1	Chr07	479	7	1440	480	64.85	9.12
<i>CmoMLO11^a</i>	CmoCh03G006470.1	Chr03	483	8	1452	484	65.10	9.20
<i>CmoMLO12</i>	CmoCh03G012940.1	Chr03	456	7	1371	457	61.49	9.60
<i>CmoMLO13</i>	CmoCh20G010570.1	Chr20	465	8	1398	466	55.86	9.31
<i>CmoMLO14</i>	CmoCh08G009620.1	Chr08	490	7	1473	491	57.81	8.03
<i>CmoMLO15</i>	CmoCh17G000460.1	Chr17	493	7	1482	494	58.25	9.14
<i>CmoMLO16</i>	CmoCh04G005710.1	Chr04	251/93/87	6	1302	434	64.59	8.71
<i>CmoMLO17^b</i>	CmoCh16G012870.1	Chr16	436	5	1311	437	58.93	6.15
<i>CmoMLO18^b</i>	CmoCh15G003290.1	Chr15	476	7	1431	477	64.16	7.70
<i>CmoMLO19</i>	CmoCh01G012560.1	Chr01	477	7	1458	486	63.16	9.14
<i>CmoMLO20</i>	CmoCh09G008640.1	Chr09	364	5	1095	365	42.95	7.75
<i>CmaMLO01</i>	CmaCh20G004770.1	Chr20	487	7	1464	488	68.63	9.28
<i>CmaMLO02</i>	CmaCh13G001880.1	Chr13	489	7	1470	490	66.72	9.17
<i>CmaMLO03</i>	CmaCh02G008830.1	Chr02	487	7	1464	488	67.36	8.93
<i>CmaMLO04</i>	CmaCh04G013590.1	Chr04	482	7	1449	483	65.53	9.31
<i>CmaMLO05</i>	CmaCh18G008880.1	Chr18	478	7	1437	479	94.41	8.72
<i>CmaMLO06</i>	CmaCh01G005380.1	Chr01	525	9	1578	526	143.37	9.17
<i>CmaMLO07</i>	CmaCh13G001900.1	Chr13	496	8	1491	497	132.26	9.33
<i>CmaMLO08</i>	CmaCh05G009680.1	Chr05	485	7	1458	486	61.15	9.11
<i>CmaMLO09</i>	CmaCh06G001680.1	Chr06	475	8	1428	476	70.96	9.20
<i>CmaMLO10^a</i>	CmaCh07G003790.1	Chr07	479	7	1494	498	64.78	9.16
<i>CmaMLO11^a</i>	CmaCh03G006190.1	Chr03	483	8	1452	484	65.16	9.11
<i>CmaMLO12</i>	CmaCh02G001970.1	Chr02	472	8	1419	473	61.01	9.50
<i>CmaMLO13</i>	CmaCh03G012970.1	Chr03	456	7	1371	457	66.55	9.87
<i>CmaMLO14</i>	CmaCh20G010510.1	Chr20	445	8	1338	446	53.81	8.80
<i>CmaMLO15</i>	CmaCh08G009910.1	Chr08	491	7	1476	492	57.96	8.27
<i>CmaMLO16</i>	CmaCh17G000440.1	Chr17	493	7	1482	494	58.28	9.14
<i>CmaMLO17</i>	CmaCh04G005350.1	Chr04	480	5	1443	481	64.33	8.74
<i>CmaMLO18^b</i>	CmaCh16G012410.1	Chr16	467	6	1404	468	109.03	5.28
<i>CmaMLO19^b</i>	CmaCh15G003160.1	Chr15	476	7	1431	477	64.15	8.52
<i>CmaMLO20</i>	CmaCh01G012040.1	Chr01	477	7	1434	478	63.16	9.32
<i>CmaMLO21</i>	CmaCh09G008750.1	Chr09	478	7	1437	479	63.28	8.63
<i>CpeMLO01</i>	Cp4.1LG16g05390.1	Chr16	309	4	930	310	48.69	9.53
<i>CpeMLO02</i>	Cp4.1LG05g08330.1	Chr05	357/79	6	1314	438	61.00	8.90
<i>CpeMLO03</i>	Cp4.1LG01g14830.1	Chr01	292/98/94	6	1461	487	63.85	9.44

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Table S1 to be continued

Gene	Gene ID	Chr	LMD (aa)	TM	ORF (bp)	AA (aa)	MW (KDa)	PI
<i>CpeMLO04</i>	Cp4.1LG09g04350.1	Chr09	500	7	1503	501	69.73	9.17
<i>CpeMLO05</i>	Cp4.1LG02g12880.1	Chr02	456	4	1371	457	59.02	6.84
<i>CpeMLO06</i>	Cp4.1LG20g09050.1	Chr20	468	5	1530	510	70.09	6.44
<i>CpeMLO07</i>	Cp4.1LG11g07830.1	Chr11	340	4	1110	370	51.65	7.11
<i>CpeMLO08^a</i>	Cp4.1LG08g12850.1	Chr08	461	9	1386	462	63.44	9.03
<i>CpeMLO09^a</i>	Cp4.1LG19g08380.1	Chr19	479	7	1440	480	64.73	9.10
<i>CpeMLO10^a</i>	Cp4.1LG10g10540.1	Chr10	472	8	1419	473	63.64	9.20
<i>CpeMLO11</i>	Cp4.1LG10g05200.1	Chr10	456	7	1371	457	61.44	9.64
<i>CpeMLO12</i>	Cp4.1LG16g00900.1	Chr16	209/165/187	10	1692	564	67.23	8.74
<i>CpeMLO13</i>	Cp4.1LG17g02980.1	Chr17	496	7	1491	497	58.65	8.45
<i>CpeMLO14</i>	Cp4.1LG12g00390.1	Chr12	248/290	7	1620	540	62.35	9.06
<i>CpeMLO15</i>	Cp4.1LG01g01830.1	Chr01	194/227	5	1269	423	56.98	7.14
<i>CpeMLO16^b</i>	Cp4.1LG14g10200.1	Chr14	250/202	6	1362	454	60.31	7.16
<i>CpeMLO17^b</i>	Cp4.1LG13g08770.1	Chr13	480	7	1443	481	64.61	8.05
<i>CpeMLO18</i>	Cp4.1LG06g07040.1	Chr06	451	6	1356	452	61.00	8.42

^athe sequences contained a signal peptide domain; ^bthe sequences contained a fungal_trans domain

Table S2. Sequences of the primers for the RT-qPCR analysis of the *MLOs* in *Cucurbita pepo*

Gene	ID	Primer1	Primer2
<i>CpeMLO01</i>	Cp4.1LG16g05390.1	CTTCGCCGTCGCACCATTTTC	AATTCCTTCGGGCCCCACGTC
<i>CpeMLO02</i>	Cp4.1LG05g08330.1	GCTGCTGCTCACGGTAGGAC	CGCCGGAAAGTGGCATTGAC
<i>CpeMLO03</i>	Cp4.1LG01g14830.1	GCACCCGCACAACCCAGATA	GGGAGATGTGCTGCTGTGCT
<i>CpeMLO04</i>	Cp4.1LG09g04350.1	ACAACGTTTGGACGCCGACA	ACTTCCGGGCGCCAAATGAG
<i>CpeMLO05</i>	Cp4.1LG02g12880.1	CGGTAACGCAACAGCCGGTA	CTGCTGCGAGGCTCACGAAT
<i>CpeMLO06</i>	Cp4.1LG20g09050.1	TTTGCGCAGTGGTTGAAGCG	ACTGGCTGTTGCGTTACCGT
<i>CpeMLO07</i>	Cp4.1LG11g07830.1	GTGGAAGCCCCCTCCGAGTCA	GAAGGAACGGCGGAGGCTT
<i>CpeMLO08</i>	Cp4.1LG08g12850.1	CGAGGGCGATTACACAGCAA	TCCGGTTGTTCCCTTTTACCA
<i>CpeMLO09</i>	Cp4.1LG19g08380.1	ACTCCGACATGGGCTGTTGC	CCTTAGCTGCTGCACACGGT
<i>CpeMLO10</i>	Cp4.1LG10g10540.1	GGGTGTTGGCTGGTCATGGT	AGTGAGCCGAAATCGTGCGT
<i>CpeMLO11</i>	Cp4.1LG10g05200.1	GGCCGGCCTAAGTTGCTTCT	GAACTGCACCAGCACACCCA
<i>CpeMLO12</i>	Cp4.1LG16g00900.1	CGTCGCCGTTGTTTCCTCCA	TCAGCACGGCGTGATTCAGT
<i>CpeMLO13</i>	Cp4.1LG17g02980.1	ACCCTGCCGCTCTACGCTAT	GCTTCCTTGCTTCCGTGGCT
<i>CpeMLO14</i>	Cp4.1LG12g00390.1	GCACCCTACCGCTCTATGCC	ACCTTCCTTGCCCTCCTTGGC
<i>CpeMLO15</i>	Cp4.1LG01g01830.1	GCAGCTACAGCACAGTGCCA	GTGACAACGTACCCGACGCA
<i>CpeMLO16</i>	Cp4.1LG14g10200.1	AGTTGTGGGTGCAACATCGC	ACCCGAGAGGAACGTGTGGA
<i>CpeMLO17</i>	Cp4.1LG13g08770.1	GGGCAAGGCAGCAAGAAGGA	GCAGAGGGTTGCAGAAGCGA
<i>CpeMLO18</i>	Cp4.1LG06g07040.1	TGGCTCTGACGCCTACTTGG	TGATGCCGTCAGAAGCAAGGA
<i>RPL44</i>	XM_023692370	AGCCTTGCTGCTCAAGGGAA	CATGCTTGCAACCCTGGCAT