

糜子 *MCM* 基因家族的鉴定及其对非生物胁迫的
响应分析

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Identification of *MCM* Gene Family in
Broomcorn Millet (*Panicum miliaceum* L.) and Its
Response to Abiotic Stress

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附表

附表 1 本研究所使用的引物序列
Additional table 1 Primer sequences used in this study

基因名称	正向引物	反向引物
Gene name	Forward primer (5'-3')	Reverse primer (5'-3')
<i>PmMCM1</i>	GGCTGCTGTCCTTCGTCTATG	TGAGTCCTGCGGTGCTCGTAT
<i>PmMCM2</i>	GCTATGCGCCTAGATATACACAAT	CGGGATATCCTGATGACGCA
<i>PmMCM3</i>	GCCCGTCTTGCTTCGCTTTCT	GACTCGTGCTTTTCCCGTTTT
<i>PmMCM4</i>	GCAGTAAGTGGAACGCACTC	ACCTTACAGAGGTTTTCCATGTGT
<i>PmMCM5</i>	CGGCAGCATGAAGAGTCCAT	ATCATGTCCCTGTTTCTGGGT
<i>PmMCM6</i>	AGTCCGTACCTTTTCGAGGGA	GGGGTTTCATCTGGTGTGGT
<i>PmMCM7</i>	ACTATGGATTCAGAGCGATGC	ATGCCTGACATCTCAACCACA
<i>PmMCM8</i>	ACCTGTTGCATGATCCGTCG	GGTTCTTGTGCTGATAATTTTGCTG
<i>PmMCM9</i>	GCCCTAATGCTACTCTGC	CTCCACAACATCTCGCACTT
<i>PmMCM10</i>	GGGAGAAAATTCGCACGCATA	GGAGCGCATAAGATTGGGACT
<i>PmMCM11</i>	CTGAGCCTGCCAGTTGTAA	CCATCATGCAATCCGCTGTG
<i>PmMCM12</i>	CAAGCAAGAAGGTCCGGTGC	TGTTAAGAGGTTTGTCTGTCTGTATG
<i>PmMCM13</i>	TCTTATGGCTGGGCAAGTCG	CCAAGGCCACCCATGTAAC
<i>PmMCM14</i>	TCCAATGACGGAACAAAACG	TGCACAATAGCAGTCAGTCAC
<i>PmMCM15</i>	GGCCACCAAGCCATCATTA	TGTCAATGGGTCTCTGACTTGAA
<i>ACT2</i>	GCGAGCTTCCTGTAGGTA	CGAACCCAGCCTTCACCATAC

附表 2 糜子 *MCM* 基因家族的理化性质和染色体定位Additional table 2 Physicochemical properties and subcellular localization in *Panicum miliaceum* *MCM* gene family

基因名称	蛋白质 ID	氨基酸长度/aa	分子量/kDa	等电点	不稳定系数	脂肪族指数	亲水性系数	亚细胞定位
Gene name	Protein ID	Number of Amino Acid	Molecular Weight	Theoretical pI	Instability Index	Aliphatic Index	Grand Average of Hydropathicity	Subcellular localization
<i>PmMCM1</i>	RLN30454.1	831	92.63	5.66	42.56	86.74	-0.343	Nucleus(1)/ Cytoplasmic(2)
<i>PmMCM2</i>	RLN28973.1	723	81.23	5.61	43.73	93.80	-0.229	Nucleus(1)/ Cytoplasmic(2)
<i>PmMCM3</i>	RLN30725.1	770	85.16	5.84	37.25	87.25	-0.329	Nucleus(1)/ Nucleus(2)
<i>PmMCM4</i>	RLN30493.1	771	85.08	6.29	38.62	89.03	-0.274	Nucleus(1)/ Nucleus(2)
<i>PmMCM5</i>	RLN00221.1	831	92.62	5.73	43.28	86.29	-0.361	Nucleus(1)/ Cytoplasmic(2)
<i>PmMCM6</i>	RLM99914.1	770	85.30	5.95	37.87	86.61	-0.353	Nucleus(1)/ Nucleus(2)
<i>PmMCM7</i>	RLN01070.1	654	73.27	5.78	40.16	92.66	-0.239	Nucleus(1)/ Cytoplasmic(2)
<i>PmMCM8</i>	RLN22648.1	760	83.73	5.95	53.12	85.57	-0.350	Nucleus(1)/ Nucleus(2)
<i>PmMCM9</i>	RLM94096.1	851	94.12	6.17	51.04	86.16	-0.360	Nucleus(1)/ Nucleus(2)
<i>PmMCM10</i>	RLN12911.1	605	67.55	6.28	34.08	92.00	-0.235	Nucleus(1)/ Nucleus(2)
<i>PmMCM11</i>	RLM55471.1	611	68.07	6.40	38.45	88.87	-0.289	Nucleus(1)/ Nucleus(2)
<i>PmMCM12</i>	RLN09616.1	711	78.43	7.91	45.37	86.05	-0.318	Nucleus(1)/ Nucleus(2)
<i>PmMCM13</i>	RLM79143.1	703	77.56	7.91	45.01	86.61	-0.307	Nucleus(1)/ Nucleus(2)
<i>PmMCM14</i>	RLM69826.1	957	108.09	5.03	45.18	80.59	-0.561	Nucleus(1)/ Nucleus(2)
<i>PmMCM15</i>	RLM57963.1	1018	114.78	5.45	45.09	83.24	-0.532	Nucleus(1)/ Nucleus(2)

注： (1)为用 Plant-mPLOC 网站预测亚细胞定位结果，(2)为用 CELLO 网站预测亚细胞定位结果。

Note: 1 Subcellular localization prediction results predicted by Plant-mPLOC website, 2 Subcellular localization prediction results predicted by CELLO website.

附表 3 *PmMCM* 基因家族片段重复基因对的 *Ka/Ks* 值Additional table 3 *Ka/Ks* ratios of segmental duplicated gene pairs in the *PmMCM* gene family

重复基因对	非同义替换率	同义替换率	非同义替换率/同义替换率
Duplicated gene pairs	Non-synonymous substitution	Synonymous substitution	Non-synonymous substitution/Synonymous substitution
	(<i>Ka</i>)	(<i>Ks</i>)	(<i>Ka/Ks</i>)
<i>PmMCM1-PmMCM5</i>	0.009	0.089	0.101
<i>PmMCM2-PmMCM7</i>	0.003	0.083	0.032
<i>PmMCM3-PmMCM6</i>	0.005	0.044	0.104
<i>PmMCM8-PmMCM9</i>	0.009	0.106	0.088
<i>PmMCM10-PmMCM11</i>	0.019	0.039	0.507
<i>PmMCM12-PmMCM13</i>	0.002	0.049	0.051
<i>PmMCM14-PmMCM15</i>	0.007	0.061	0.109

注: $Ka/Ks < 1$ 表示该基因受到纯化选择, $Ka/Ks > 1$ 表示该基因受到正选择, $Ka/Ks = 1$ 表示该基因受到中性选择

Note: $Ka/Ks < 1$ indicates the gene is under purifying selection, $Ka/Ks > 1$ indicates the gene is positive selection, $Ka/Ks = 1$ indicates the gene is neutral selection

附表 4 共线性分析所用不同植物 *MCM* 基因序列登录号Additional table 4 Accession numbers of *MCM* sequences from different plants used in collinearity analysis

糜子 ID	拟南芥 ID	水稻 ID	玉米 ID
<i>Panicum miliaceum</i> ID	<i>Arabidopsis thaliana</i> ID	<i>Oryza sativa</i> ID	<i>Zea mays</i> ID
<i>PmMCM1</i>	<i>AT3G09660.1</i>	<i>OsMCM6</i>	<i>ZmMCM3</i>
<i>PmMCM2</i>		<i>OsMCM7</i>	<i>Zm00001d030614/Zm00001eb028400</i>
<i>PmMCM3</i>		<i>OsMCM3i</i>	<i>ZmMCM9/ZmMCM8</i>
<i>PmMCM4</i>		<i>OsMCM8</i>	<i>Zm00001d010567</i>
<i>PmMCM5</i>		<i>OsMCM6</i>	<i>ZmMCM3/ZmMCM4</i>
<i>PmMCM6</i>		<i>OsMCM3i</i>	<i>ZmMCM8/ZmMCM9</i>
<i>PmMCM7</i>		<i>OsMCM7</i>	<i>Zm00001d030614/ZmMCM5</i>
<i>PmMCM8</i>		<i>OsMCM4</i>	<i>ZmMCM10</i>
<i>PmMCM9</i>		<i>OsMCM4</i>	<i>ZmMCM10</i>
<i>PmMCM10</i>		<i>OsMCM9</i>	<i>ZmMCM15</i>
<i>PmMCM11</i>			<i>ZmMCM15</i>
<i>PmMCM12</i>		<i>OsMCM5</i>	<i>ZmMCM1/ZmMCM6</i>
<i>PmMCM13</i>		<i>OsMCM5</i>	<i>ZmMCM1/ZmMCM6</i>
<i>PmMCM14</i>		<i>OsMCM2</i>	<i>Zm00001d010567</i>
<i>PmMCM15</i>			<i>Zm00001d010567</i>

附表 5 拟南芥、水稻和玉米中 *MCM* 同源基因的基因编号Additional table 5 Gene IDs of *MCM* homologs in *Arabidopsis thaliana*, *Oryza sativa* and *Zea mays*

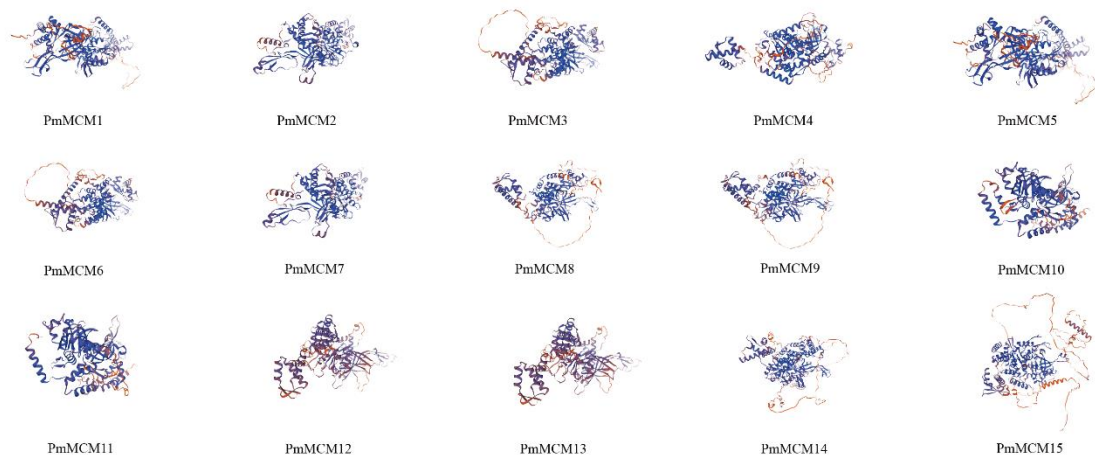
基因名字	基因符号
Gene name	Gene symbol
<i>AtMCM2</i>	AT1G44900
<i>AtMCM3</i>	AT5G46280
<i>AtMCM4</i>	AT2G16440
<i>AtMCM5</i>	AT2G07690
<i>AtMCM6</i>	AT5G44635
<i>AtMCM7</i>	AT4G02060
<i>AtMCM8</i>	AT3G09660
<i>AtMCM9</i>	AT2G14050
<i>AtMCM10</i>	AT2G20980
<i>OsMCM2</i>	LOC_Os11g29380.1
<i>OsMCM3</i>	i) LOC_Os05g39850.1/ii)LOC_Os05g08100.1
<i>OsMCM4</i>	LOC_Os01g36390.1
<i>OsMCM5</i>	LOC_Os02g55410.1
<i>OsMCM6</i>	LOC_Os05g14590.1
<i>OsMCM7</i>	LOC_Os12g37400.1
<i>OsMCM8</i>	LOC_Os05g38850.1
<i>OsMCM9</i>	LOC_Os06g11500.1
<i>OsMCM10</i>	LOC_Os09g36820.1
<i>ZmMCM1</i>	Zm00001d018384
<i>ZmMCM2</i>	Zm00001d049190
<i>ZmMCM3</i>	Zm00001d010406
<i>ZmMCM4</i>	Zm00001d037781
<i>ZmMCM5</i>	Zm00001d041606
<i>ZmMCM6</i>	Zm00001d052021
<i>ZmMCM7</i>	Zm00001d009374
<i>ZmMCM8</i>	Zm00001d010611
<i>ZmMCM9</i>	Zm00001d038467
<i>ZmMCM10</i>	Zm00001d044540
<i>ZmMCM11</i>	Zm00001d010614
<i>ZmMCM12</i>	Zm00001d037195
<i>ZmMCM13</i>	Zm00001d013372
<i>ZmMCM14</i>	Zm00001d042967
<i>ZmMCM15</i>	Zm00001d037196
<i>ZmMCM16</i>	Zm00001d040595
<i>ZmMCM17</i>	Zm00001d009392

附表 6 PmMCM 蛋白二级结构占比

Additional table 6 PmMCM protein secondary structure content

蛋白名称	α -螺旋 (%)	β -转角 (%)	无规则卷曲 (%)	延伸链 (%)
Protein name	Alpha helix (%)	Beta turn (%)	Random coil (%)	Extended strand (%)
PmMCM1	49.94%	0.00%	38.87%	11.19%
PmMCM2	47.03%	0.00%	40.94%	12.03%
PmMCM3	46.88%	0.00%	41.56%	11.56%
PmMCM4	40.99%	0.00%	14.27%	13.75%
PmMCM5	47.29%	0.00%	41.16%	11.55%
PmMCM6	49.48%	0.00%	39.74%	10.78%
PmMCM7	48.32%	0.00%	38.53%	13.15%
PmMCM8	40.79%	0.00%	49.61%	9.61%
PmMCM9	38.19%	0.00%	50.41%	11.40%
PmMCM10	41.16%	0.00%	44.46%	14.38%
PmMCM11	41.24%	0.00%	44.03%	14.73%
PmMCM12	45.71%	0.00%	42.19%	12.10%
PmMCM13	44.95%	0.00%	41.96%	13.09%
PmMCM14	41.90%	0.00%	48.59%	9.51%
PmMCM15	43.52%	0.00%	47.25%	9.23%

附图



附图 1 Swiss-Model 预测 PmMCMs 蛋白空间结构

Additional figure 1 Spatial structure of PmMCMs protein predicted by Swiss-Model

A	PmMCM1	MEAFGGFFVDEKAARVENI FLEFLKRFKESDGAPEPTFYEEMEAAMRSRESTIMVDFAHVMRFNDI LQKAI AEEYLRFEFYLNRACKRFVLEHRAGENRA	100
	PmMCM5	MEAFGGFFVDEKAARVENI FLEFLKRFKESDGAPEPTFYEEMEAAMRSRESTIMVDFAHVMRFNDI LQKAI AEEYLRFEFYLNRACKRFVLEHRAGENRA	100
	PmMCM1	PII SDDSPNKDI NI AFYNI PMKKRLRELGTAEI GKLTSVMGVVTRISEVRPELLQGTFKCLYCGNVKNVEQQFKYTEPII CVNATCQNRSKWALLRQES	200
	PmMCM5	PII SDDSPNKDI NI AFYNI PMKKRLRELGTAEI GKLTSVMGVVTRISEVRPELLQGTFKCLDCGNVKNVEQQFKYTEPII CVNATCQNRSKWALLRQES	200
	PmMCM1	KFTDQVRVMQETSKETI PAGSLPRSLDM LRHEI VEKARAGDTVFTGTIVAVPDVMAITSPGERAECCRREAPQRKNGGVQGVKGKLSLGVRLSYHLA	300
	PmMCM5	KFTDQVRVMQETSKETI PAGSLPRSLDM LRHEI VEKARAGDTVFTGTIVAVPDVMAITSPGERAECCRREAPQRKNGGVQGVKGKLSLGVRLSYHLA	300
	PmMCM1	FVANSVQVADGRREVDI RDRDITDGDSEKQFTTEEEDEVVRMNPDPDFNKI VDSI CPTVFGHQEI KRAVLILMLGGVHKI THEGI NLRGDI NVCI VGD	400
	PmMCM5	FVANSVQVADGRREVDI RDRDITDGDSEKQFTTEEEDEVVRMNPDPDFNKI VDSI CPTVFGHQEI KRAVLILMLGGVHKI THEGI NLRGDI NVCI VGD	400
	PmMCM1	PSCAKSQFLKYTAGI VPRSVYTS GKSSS AAGI TATVAKEPETGEFCI EAGALMADNGI CCTDEFDKMDI KDQVAI HEAMEQQTISI TKAGI QATLNART	500
	PmMCM5	PSCAKSQFLKYTAGI VPRSVYTS GKSSS AAGI TATVAKEPETGEFCI EAGALMADNGI CCTDEFDKMDI KDQVAI HEAMEQQTISI TKAGI QATLNART	500
	PmMCM1	SILAAANPTGGRYDKSKPI LKYNVALPPAI LSRFDLVYI M DEPIDENTYHI AHHI VRVHQREEALAPAFS TAEIKRYI VFAKSLKPQLSSEAKKVLVES	600
	PmMCM5	SILAAANPTGGRYDKSKPI LKYNVALPPAI LSRFDLVYI M DEPIDENTYHI AHHI VRVHQREEALAPAFS TAEIKRYI VFAKSLKPQLSSEAKKVLVES	600
	PmMCM1	VYTLRRGDS TPGRVAYRMI VRQLEALI RLSEAI ARSHLERTVLP AHMRLAVKLKTSI I SVESSEVDI SDFQDAEDGTNPDPNDACQPAEADAAPQQQ	700
	PmMCM5	VYTLRRGDS TPGRVAYRMI VRQLEALI RLSEAI ARSHLERTVLP AHMRLAVKLKTSI I SVESSEVDI SDFQDAEDGTNPDPNDACQPAEADAAPQQQ	700
	PmMCM1	GAENDQADNGKKKLM I TEHFQRVTQALVMRLRQHEESVMDGGLAGMQGDII I WVEQQAQAYSS TAEVKEEVKTI KAI I ERLI QREGHILM I D	800
	PmMCM5	DAENQADNGKKKLM I TEHFQRVTQALVMRLRQHEESI MDGGLAGMQGDII I WVEQQAQAYSS TAEVKEEVKTI KAI I ERLI QREGHILM I D	800
	PmMCM1	EGTAAVAEDGAGARRI SESRI LAWNPNYI I	830
	PmMCM5	EGTAAVAEDGAGARRI SESRI LAWNPNYI I	830

B	PmMCM2	MKNPDEAADKALAKIFLSNFADPRGEPKYLNI LQDVANRKI RAVQIELDLDFHYKMDIEEFLQRVTEINTRRYI G FAEAMDELMPEPTEAYTVDEDRDI L	100
	PmMCM7	MKNPDEAADKALAKIFLSNFADPRGEPKYLNI LQDVANRKI RAVQIELDLDFHYKMDIEEFLQRVTEINTRRYI G FAEAMDELMPEPTEAYTVDEDRDI L	100
	PmMCM2	MIQRVDEGADGGADGDTPLQRMPEI KRFEVYI KAFSKVITPLI I ROVKASNI GQLVKI SGI VTRCSDVKPLMQVAVYTCEECCFEI YQEVTVARVFMPLF	200
	PmMCM7	MIQRVDEGADGGADGDTPLQRMPEI KRFEVYI KAFSKVITPLI I ROVKASNI GQLVKI SGI VTRCSDVKPLMQVAVYTCEECCFEI YQEVTVARVFMPLF	200
	PmMCM2	ECPSQRCKLNKAKGNLI LQRASKFLKFQEVKIQEL AEHVPKGHI PRSLTVHLRGEL TRKVAPGDVWEMGI FLPMYYGFRAMRAGLVADTYLEAMSVI	300
	PmMCM7	ECPSQRCKLNKAKGNLI LQRASKFLKFQEVKIQEL AEHVPKGHI PRSLTVHLRGEL TRKVAPGDVWEMGI FLPMYYGFRAMRAGLVADTYLEAMSVI	300
	PmMCM2	HFKKYHFHYELKGGDEQQL DRLEADGDI YSKLARSLAPEI FGHEDVKALLLLVGAPHRKLGDMKI RGDHI CLMDPGVAKSQLLKHII I NVAPRGVY	400
	PmMCM7	HFKKYHFHYELKGGDEQQL DRLEADGDI YSKLARSLAPEI FGHEDVKALLLLVGAPHRKLGDMKI RGDHI CLMDPGVAKSQLLKHII I NVAPRGVY	400
	PmMCM2	TTGRGSSGGLTAAVQKDI TSEFVLEGGALVADMI CAIDETFKMEESDRTAI HEVMEQQTIVSI AKAGI TTSLNARTAI LAAANPAWGRYDMRRITPAE	500
	PmMCM7	TTGRGSSGGLTAAVQKDI TSEFVLEGGALVADMI CAIDETFKMEESDRTAI HEVMEQQTIVSI AKAGI TTSLNARTAI LAAANPAWGRYDMRRITPAE	491
	PmMCM2	NI NLPPALLSRFDLLWLI LDRADMESDLEMRHIVHMQNLESPALGFPTLEPSVLRQVAYI SAARRVI PSVPRELEFYI ATAYSSI RQEEAKSNAPTS	600
	PmMCM7	NI NLPPALLSRFDLLWLI LDRADMESDLEMRHIVHMQNLESPALGFPTLEPSVLRQVAYI SAARRVI PSVPRELEFYI ATAYSSI RQEEAKSNAPTS	531
	PmMCM2	YTTI RTLLSI LRI SI ALARLRFSETVAQSDVDEALRMQSKYLSYSDRQRSGLDAI SDI YSI LRDEAARTSSMDRYAHALNI I SRKGYSEAQKECT	700
	PmMCM7	YTTI RTLLSI LRI SI ALARLRFSETVAQSDVDESLRMQSKYLSYSDRQRSGLDAI SDI YSI LRDEAARTSSMDRYAHALNI I SRKGYSEAQKECT	631
	PmMCM2	EEYASLNWQI HPNTFDI HEI D	722
	PmMCM7	EEYASLNWQI HPNTFDI HEI D	653

C	PmMCM3	MDVNEEAMAAHKRAFLDFLDQDVGGGYMQAVRDMQNGRIHLI I GMDLRNFI L LARRVI RSPGEYMQPASDAVEVARNIDPKFLKEGERVMGFSG	100
	PmMCM6	MDVNEEAMAAHKRAFLDFLDQDVGGGYMQAVRDMQNGRIHLI I GMDLRNFI L LARRVI RSPGEYMQPASDAVEVARNIDPKFLKEGERVMGFSG	100
	PmMCM3	PFGRHRTVPRDLMSSEI GIMC'VEGI VTKCSLVRPKVKS'VHF'CPVTGAFLSREYRDI TSFVGLPTGS VYPTRIDNGNLLVIEYGM'EYKHQILSMQEV	200
	PmMCM6	PFGRHRTVPRDLMSSEI GIMC'VEGI VTKCSLVRPKVKS'VHF'CPVTGAFLSREYRDI TSFVGLPTGS VYPTRIDNGNLLVIEYGM'EYKHQILSMQEV	200
	PmMCM3	PENSAPQQLPRIVDI VEIDLVDCCKPGDRVSI VGVYKALPGSKGSVSGVFTVLI ANWSLLNKEANAPVYTREDIKRMEI SRNRDITDILGNSLAP	300
	PmMCM6	PENSAPQQLPRIVDI VEIDLVDCCKPGDRVSI VGVYKALPGSKGSVSGVFTVLI ANWSLLNKEANAPVYTREDIKRMEI SRNRDITDILGNSLAP	300
	PmMCM3	SI YGHLWIKKAVLLMLGGVEKNLNGITHLRGDI NMMMGDP'SVAKSQLLRAVMNI APLAI STTGRGSSGGLTAAVTS'DQETGERRLEAGAMLADRGV	400
	PmMCM6	SI YGHLWIKKAVLLMLGGVEKNLNGITHLRGDI NMMMGDP'SVAKSQLLRAVMNI APLAI STTGRGSSGGLTAAVTS'DQETGERRLEAGAMLADRGV	400
	PmMCM3	VCI DEFDKMNDLRVAI HEVMEQQTIVTI AKAGIHASLNARCSVI AAANPI YGYDRSLTPITKNI GLPDSLLSRFDLLFI VLDQMDPEI DRQ SEHVARMH	500
	PmMCM6	VCI DEFDKMNDQRVAI HEVMEQQTIVTI AKAGIHASLNARCSVI AAANPI YGYDRSLTPITKNI GLPDSLLSRFDLLFI VLDQMDPEI DRQ SEHVARMH	500
	PmMCM3	RYCTDDGGARSLDKAGYAEEDDGEANAAI FVKYDRMHGQDRRRGGKARQDGLTVKFLKKYI HYAKNLI QPKLTDEASDHI ATSYAELRDGNANAKSGG	600
	PmMCM6	RYCTDDGGARSLDKAGYAEEDDGEANAAI FVKYDRMHGQDRRRGGKARQDGLTVKFLKKYI HYAKNLI QPKLTDEASDHI ATSYAELRDGNANAKSGG	600
	PmMCM3	TLPI TARTILETI I RLSTAHAKMLRHEVLS'DVEAALQVLF'AI YHKEI TEMEEREQREM'KQADHDAGATDGAADNGSSGNDPMDVDVGNISNDQD	700
	PmMCM6	TLPI TARTILETI I RLSTAHAKMLRHEVLS'DVEAALQVLF'AI YHKEI TEMEEREQREM'KQADHDAGATDGAADNGSSGNDPMDVDVGNISNDQD	700
	PmMCM3	VP'ARI EAFEAI LQGHVLANHVDQM6I DOI EQIVNRESAAPYTRRQVEFI LERMQDANRI M RDGI VRI	769
	PmMCM6	VP'ARI EAFEAI LQGHVLANHVDQM6I DOI EQIVNRESAAPYTRRQVEFI LERMQDANRI M RDGVVRI	769

D	PmMCM8	MSNNGGSSPPPASSPDASPSPLPVNTSSPTQSTRSGRRRRGASPYASSPSLGGFETPPHPGRRTPSGGGAGGAGGARQQRQNWGRFPPTPTSTM	100
	PmMCM9	MSNNGGSSPPPASSPDARPPSSPLPVNTSSPTQSTRSGRRRRGASPYASSPSLGGFETPPHPGRRTPSGGGAG...AARQKQNWGRFPPTPTSTM	97
	PmMCM8	STDDI PPSSDAGEDETDGGGAGVDAIPVFWGTNI SVQDVNAALIRFLRHF RDPDRAGRVDPVMDGKYMRAI HRI LELEGGESLDVDAHDFDHPDLY	200
	PmMCM9	STDDI PPSSDAGEDETDGGGAGVDAIPVFWGTNI SVQDVNAALIRFLRHF RDPDRAGRVDPVMDGKYMRAI HRI LELEGGESLDVDAHDFDHPDLY	197
	PmMCM8	SKMRYPLEVLAI FDI VMLDLVARI EPLFEKHI QIRLYNLKSSI CLRNLPDSI EKMSI KGM I RCSSVI PELKEAVFRCLVCGFYSEPVMDR....	295
	PmMCM9	SKMRYPLEVLAI FDI VMLDLVARI EPLFEKHI QIRLYNLKSSI CLRNLPDSI EKMSI KGM I RCSSVI PELKEAVFRCLVCGFYSEPVMDRGRVTE	297
	PmMCM8	DKQI I KLQETPDEI PEGGPHIVSVLMHDKLVDAGKPGORVEI TGI YRAMSI RVGP AQRTVKSI FKTYL DCLHIK	370
	PmMCM9	PHI CQKEQCKATNSMLVHNRCPADKQI I KLQETPDEI PEGGPHIVSVLMHDKLVDAGKPGORVEI TGI YRAMSI RVGPSQRTVKSI FKTYL DCLHIK	397
	PmMCM8	KITKSR LHVEDTMDI DKVNANKSTEEDFLSDKVEKLKELSKLPDIYDRLTRSLAPNI WELDDVKRGLLCQL.....	442
	PmMCM9	KITKSR LHVENTMDI DNADANKSTEEDFLSDKVEKLKELSKLPDIYDRLTRSLAPNI WELDDVKRGLLCQLFGGNPLRPSGASFRGDI NLLVGDPTGS	497
	PmMCM8	QYMKLSPRGIYTSGRGSSAVGLTAYVTKDPETGETVLESGLVMSDKGACCI DEFDKMDNARSMHEVMEQQTISI AKAGI I ASLNARTSVLA	537
	PmMCM9	KSQLLQYMKLSPRGIYTSGRGSSAVGLTAYVTKDPETGETVLESGLVMSDKGACCI DEFDKMDNARSMHEVMEQQTISI AKAGI I ASLNARTSVLA	597
	PmMCM8	CANPTESRYNPRLSVI DNIHLAPTLLSR.....QLELEFLVLDLPTLVAYI SYARKYI QPQLSDEAAEELTRGVV	606
	PmMCM9	CANPTESRYNPRLSVI DNIHLAPTLLSRFDLI YLI LDKADEQITRRLAKHI VSLHFENPNLELEFLVLDLPTLVAYI SYARKYI QPQLSDEAAEELTRGVV	697
	PmMCM8	EMRKQSPGSRKKVI TATARQIESLI RLSEALARMFSEVVEVRDWEAFRLLEVAMQQSATDHATGTLDDLI MGI SASERQRRENVAATRNLI ME	706
	PmMCM9	EMRKQSPGSRKKVI TATARQIESLI RLSEALARMYSEVVEVRDWEAFRLLEVAMQQSATDHATGTLDDLI MGI SASERQRRENVAATCNLI ME	797
	PmMCM8	KMQLGGPSMRMTELEEMRKQSSMEI HLHDLRSALGILMTEGAVV HGDNVKR	759
	PmMCM9	KMQLGGPSMRMTELEEMRKQSSMEI HLHDLRSALGILMTEGAVV HGDNVKR	850
E	PmMCM12	M6GWDEGAVFYSDQAQFPRGGPGGPAAGADLSRHSALRKFEFLRGFTGPTGDFPYRESI VHNRDHVTVAI EDLDAPDAELSDKI RKSPADYLP LFETAA	100
	PmMCM13	M6GWDEGAVFYSDQAQFPRGGPGGPA ADLSRHSALRKFEFLRGFTGPTGDFPYRESI VHNRDHVTVAI EDLDAPDAELSDKI RKSPADYLP LFETAA	99
	PmMCM12	AEVLASLRSKVAGETGEMEEPVTGDMQIFLSSKENCLSMSI GADYMKLVKI AGI AI AASRVKAKATHVTLLCNCRSVRI VSCRPLGGAI VPRSCDH	200
	PmMCM13	AEVLASLRSKVAGETGEMEDPVTGDMQIFLSSKENCLSMSI GADYMKLVKI AGI AI AASRVKAKATHVTLLCNCRSVRI VSCRPLGGAI VPRSCDH	199
	PmMCM12	VPQGEPCPLDPW PVPDKSKYMLQITLKMENPEDPTGELPRNVLLSVDRHLVQII VPGIRLTVAGI YSVYQASANQKQAVGVKQPI RVVGLQ	300
	PmMCM13	VPQGEPCPLDPW PVPDKSKYMLQITLKMENPEDPTGELPRNVLLSVDRHLVQII VPGIRLTVAGI YSVYQASANQKQAVGVKQPI RVVGLQ	297
	PmMCM12	SRDNNNGPSNFTLDEEMFEKEFAQRPDAYAKLCSM GPSI YGHSDAKKAI ACLIFGSKKRLPDGFLKFEKI API AVYTSQGSSAAGLTASVTRDSS	400
	PmMCM13	SRDNNNGPSNFTLDEEMFEKEFAQRPDAYAKLCSM GPSI YGHSDAKKAI ACLIFGSKK...FLKFEKI API AVYTSQGSSAAGLTASVTRDSS	392
	PmMCM12	SREFYLEGGAMTLADGGVACI DEFDKRPEDRVAI HEAMEQITI SI AKAGITTVLNSRTSVLAAANPI AGRYDILKTAQONI DLQITLLSRFDLI FIVKD	500
	PmMCM13	SREFYLEGGAMTLADGGVACI DEFDKRPEDRVAI HEAMEQITI SI AKAGITTVLNSRTSVLAAANPI AGRYDILKTAQONI DLQITLLSRFDLI FIVKD	492
	PmMCM12	VRMDQDKRI ASHI I KVHASGAAASSKNTEASEGENWLKRYI EYCRATCKPRI SEKAAEMQNKYVEI RQKVRQQAHEHETGAAAI PI TVRQLEAI I RLSE	600
	PmMCM13	IRMDQDKRI ASHI I KVHASGAAASSKNTEASEGENWLKRYI EYCRATCKPRI SEKAAEMQNKYVEI RQKVRQQAHEHETGAAAI PI TVRQLEAI I RLSE	592
	PmMCM12	SLAKMRLTSVAIPEHVEEAFRLFNSTVDAARSGI NEHLNLSPEI ANEI KQAEAQ KRRMGI GSHI SERRLI DELTRMGNESI I RRALLI MHORDEV EY	700
	PmMCM13	SLAKMRLTSVAIPEHVEEAFRLFNSTVDAARSGI NEHLNLSPEI ANEI KQAEAQ KRRMGI GSHI SERRLI DELTRMGNESI I RRALLI MHORDEV EY	692
	PmMCM12	KRERHIVRK	710
	PmMCM13	KRERHIVRK	702

注： 红框代表 α -螺旋，蓝框代表 β -折叠区域。

Note: α -helix and β -sheet are highlighted with red and blue squares, respectively.

附图 2 PmMCM 氨基酸序列比对分析

Additional figure 2 Alignment and analysis of sequences of PmMCM amino acid