

# Identification of candidate genes required for susceptibility to powdery or downy mildew in cucumber

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**Abstract** Powdery mildew (PM, caused by *Podosphaera fusca*) and downy mildew (DM, caused by *Pseudoperonospora cubensis*) are important diseases of cucumber (*Cucumis sativus*). Breeding for resistance has been undertaken since the 1940s, but underlying resistance genes have not been functionally analysed yet. The published genome sequence of cucumber catalyses the search for such genes. Genetic studies have indicated that resistances to PM and DM in cucumber are often inherited recessively, which indicates the presence of susceptibility genes (S-genes). Therefore we analyzed the cucumber genome for homologs of functionally proven S-genes known from other plant species. We identified 13 *MLO*-like genes in cucumber, three of which cluster in Clade V, the clade that contains all known *MLO*-like susceptibility genes to powdery mildews in other dicots. The expression of one of these three genes, *CsaMLO1*,

located on chromosome 1, was upregulated after PM inoculation. It co-localizes with a QTL for PM resistance previously identified. Also homologs of the susceptibility genes *PMR4* and *PMR5* are located at this QTL. The second *MLO*-like gene from Clade V (*CsaMLO8*) resides in a recessively inherited major QTL for PM resistance at the bottom of chromosome 5, together with a *PMR6*-like gene. Two major QTL for DM recessive resistance at the top of chromosome 5 co-localize with *CsaDMR6-2*, which is homologous to the *DMR6* susceptibility gene in *Arabidopsis*. This study has identified several candidate genes for susceptibility to PM and DM in cucumber that may explain QTL for recessively inherited resistance, reported earlier.

**Keywords** Powdery mildew · Downy mildew · Cucumber · Susceptibility genes · *MLO* · *PMR* · *DMR*

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## Introduction

Disease resistant crops are commonly bred by the introgression of resistance (R) genes from wild relatives. However, race-specific resistance conferred by R-genes asserts selective pressure on pathogen populations, therewith overcoming resistance. Also resistance to powdery mildew (PM) in cucumber (*Podosphaera fusca* (Fr.) Braun & Shishkoff, syn. *Sphaerotheca fuliginea* Schlech ex Fr. Poll) has been

bred through introgression of race specific resistance genes, which led to emergence of virulent races (Cohen et al. 2004; Torés et al. 2009). Pyramiding of R-genes has been proposed as a solution to this problem. An alternative strategy for achieving durable resistance is disabling genes that are required for susceptibility, namely susceptibility genes (S-genes) (Pavan et al. 2009).

Several natural loss-of-function alleles of S-genes are known in agriculture, providing durable disease resistance. The most well-known examples are the barley *mlo* mutants (Acevedo-Garcia et al. 2014). These barley mutants have been successfully employed in European barley growing for more than 35 years (Lyngkjær et al. 2000), emphasizing the durability of *mlo*-mediated disease resistance under agricultural conditions. Another example is the loss-of-function mutation in the proline-containing protein Pi21 in rice, providing resistance to rice blast throughout a century of cultivation (Fukuoka et al. 2009).

After discovery of the *MLO* susceptibility gene in barley, *MLO*-like susceptibility genes have been discovered in other monocots, i.e. *OsMLO3* in rice (Devoto et al. 2003), *TaMLO\_A1* and *TaMLO\_B1* in wheat (Devoto et al. 2003; Várallyay et al. 2012). But also in dicots *MLO*-like susceptibility genes have been discovered, such as *AtMLO2*, *AtMLO6* and *AtMLO12* in *Arabidopsis* (Consonni et al. 2006), *SIMLO1* in tomato (Bai et al. 2008), *PsMLO1* in pea (Humphry et al. 2011; Pavan et al. 2011; Santo et al. 2013), *CaMLO2* in pepper (Kim and Hwang 2012; Zheng et al. 2013), *LjMLO1* in lotus (Humphry et al. 2011), and *MtMLO1* in barrel clover (Humphry et al. 2011). The *MLO*-genes have about seven transmembrane domains, and are located in the plasma membrane with an extracellular amino terminus and an intracellular carboxy terminus with a calmodulin binding domain (Kim et al. 2002). In spite of many efforts to elucidate the biochemical mechanism of the *MLO*-mediated susceptibility to PM, this still remains a mystery to a large extent (Acevedo-Garcia et al. 2014).

In addition to *MLO* other genes that are required for susceptibility to PM have been detected in *Arabidopsis*, i.e. *PMR4* (*powdery mildew resistance 4*; Nishimura et al. 2003; Ellinger et al. 2013), *PMR5* (Vogel et al. 2004) and *PMR6* (Vogel et al. 2002). These three genes appear to influence the cell wall of the plant. Loss-of-function mutations in these *PMR*

genes resulted in PM resistance in *Arabidopsis*. *PMR4* encodes callose synthase (Nishimura et al. 2003). When PM infection occurred in *Arabidopsis thaliana*, the plant cells responded by depositing callose, a (1,3)- $\beta$ -glucan polymer, at the penetration site, thus thickening the cell wall to block the fungal penetration (Nishimura et al. 2003). In view of this, *PMR4* would encode a resistance gene (PM Resistance), rather than a susceptibility gene. Nishimura et al. (2003) provide a possible explanation for this paradox, as callose or callose synthase would negatively regulate the defence by the salicylic acid pathway. Ellinger et al. (2013) confirmed that overexpression of *PMR4* in *A. thaliana* leads to callose deposition at PM penetration sites, but in their findings this leads to resistance, rather than to susceptibility. However, Huibers et al. (2013) showed that down-regulation of the *PMR4* ortholog in tomato reduced the susceptibility to PM, indicating the S-gene effect of *PMR4*. *PMR5* belongs to a large family of plant-specific genes with unknown function. The *pmr5* mutant exhibited pectin enrichment and had smaller cells (Vogel et al. 2004). *PMR6* encodes a pectate lyase-like protein (Vogel et al. 2002).

For downy mildew (DM), several S-genes were revealed in *Arabidopsis*, i.e. *DMR1* (van Damme et al. 2009) and *DMR6* (van Damme et al. 2008). The *DMR1* gene encodes homoserine kinase. *dmr1* mutants contained high levels of homoserine, that would trigger a novel form of DM resistance, independent of known immune responses (van Damme et al. 2009). Interestingly, the tomato ortholog of *DMR1* was found to be required for PM susceptibility in this crop (Huibers et al. 2013). *DMR6* encodes a putative 2OG-Fe(II) oxygenase and the *Arabidopsis dmr6*-mutant was resistant to the DM pathogen *Hyaloperonospora arabidopsidis* (van Damme et al. 2008). In both tomato and cucumber, *DMR6* orthologs have been identified, which could partially restore the DM resistance in the *Arabidopsis dmr6*-mutant (Zeilmaker (2012), indicating that tomato and cucumber have *DMR6*-like genes that provide susceptibility to DM.

PM and DM limit the production of cucumbers throughout the world (Morishita et al. 2003). Both dominant resistances and recessively inherited resistances to PM have been found in cucumber (Sitterly 1972; Morishita et al. 2003; He et al. 2013), whereas resistance to DM is in most of the cases inherited recessively in this crop (Olczak-Woltman et al. 2011).

The recessively inherited resistances potentially resulted from loss-of-function of S-genes.

We describe here the search for *MLO*-, *PMR*- and *DMR*-like genes in cucumber that could be responsible for recessively inherited resistance. Zhou et al. (2013) searched for *MLO*-like genes in a previous version (version 1) of the published sequence of the cucumber genome. In this study, we used the improved version (version 2) of the cucumber genome to identify *MLO*-, *PMR*- and *DMR*-like genes in this crop. Further, we related the genetic loci of the putative S-genes with QTL for recessively inherited resistance to PM and/or DM in cucumber, described in literature.

## Materials and methods

### Identification of putative MLO-like proteins in cucumber

The amino acid sequences of the 15 MLO family members in the genome of *A. thaliana* (AtMLO1 to AtMLO15) were extracted from the NCBI protein database and used for blast searches for MLO-like predicted proteins of cucumber in the Cucurbit Genomics Database version 2 ([www.icugi.org](http://www.icugi.org) using the default blast search settings; Huang et al. 2009). For each MLO protein from *A. thaliana*, the best five hits in the cucumber database were stored in a list, and duplications were removed. The genomic positions of the yielded *MLO*-like genes in cucumber were extracted from the mentioned Cucurbit Genomics Database, using the genome browser.

### Cluster analysis

Twelve orthologous MLO-proteins that have a proven function in susceptibility to powdery mildews were selected, i.e. HvMLO in barley (GenBank identification number P93766), OsMLO3 in rice (AAK94907), TaMLO\_A1 and TaMLO\_B1 in wheat (AAK94904 and AAK94905), AtMLO2, AtMLO6 and AtMLO12 in *Arabidopsis* (NP172598, NP176350, NP565902), SIMLO1 in tomato (NP001234814), PsMLO1 in pea (ACO07297), CaMLO2 in pepper (AFH68055), LjMLO1 in lotus (AAX77015), and MtMLO1 in barrel clover (ADV40949). For clade annotation according to Devoto et al. (2003), the sequences of the remaining MLO proteins in *A. thaliana* that are not known to be

susceptibility proteins were added. All these sequences were aligned with the MLO-like putative proteins in cucumber, using the default settings in the CLC Main Workbench 6.8.4 (<http://clcbio.com>), and a phylogenetic tree was created using UGPMA clustering.

### Conserved domains of Clade V proteins

Clade V contains all functionally proven MLO-like susceptibility proteins of other dicots (Fig. 1). The amino acid sequences of the cucumber proteins that clustered also in this clade were aligned to the sequences of these known susceptibility proteins of other dicots, using CLC. We regarded an amino acid as conserved if at least 7 out of 8 MLO-like susceptibility proteins of Clade V shared this amino acid, or if it was substituted with an amino acid with similar chemical properties according to the Rasmol colour scheme (Sayle 1994). We counted the number of these conserved amino acids in the susceptibility proteins, and counted for these amino acids the number of deviating amino acids in the Clade V proteins of cucumber. Further we counted for each known susceptibility gene the number of amino acids that deviated from the conserved amino acids in the other susceptibility genes. This allowed us to judge whether the degree of similarity of the cucumber Clade V proteins was within the variation range of the Clade V susceptibility genes for the conserved regions.

### Transcriptomics

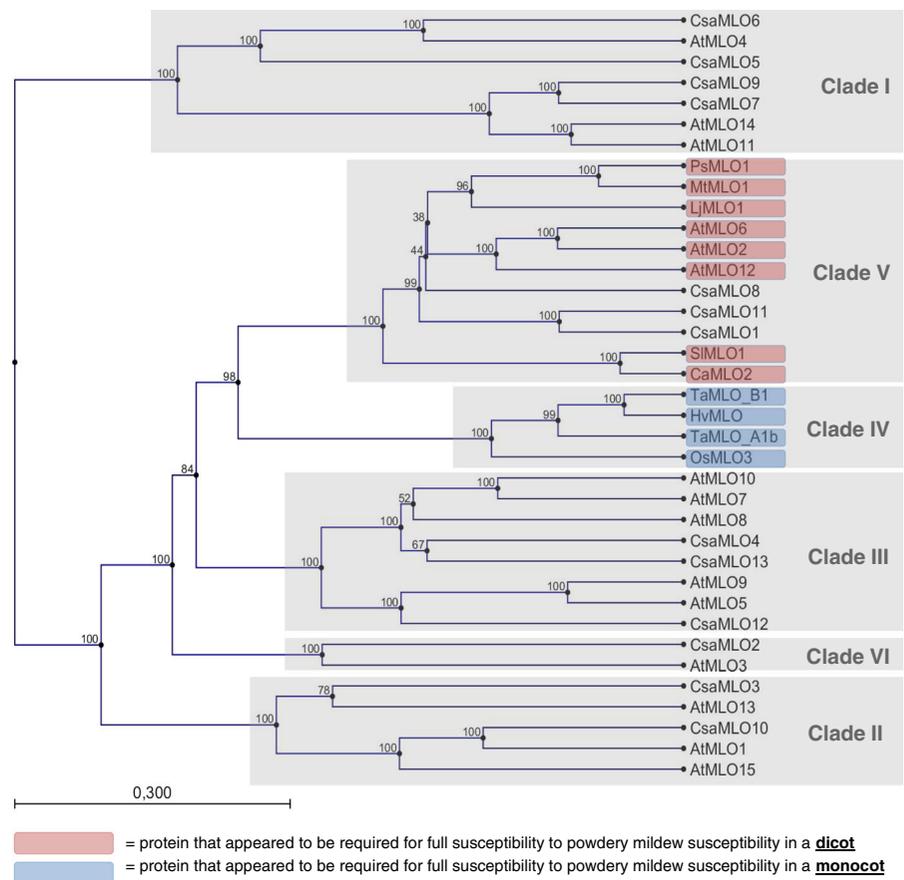
The ‘Chinese long’ inbred line 9,930 that was used for sequencing the whole cucumber genome (Huang et al. 2009), was cultivated in a greenhouse at Nickerson-Zwaan, The Netherlands. The plants were inoculated with the PM fungus *P. fusca* or the DM oomycete *Pseudoperonospora cubensis*. Leaf samples were harvested before inoculation, as well as 8, 24, 48, and 72 h after inoculation. Leaves were immediately frozen in liquid N<sub>2</sub>, ground. Material was sent to KeyGene, The Netherlands, for RNA-Seq. Total RNA was isolated using the Qiagen RNeasy Plant Mini Kit, following the manual included in the kit. Subsequently, RNA Seq libraries were made following the TruSeq<sup>TM</sup> RNA Sample Preparation v2 Guide protocol. After concentration measurement by qPCR (LightCycler<sup>®</sup> 480; Roche), the libraries were pooled, and sequenced using two lanes of the Illumina HiSeq 2000 sequencer. PhiX (~0.6 %) was spiked in according to manufacturer’s



**Table 1** Members of the *CsaMLO* gene family as predicted in the genomic sequence of *Cucumis sativus* var. *sativus* L. in the Cucurbit Genomics Database version 2, clade (Fig. 2), and genomic position (Fig. 1)

Gene	Name in the Cucurbit Genomics Database	Clade	Position in the genome
<i>CsaMLO1</i>	Csa1M085890.1	V	Chr1: 8,159,427..8,165,253
<i>CsaMLO2</i>	Csa1M086900.1	VI	Chr1: 8,208,913..8,218,077
<i>CsaMLO3</i>	Csa2M336140.1	II	Chr2: 15,106,794..15,111,765
<i>CsaMLO4</i>	Csa3M000160.1	II	Chr3: 126,096..130,305
<i>CsaMLO5</i>	Csa3M002740.1	I	Chr3: 466,457..470,782
<i>CsaMLO6</i>	Csa3M223310.1	I	Chr3: 14,768,562..14,776,294
<i>CsaMLO7</i>	Csa4M637780.1	I	Chr4: 20,814,671..20,822,329
<i>CsaMLO8</i>	Csa5M623470.1	V	Chr5: 24,827,408..24,831,456
<i>CsaMLO9</i>	Csa5M631480.1	I	Chr5: 25,795,758..25,802,792
<i>CsaMLO10</i>	Csa6M078520.1	II	Chr6: 5,267,286..5,273,051
<i>CsaMLO11</i>	Csa6M292430.1	V	Chr6: 14,120,024..14,125,039
<i>CsaMLO12</i>	Csa6M355430.1	III	Chr6: 15,892,884..15,897,933
<i>CsaMLO13</i>	Csa6M509690.1	III	Chr6: 26,165,903..26,171,238

**Fig. 2** Phylogenetic tree of 13 MLO-like putative proteins in cucumber, 12 MLO-like proteins known to be required for susceptibility to powdery mildew (PM) in monocots or dicots, and 12 MLO-like proteins in *A. thaliana* that are not known as susceptibility proteins. The numbering of the six clades is according to Devoto et al. (2003). The proteins that have been reported as required for susceptibility to PM in monocotyledons or dicotyledons are highlighted. Bootstrap values at 100 replicates are displayed



proteins, yielded 13 putative members of the MLO family (Table 1). All chromosomes appear to contain at least one *MLO*-like gene, apart from chromosome 7,

which lacks such genes (Fig. 1). Most *MLO*-like genes are scattered among the genome, but in three cases two genes are located close together, i.e. the pairs

*CsaMLO1* and *CsaMLO2*, *CsaMLO4* and *CsaMLO5*, and *CsaMLO8* and *CsaMLO9* (Fig. 1). For these three cases of tight linkage, the genes were not tandem repeats, but clustered in different clades (Fig. 2).

*CsaMLO1*, *CsaMLO8* and *CsaMLO11* cluster with the known MLO-like susceptibility proteins in dicots

The amino acid sequences of the 13 MLO-like putative proteins in cucumber were aligned to the sequences of the 15 MLO proteins in *A. thaliana*, and the 12 MLO proteins that have a proven function in susceptibility to PM in monocots or dicots. This multiple alignment was used for construction of the phylogenetic tree shown in Fig. 2. The six clades were numbered according to the annotation by Devoto et al. (2003). All MLO proteins that have proven to play a role in susceptibility to PM in monocots, i.e. in barley, rice and wheat, group in Clade IV, and all MLO proteins that are important for susceptibility to PM in dicots group in Clade V (Fig. 2), which resembles the results shown by others, such as Devoto et al. (2003) and Acevedo-Garcia et al. (2014). Three putative proteins (*CsaMLO1*, *CsaMLO8*, and *CsaMLO11*) from cucumber, which is a dicot, were positioned in this Clade V (Fig. 2). Based on this phylogenetic tree, the three underlying genes *CsaMLO1*, *CsaMLO8* and *CsaMLO11* are considered as candidate genes for susceptibility to PM.

All three candidates harbour the conserved regions of MLO-like susceptibility proteins

We aligned the amino acid sequences of the three predicted cucumber proteins from Clade V (*CsaMLO1*, *CsaMLO8*, and *CsaMLO11*) to the sequences of the known MLO-like susceptibility proteins from the same clade (Fig. 2, and Online Resource 1). The three Clade V cucumber proteins showed 97.3–98.5 % similarity to the susceptibility proteins in other dicots in the conserved regions (Table 2). This similarity of the cucumber proteins is well within the range of conservation of the proven susceptibility proteins of dicots (94.2–98.9 %), as far as the conserved regions are concerned. The LjMLO1 protein from lotus deviated more (94.2 %) in these regions, but in spite of that is still a functional susceptibility gene, according to Humphry et al. (2011). Further, the multiple alignment illustrates that

**Table 2** Degree of similarity of the amino acid sequences of MLO-like proteins to the consensus MLO-sequence of dicots in conserved domains

Protein	Number of deviating amino acids in conserved regions	Similarity to consensus sequence in conserved regions (%)
AtMLO2	6	97.8
AtMLO6	5	98.1
AtMLO12	7	97.4
CaMLO2	3	98.9
LjMLO1	16	94.2
MtMLO1	3	98.9
PsMLO1	6	97.8
SIMLO1	4	98.5
<i>CsaMLO1</i>	4	98.5
<i>CsaMLO8</i>	7	97.3
<i>CsaMLO11</i>	5	98.1

If an amino acid deviated from the consensus sequence but kept the same colour in the Rasmol colour scheme (Sayle 1994), the change in amino acid was neglected

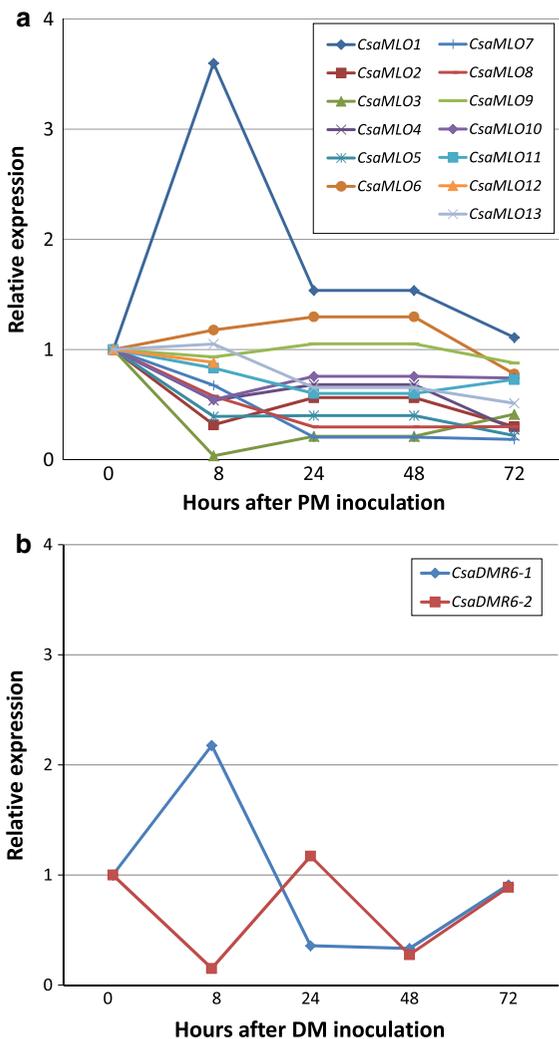
none of the three cucumber genes harbours an early stop codon that would have given rise to a truncated protein. Therefore, none of the three cucumber proteins can be excluded as a candidate gene based on absence of one or more conserved regions.

*CsaMLO1* expression is upregulated after PM inoculation

A characteristic of *MLO*-susceptibility genes is that their transcript abundances are increased about 8 h after inoculation with the PM causing fungus (e.g. Zheng et al. 2013). Therefore we investigated the expression of the MLO-like genes in cucumber after inoculation with PM, using RNA-Seq. Only the expression of *CsaMLO1* was clearly upregulated 8 h after inoculation (Fig. 3).

*PMR*- and *DMR*-like genes in the cucumber genome

We searched for homologs of the *PMR4*, *PMR5* and *PMR6* susceptibility genes for PM. These genes do not belong to the *MLO*-gene family. For *PMR4* in *A. thaliana* we found ten homologous predicted proteins in cucumber (Table 3), named *CsaPMR4*-1 to 10. Two predicted proteins (*CsaPMR4*-2 and *CsaPMR4*-9)



**Fig. 3** Transcript abundances of *MLO*- and *DMR6*-like genes in cucumber leaves after inoculation with the pathogen, measured by means of RNA-Seq. **a** Transcript abundances of *MLO*-like genes upon powdery mildew (PM) infection. **b** Transcript abundances of *DMR6*-like genes upon downy mildew (DM) infection. The transcript abundances before inoculation were set at 1

appeared to be highly similar to AtPMR4 (Fig. 4). For PMR5, only one homologous protein was found in cucumber, which we named CsaPMR5 (Table 3). For PMR6, 13 homologous predicted proteins were detected. Construction of a phylogenetic tree for these 13 predicted proteins revealed that CsaPMR6-5, 12 and 13 show the highest homologies to the PMR6 susceptibility protein in *A. thaliana*. For DMR1 and DMR6 we found only one and two homologous proteins, respectively (Table 3).

We consulted literature on induction of expression of *PMR4*, *PMR5*, *PMR6*, *DMR1*, *DMR6* by PM or DM, and did not find indications of elevated transcript abundance after infection, apart from *DMR6* in *Arabidopsis*. This gene was locally induced after infection with DM in *A. thaliana* (van Damme et al. 2008). Therefore we analyzed the expression to *DMR6* upon infection. However, the *CsaDMR6*-like genes did not show a strong induction (Fig. 3b).

## Discussion

The cucumber *MLO*-like genes as potential S-genes to PM

We searched for *MLO*-like genes in the cucumber genome, and found 13 putative *MLO*-like genes, scattered among the chromosomes (Table 1; Fig. 1). Out of these 13 *MLO*-like genes, three (*CsaMLO1*, *CsaMLO8*, and *CsaMLO11*) code for predicted proteins that belong to Clade V (Fig. 2). Not all *MLO*-like genes that cluster in this clade are susceptibility genes (Zheng et al. 2013), but until now all *MLO*-like genes of dicots that have shown to be required for susceptibility to PM, belong to Clade V (Fig. 2). Therefore, the clustering in this clade is a strong selection criterion for *MLO*-like susceptibility genes. The predicted proteins from these three genes appear to have high similarity to proven *MLO*-like susceptibility genes, and none of the three candidate could be excluded based on deviation in conserved regions or an early truncation of the protein (Online Resource 1).

Transcript abundances of *MLO*-like susceptibility genes tend to increase after PM infection already 5 h after inoculation (e.g. Piffanelli et al. 2002; Zheng et al. 2013). Therefore we investigated the transcript abundances of all *MLO*-like genes in cucumber, using RNA-Seq. Only the expression of *CsaMLO1* was upregulated soon after PM infection. *CsaMLO1* is one of the three putative genes for which the predicted proteins belong to Clade V. This implies that *CsaMLO1* is the most likely candidate for being a susceptibility gene for PM in cucumber according to the transcript induction. However, Zheng et al. (2013) also found an *MLO*-like gene in pepper that was not induced by PM, but still seemed to be a susceptibility gene. Therefore, induction of expression should not be regarded as an absolute selection criterion.

**Table 3** Members of the *CsaPMR* and *CsaDMR* gene family as predicted in the genomic sequence of *C. sativus* var. *sativus* L. in the Cucurbit Genomics Database version 2

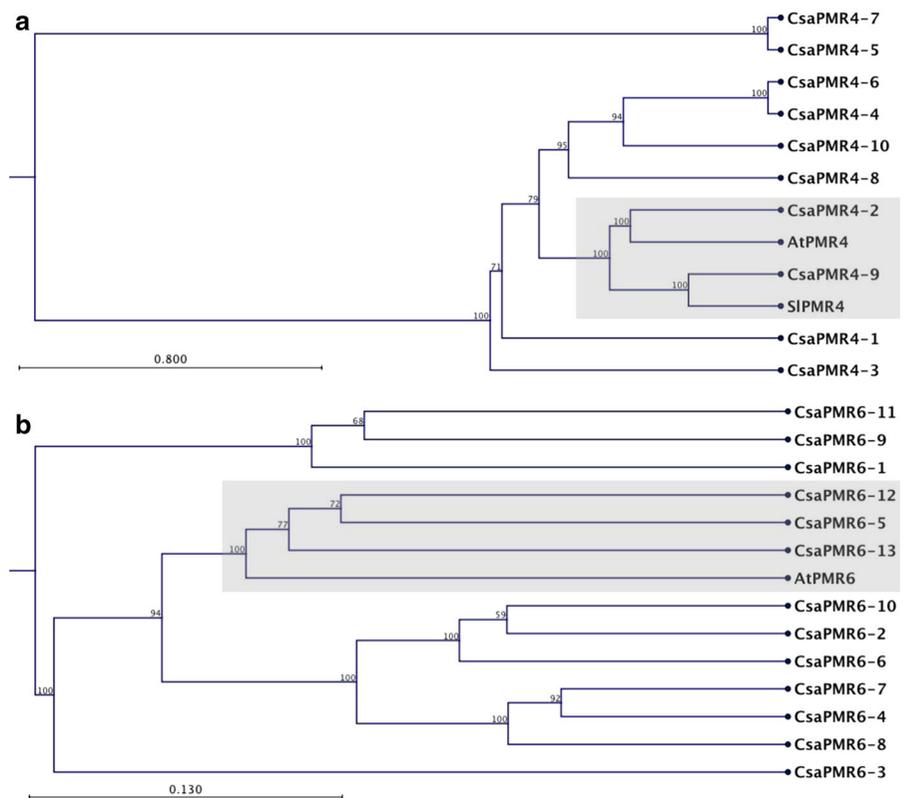
Susceptibility proteins in <i>A. thaliana</i>	Homologues in cucumber	Protein in the Cucurbit Database	Score (bits)	E-value
AtPMR4	CsaPMR4-1	Csa1M002710.1	1,440	0
	CsaPMR4-2	Csa1M073850.1	2,349	0
	CsaPMR4-3	Csa1M605110.1	1,529	0
	CsaPMR4-4	Csa2M302170.1	1,092	0
	CsaPMR4-5	Csa2M302180.1	496	e-140
	CsaPMR4-6	Csa2M302250.1	1,058	0
	CsaPMR4-7	Csa2M302260.1	494	e-139
	CsaPMR4-8	Csa4M621160.1	1,401	0
	CsaPMR4-9	Csa6M128000.1	2,710	0
	CsaPMR4-10	Csa7M236800.1	1,464	0
AtPMR5	CsaPMR5	Csa1M532290.1	503	e-143
AtPMR6	CsaPMR6-1	Csa1M045510.1	435	e-122
	CsaPMR6-2	Csa1M049960.1	490	e-139
	CsaPMR6-3	Csa1M059200.1	381	e-106
	CsaPMR6-4	Csa2M155600.1	489	e-138
	CsaPMR6-5	Csa2M326460.1	568	e-162
	CsaPMR6-6	Csa2M350210.1	484	e-137
	CsaPMR6-7	Csa3M133180.1	492	e-139
	CsaPMR6-8	Csa3M624020.1	471	e-133
	CsaPMR6-9	Csa3M827350.1	396	e-110
	CsaPMR6-10	Csa5M517820.1	468	e-132
	CsaPMR6-11	Csa5M604340.1	399	e-111
	CsaPMR6-12	Csa5M622520.1	573	e-164
	CsaPMR6-13	Csa6M447060.1	559	e-159
AtDMR1	CsaDMR1	Csa7M025730.1	453	e-128
AtDMR6	CsaDMR6-1	Csa4M091870.1	468	e-132
	CsaDMR6-2	Csa5M146870.1	359	e-100

In a patent application Diergaarde et al. (2012) describe a functional test of three Clade V *MLO*-genes from melon (*Cucumis melo*). They used these genes for complementation of *mlo* mutants of *A. thaliana*, lacking two out of three functional *MLO* susceptibility genes (*Atmlo2* and *Atmlo6*) or lacking all three functional genes (*Atmlo2*, *6* and *12*). The complementation by one of these genes, named *CmMLO1*, partially restored the PM susceptibility in *A. thaliana*, indicating that *CmMLO1* is a S-gene (Diergaarde et al. 2012). Cucumber and melon are closely related and belong to the same genus. We aligned the putative cDNA sequence of *CmMLO1* with the putative cDNA sequences of the three Clade V genes of cucumber. The phylogenetic tree revealed that *CmMLO1* is most

related to *CsaMLO8* (Online Resource 2). This result provides evidence that *CsaMLO8* is also a likely candidate.

Zhou et al. (2013) also searched for *MLO*-like gene in the cucumber genome. They used an older version (version 1) of the published genome sequence of cucumber '9930', compared to the sequence we used (version 2). As the gene ID codes changed between these versions, direct comparison is a bit hampered. Zhou et al. detected 14 *MLO*-like sequences, whereas we detected one less. They indicated that Chr. 1 contains three *MLO*-like genes, whereas we detected here only two *MLO*-candidates (Fig. 1). The predicted ORFs of two neighbouring *MLO*-like genes on this chromosome mentioned by Zhou et al. are shorter (513

**Fig. 4** Phylogenetic trees of PMR-like proteins in cucumber. **a** Ten PMR4-like putative proteins in cucumber, and the PMR4 protein, required for susceptibility to powdery mildew in *A. thaliana*; **b** 13 PMR6-like putative proteins in cucumber, and the PMR6 susceptibility protein in *A. thaliana*. Bootstrap values at 100 replicates are displayed



and 1,080 bp) than the ORFs of the other predicted *MLO*-like genes (1,606 bp on average), and the number of transmembrane domains was only one and three respectively, although *MLO*-proteins usually have about seven transmembrane domains (Devoto et al. 2003). However, version 2 of the genome browser combines the two short genes into one gene (i.e. Csa1M086900.1 = *CsaMLO2*), with a ORF size of 1,755 bp that is within the normal range of *MLO*-like genes. Zhou et al. indicated that the two short *MLO*-like genes coded for proteins that clustered in Clade VI and a new Clade VII. However, the *CsaMLO2* predicted in the version 2 cucumber genome clusters in Clade VI (Fig. 2). Therefore, the new Clade VII of Zhou et al., which was also mentioned by Acevedo-Garcia et al. (2014), probably resulted from an error in version 1 of the genome sequence, and refers to a fragment of a Clade VI protein.

In view of the references to the older genome sequence, the two short genes on Chr 1 that should be one gene, and some lengthy gene (such as *CsMLO1415*) coded by Zhou et al., we decided to

keep our own numbering for *MLO*-like genes. Also we decided to use *Csa* as genus code rather than *Cs*, in view of consistency with the genus code *Csa* applied for all putative genes in the whole genome sequence (Huang et al. 2009).

#### Co-localization of *MLO*-, *PMR*-like genes with QTLs for resistance to PM in cucumber

In Fig. 1 we depicted QTL for PM resistance, detected by others. We limited to QTL that explained more than 20 % of the variation. The QTL found by Sakata et al. (2006) and He et al. (2013) represent recessively inherited resistances, but for the other QTL it is not clear from the papers whether the resistances inherited dominantly or recessively. The *CsaMLO1* gene is located at the border of the PM resistance region detected by Fukino et al. (2013), and might be the causal gene for these QTL. However, a more detailed mapping of the QTL or a functional analysis of *CsaMLO1* would be required to provide an answer on the question whether a loss of function mutation in *CsaMLO1* caused this QTL, or whether such a

mutation in this gene or in its regulatory sequences may cause resistance in other genotypes.

At the position of *CsaMLO8*, a second Clade V gene, He et al. (2013) detected a strong, recessively inherited QTL for PM resistance from the cucumber-inbred line WI 2757. *CsaMLO8* is an interesting candidate gene for this QTL. This is also supported by the functional analysis of the *CmMLO1* gene in melon by Diergaarde et al. (2012), as discussed above.

Liu et al. (2008) found a QTL for PM resistance at *CsaMLO13*, but this gene does not cluster in Clade V (Fig. 2), nor was it induced by PM infection (Fig. 3), and consequently it is a less likely candidate gene for the PM QTL. On Chr. 5 three other QTL for PM resistance are displayed, close to *CsaPMR6-10* (Fig. 1). However, this candidate gene is less homologous to *AtPMR6* compared to some other *CsaPMR6*-homologs (Fig. 4b).

*PMR4*, *PMR5*, and *PMR6* are required for susceptibility to PM in *A. thaliana* and tomato (Nishimura et al. 2003; Vogel et al. 2002, 2004; Huibers et al. 2013). We found a series of *PMR4*-, *PMR5*-, and *PMR6*-like genes in the cucumber genome. Six out of these showed high homology to the known *PMR*-genes. Two out of these six genes (*CsaPMR4-2* and *CsaPMR5*) are located at the borders of QTL on chromosome 1 (Fig. 1), and one (*CsaPMR6-12*) is located in the strong recessively inherited QTL for PM resistance at the bottom of chromosome 5, detected by He et al. (2013). The last *PMR6*-like gene is closely linked to the Clade V gene *CsaMLO8*, and both are serious candidates that could explain the strong QTL detected. For the mentioned QTL, a more thorough analysis is required for investigation of a hypothetical causal relationship between a possible loss of function of one of the mentioned candidate susceptibility genes at these loci and the recessively inherited QTL.

#### Co-localization of *DMR*-like genes with QTLs for resistance to DM in cucumber

The number of *DMR*-like genes is far lower compared to *PMR*-like genes, as only one *DMR1*-like gene was detected in the cucumber genome, and only two *DMR6*-like genes (Table 3; Fig. 1). *DMR1* and *DMR6* are susceptibility genes for DM in *A. thaliana* (van Damme et al. 2008, 2009). A homologous gene of *DMR1* in tomato (*SIDMR1*) appeared to be required for PM susceptibility in that crop (Huibers et al. 2013).

Several QTL for DM in cucumber have been described, listed in a review paper from Olczak-Woltman et al. (2011). The majority of the DM resistances in cucumber are inherited recessively (Olczak-Woltman et al. 2011), which indicates the presence of susceptibility genes. We selected for QTL that explained more than 20 % of the variation, and could be positioned on the genome map, using primer sequences and the cucumber genome sequence. We found a QTL that met these criteria at the top of chromosome 5 (Fig. 1; Pang et al. 2013). A recently described QTL with recessively inheriting resistance to DM was detected at the same location by Yoshioka et al. (2014). Surprisingly, also *CsaDMR6-2* resides at this location. Also for this gene, it would be worthwhile to study whether a loss of function mutation, or a low expression level of this gene caused the resistance.

Zeilmaker (2012) cloned a *DMR6*-like gene from cucumber, and over-expressed it under control of the CaMV 35S promoter in a *dmr6* mutant of *A. thaliana*. This restored to some extent the susceptibility to DM, indicating that the cloned *DMR6*-like gene from cucumber is indeed a susceptibility gene to DM. We aligned the sequences of the primers that Zeilmaker used to amplify this cucumber gene, and found that he had amplified the *DMR6*-like gene on Chr 4 (*Csa4M091870.1*), that we named *CsaDMR6-1* (Table 3). Surprisingly, at the position of *CsaDMR6-1* no strong QTL for DM resistance was mapped yet (Fig. 1).

Zhang et al. (2013) also mapped DM resistance in cucumber, and found several weak QTL in three consecutive years. The QTL on Chr 5 appeared in all 3 years. Therefore we included it in Fig. 1, although it explained slightly less than 20 % of the variation. However, the QTL interval is besides the *CsaDMR6-2* gene (Fig. 1), and therefore does not support this gene as the candidate gene in the resistant parent used by Zhang et al. (2013).

We summarize that analysis of the cucumber genome yielded several candidate genes for susceptibility to PM, i.e. *CsaMLO1*, *CsaPMR4-2*, and *CsaPMR5* on chromosome 1, and *CsaMLO8* and *CsaPMR6-12* at the bottom of chromosome 5. These candidate genes are located at QTL for recessively inherited resistance to PM. Two strong QTL for DM resistance at the top of chromosome 5 may be caused by *CsaDMR6-2*, in view of their genetic locations, and in view of the recessive inheritance of the resistances.

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