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Dissimilar evolutionary histories of two resistance gene families in the genus *Solanum*

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ABSTRACT

Genomic analyses have shown that most genes in eukaryotic lineages belong to families. Gene families vary in terms of number of members, nucleotide similarity, gene integrity, expression, and function. Often, the members of gene families are arranged in clusters, which contribute to maintaining similarity among gene copies and also to generate duplicates through replication errors. Gene families offer us an opportunity to examine the forces involved in the evolution of the genomes and to study recombination events and genomic rearrangements. In this work, we focused on the evolution of two plant resistance gene families, *Sw5* and *Mi-1*, and analyzed the completely sequenced nuclear genomes of potato and tomato. We first noticed that the potato genome carries larger resistance gene families than tomato, but all gene copies are pseudogenes. Second, phylogenetic analyses indicated that *Sw5* and *Mi-1* gene families had dissimilar evolutionary histories. In contrast to *Sw5*, *Mi-1* homologues suffered repeated gene conversion events among the gene copies, particularly in the tomato genome.

Keywords: resistance, *Solanum*, evolution, *Mi-1*, *Sw5*.

INTRODUCTION

New genes in a genome are commonly originated by duplication, chromosomal rearrangements, and subsequent divergence from pre-existing genes (Lawton-Rauh 2003). Gene duplication may occur by local or genome-wide events, such as polyploidization, and lead to the formation of a gene family. A gene family is a set of similar genes formed by duplication that generally share related biochemical functions. Most genes within a plant genome belong to gene families that originated as tandem duplicates, dispersed duplications, or genome-wide duplications, and are often arranged in clusters (Chen *et al.* 2007; Jia *et al.* 2015; Wu *et al.* 2014). A great number of gene families were described in plant genomes, including the phytochrome photoreceptor family in tomato (Alba 2000), the apyrase family in legumes that plays an important role in nutrition, photomorphogenesis, and nodulation (Cannon *et al.* 2003), and the calmodulin family in Solanaceae, which codes for different calcium sensor isoforms (Zhao *et al.* 2013). In addition, most resistance genes belong to gene families and are found in clusters (Hulbert *et al.* 2001; Andolfo *et al.* 2013). In some cases, gene family members are highly similar and produce large amounts of a single product, usually needed in a demanding metabolic process (Walsh *et al.* 2001). These gene families are subject to concerted evolution, maintaining highly similar copies by repeated gene conversion. In contrast, other gene families present dissimilar copies that recombine and exchange fragments, generating new allelic forms and increased variability (Ashfield *et al.* 2012). In addition, gene families whose members are arranged in clusters can suffer gene-size amplification by tandem duplications (due to replication slippage or unequal recombination), duplications of large regions (even the whole genome), transposition of DNA sequences, or retrotransposition of RNA transcripts (Thornton *et al.* 2000). The birth-and-death model of gene families implies that whereas some duplicated genes are maintained in the genome for a long time, others are deleted or inactivated through deleterious mutations (Nei and Rooney 2005). It has been suggested that disease resistance loci followed this model of evolution in plants (Michelmore and Meyers 1998; Nam *et al.* 2004).

Their selective effects and population genetic parameters, such as effective population size, will determine the fate of these genomic changes.

In this work, we studied the evolution of two resistance gene families in the genus *Solanum*, family Solanaceae. We focused on resistance gene families because they show a complex evolution in previous studies of the family Solanaceae (Bakker *et al.* 2011; Lozano *et al.* 2012). The resistance gene family, *Sw5*, which was described in the wild tomato *Solanum peruvianum* (Spassova *et al.* 2001), is involved in the resistance to the Tomato Spotted Wilt Virus. In particular, the *Sw5-b* gene copy confers resistance to this virus, and it has been mapped to the long arm of chromosome 9 in the tomato genome (Chagué *et al.* 1996; Stevens *et al.* 1992, 1995). The gene *Mi-1.2* confers resistance to the potato aphid *Macrosiphum euphorbiae*, the whitefly *Bemisia tabaci*, and a group of root-knot nematodes of the genus *Meloidogyne* (Dropkin 1969; Nombela *et al.* 2003; Rossi *et al.* 2003; Jablonska *et al.* 2007). This gene belongs to the *Mi-1* gene family, which forms a cluster of seven copies located in the short arm of chromosome 6 and two copies located in chromosome 5 of the *Solanum lycopersicum* nuclear genome (Seah *et al.* 2004; 2007). Approximately 45 *Mi-1* homologues were identified in the genome of *Solanum tuberosum* diploid heterozygous line RH89-039-16; five times more than those in tomato (Sanchez-Puerta and Masuelli 2011). However, because the potato line analyzed was heterozygous, it was difficult to determine whether those homologues were actual genes or different alleles (Sanchez-Puerta and Masuelli 2011). The genomic arrangement, number of copies, integrity, and evolution of these gene families in solanaceous species remain unclear.

Recently, complete genomic sequences of three *Solanaceae* species were published: the double monoploid line *S. tuberosum* Group Phureja DM1-3 516R44 (The Potato Genome Sequencing Consortium 2011), *S. lycopersicum* cultivar 'Heinz 1706' (The Tomato Genome Consortium 2012), and *Capsicum annuum* cultivar CM334 (Kim *et al.* 2013). The availability of these genomes enabled us to study gene families in three important and closely related crops by comparative genomics. To contrast the evolution of the multigene families *Sw5* and *Mi-1*, we included three smaller resistance genes families (*Hero*, *Hpa2*, and *Pto*) and three single-copy

genes (*Waxy*, *Atg-1*, *Ufm-1*) not related to pathogen resistance.

MATERIALS AND METHODS

Nucleotide data

The genomes of *Solanum lycopersicum* cultivar 'Heinz 1706' and a double monoploid of *Solanum tuberosum* Group Phureja DM1-3 516R44 were analyzed with Blast. Query sequences included the *Sw5-b* gene from *S. lycopersicum* cultivar Stevens (AY007366; 3740 bp), the *Mi-1.2* gene from *S. lycopersicum* variety Motelle (AF091048, 3849 bp), *Hero* from *S. lycopersicum* (NM_001247066; 4280 bp), *Gpa2* from *S. tuberosum* (AF195939; 2710 bp), *Pto* from *S. peruvianum* (DQ019220; 915 bp), *Ufm-1* from *Arabidopsis thaliana* (NM_106420.4; 647 bp), *Waxy* from *S. tuberosum* (EU548081.1; 1320 bp), and *Agt1* from *A. thaliana* (NM_126925.4; 1540 bp). All hits with coverage >450 bp and E-value <1e⁻⁵⁰, including full length and truncated copies, were extracted from the genomic sequences. Coding sequences from *Capsicum annuum* cultivar CM334 genome (Kim *et al.* 2014) were analyzed with BLAST to identify all homologues to the genes *Sw5-b* and *Mi-1.2*. *C. annuum* is closely related to the genus *Solanum* and it can be helpful to analyze the evolutionary history of resistance gene families in potato and tomato. Chromosome maps were drawn with Vector NTI (Lu *et al.* 2005) and edited with Adobe Illustrator. The approximate location of centromeres in the potato and tomato chromosomes was estimated from Park *et al.* (2007) and SolGenomics Network, respectively.

Phylogenetic analyses

Sw5 and *Mi-1* homologues identified in potato, tomato, and hot pepper were aligned individually using MacClade (Maddison and Maddison, 2000). Each nucleotide alignment was subjected to manual editing taking into account the encoded amino acid sequences to identify positional homology. Maximum likelihood analyses were performed with Garli 0.951 (Zwickl 2006) under the General Time Reversible model with parameters for invariant sites and gamma-distributed rate heterogeneity (4 categories). One hundred bootstrap replicates were performed.

RESULTS

Sw5 gene family is four times greater in potato than in tomato

BLAST searches of *Sw5-b* against the nuclear genomes of *S. lycopersicum* and *S. tuberosum* yielded 9 (SlySw5h) and 36 (StbSw5h) homologues, respectively (Table S1). Only one homologue (SlySw5h3 from tomato) covered the entire gene length (3740 bp) and the rest were variable in size (due to indels), ranging from 490 to 4,572 bp (Table S1). Out of 45 *Sw5* homologues identified in both *Solanum* species, 44 were classified as pseudogenes because they were truncated, contained premature stop codons, or had indels that led to frameshifts. The identity between potato homologues and the gene *Sw5-b* was 73-94%; and between tomato homologues and *Sw5-b* was 77-97% (Table S1). We identified 26 *Sw5* homologues in *Capsicum annuum*, which were located in chromosomes 3, 7, and 10 (Table S3). The *Sw5* tomato homologues were found in four chromosomes (chr 1, 6, 9 and 12), while those in the potato genome were identified in seven different chromosomes (chr 1, 5, 6, 7, 8, 9 and 11) (Figure 1). There were several non-syntenic *Sw5* homologues between potato and tomato genomes, such as those found in the potato chromosomes 1, 5, 6, 7, 8 and 11 and those in chromosomes 6 and 12 of tomato (Figure 1). Most *Sw5* homologues were clustered in chromosomes 9 of both tomato and potato genomes. A particularly dense area encompassed 17 *Sw5* homologues clustered within ~360 kb of chromosome 9 of *S. tuberosum*.

Mi-1 homologues were mainly pseudogenes and clustered in chromosome 6 of tomato and potato

A BLAST search of *Mi-1.2* homologues against the complete nuclear genomes of *Solanum lycopersicum* and *S. tuberosum* found 16 (SlyMih) and 38 (StbMih) gene copies, respectively, although most of them were not full-length (Table S2). The functional gene copy *Mi-1.2* of *S. lycopersicum* has three exons, two of which (exons 2 and 3) are protein-coding exons. The first two exons and introns encompass 1,532 bp and were identified only in 5 homologues of the tomato genome under analysis (SlyMih10, SlyMih11, SlyMih12, SlyMih13, and SlyMih14), and in 8 of the 38 homologues in the potato genome (StbMih3, StbMih6, StbMih7, StbMih8, StbMih12,

StbMih14, StbMih17, and StbMih18). Exon 3 sequences were recognized in all homologues of tomato and potato showing variable lengths (Table S2). Out of the 54 *Mi-1* homologues identified in both genomes, 51 were classified as pseudogenes because they were truncated, contained premature stop codons, or had indels that led to frameshifts. Pseudogenes were variable in size, ranging from 717 to 5077 bp due to the occurrence of indels. The identity of each potato gene sequence to the tomato *Mi-1.2* copy ranged between 76-92%. The three full-length *Mi-1* copies (SlyMih11, SlyMih13, and SlyMih14) were found in the tomato genome and no complete genes were found in the potato genome. The *Mi-1* gene family in *Capsicum annuum* had 71 members located in chromosomes 2, 5 and 6 (Table S3). *Mi-1* homologues were found in three tomato chromosomes (chr 5, 6 and 9), and five chromosomes of potato (chr 2, 4, 5, 6 and 9) (Figure 1). Tomato *Mi-1* homologues present in chromosome 6 clustered in 2 loci, while those in potato clustered in five loci of the same chromosome (Figure 1). The three potato-specific clusters in chromosome 6, along with the homologues StbMih1 (in chromosome 2), StbMih2 (in chromosome 4) and several copies in chromosome 5 have no syntenic copies in tomato (Figure 1).

Comparison with other resistance gene families and single copy genes

Blast searches of additional resistance gene families, *Hero*, *Gpa2*, and *Pto*, against the nuclear genomes of potato and tomato also yielded a greater number of gene copies in *S. tuberosum* than in *S. lycopersicum* and those copies were distributed in a higher number of chromosomes of the potato genome (Table 1). In contrast, low-copy genes (*Ufm-1*, *Waxy* and *Agt1*) had only one copy of each gene in the nuclear genomes of potato and tomato and they were in syntenic locations (Table 1).

Evolutionary analyses of Sw5 homologues and their genomic distribution

The phylogenetic tree based on *Sw5* sequences showed that tomato, potato, and hot pepper *Sw5* homologues did not form species-specific monophyletic groups (Figure 2A). In most

cases, homologues found in the same chromosomes in both potato and tomato did not group together in the tree. The distribution of the *Sw5* in chromosomes 9 of potato and tomato was compared to their evolutionary relationships (Figure 2B). Along chromosome 9, tomato *Sw5* homologues were found in three loci (A', B' and C'), and potato homologues in six, where loci D, E and F were not present in tomato. In addition, 17 potato homologues formed a large cluster (Figure 2B, cluster C). Based on the phylogenetic tree (Figure 2A), most of these clustered homologues were closely related to each other, except for *StbSw5h8* and *StbSw5h21*. Finally, we observed a strongly supported sister relationship between the gene copy used as query for the Blast analyses (*Sw5b*) and the only putatively functional copy of *Sw5* identified in this study, *SlySw5h3* (Figure 2A).

Evolutionary analyses of Mi-1 homologues

A phylogenetic analysis of *Mi-1* homologues showed that potato and hot pepper sequences were more numerous and diverse than those from tomato (Figure 3A). All homologues from the genus *Solanum* formed a monophyletic clade divided in two main groups: i) one clade formed by all sequences from chromosome 6 of either tomato or potato, the *SlyMih1* and *SlyMih2* genes from tomato chromosome 5, and the genes *StbMih2* and *StbMih36* from potato chromosomes 4 and 5, respectively; and ii) the other clade included the majority of homologues located in chromosomes 2, 5, and 9 of either species (Figure 3A). All but one tomato homologue from chromosome 6 clustered in a single highly supported group (BS=100%) embedded within a group of potato sequences from chromosome 6. In contrast, tomato *Mi-1* homologues from chromosomes 5 and 9 were interspersed with potato homologues from chromosomes 2, 5, and 9. Individual tomato and potato sequences were not found as sister taxa, except for three pairs of homologues from different chromosomes (Figure 3A, brackets). In addition, we observed a strongly supported sister relationship between the gene copy used as query for the Blast analyses (*Mi-1.2*) and one of the functional copies of *Mi-1* identified in this study, *SlyMih11* (Figure 2A).

Comparing the physical location of *Mi-1* homologues in chromosome 6 of both *Solanum* species, we observed that *Mi-1* copies formed clusters in two and five loci in tomato and potato, respectively (Figure 3B). Cluster C in potato was the most highly populated. All homologues found in the two tomato clusters, except for SlyMih16, formed a well-supported clade in the evolutionary tree, closely related to the potato homologues found in chromosome 6 (Figure 3A). Comparative analyses of the potato and tomato clusters revealed the presence of highly similar intergenic regions between clusters A and A' from potato and tomato, respectively, indicating they were homologous. However, gene copies found in the clusters A and A' did not group together in the phylogenetic tree (Figure 3A).

DISCUSSION

The availability of genomic sequences from *S. tuberosum* and *S. lycopersicum* allowed us to study the evolutionary history of resistance genes in two closely related species of the family Solanaceae. Most resistance genes are organized in tandem arrays, clusters, and super-clusters (Chen *et al.* 2007; Andolfo *et al.* 2013). In this study, tomato and potato sequences of two resistance gene families were often found in clusters, with exceptional members that were distantly located possibly due to duplications followed by translocations. Large resistance gene clusters provide a huge potential for the generation of sequence variation through recombination, facilitating the creation of new alleles or genes upon which pathogen selective pressures act. The investigation of the spatial arrangement of resistance clusters is useful in reconstructing the history of the chromosomal rearrangement that shaped the genome architecture of the ancestral species.

The comparative study we undertook indicated that all gene families analyzed were more numerous in *S. tuberosum* than in *S. lycopersicum*, even though their genomes are roughly equal in size (705 Mb and 759 Mb, respectively). This phenomenon may be due to successive duplications in the potato genome or repeated gene losses in tomato. In previous surveys, syntenic comparisons between the tomato and potato genomes indicated that tomato suffered

the deletion of roughly one-third of the redundant proteome and transposable elements in euchromatic regions (The Tomato Genome Consortium 2012). This study also revealed that the tomato genome has approximately an equal number of resistance genes as *A. thaliana*, but fewer than grape, rice, and the potato genomes (The Tomato Genome Consortium 2012). Plant resistance gene family evolution has probably been influenced by polyploidization, genome size variation, natural and artificial selection including domestication breeding and cultivation, and gene family interactions (Jia *et al.* 2015; Wu *et al.* 2014; Zhong 2015). Given that the family Solanaceae evolved largely in the absence of polyploidization, except for the cultivated potato, but this event is insignificant in evolutionary times, any increase in the size of resistance gene families should be due to segmental duplications (Wu *et al.* 2010). Cross-hybridization experiments in *Solanum* showed that resistance genes have an ancient origin that predated speciation events in the Solanaceae (Quirin *et al.* 2012). After that, tomato and potato genomes suffered small and large rearrangements, along with duplications and deletions that obscured orthologous relationships because neither gene content nor order is strictly conserved (Andolfo *et al.* 2013).

The evolutionary histories of *Sw5* and *Mi-1* gene families were markedly different. Individual tomato *Sw5* homologues maintained a close phylogenetic relationship with potato and hot pepper sequences. This suggests that several gene copies were present in the ancestor of these *Solanaceae* due to early segmental duplications. In contrast, sister relationships between tomato, potato and hot pepper *Mi-1* sequences were not observed. Instead, tomato homologues formed a highly supported monophyletic group, possible due to recurring gene conversion events within the tomato (Seah *et al.* 2007) and potato (Sanchez-Puerta and Masuelli 2011) genomes, respectively.

The tomato/potato *Mi-1* homologues are distributed in less than perfectly matching positions across the two genomes, suggesting that conserved gene order on chromosomes is a mere vestige of common ancestry. *SlyMih* sequences of chromosome 6 are clustered in 2 loci, while *StbMih* sequences are found in 5 loci in the same chromosome. So, three potato clusters (C,

D and E) of chromosome 6, StbMih1 from chromosome 2, StbMih2 from chromosome 4, and some genes from chromosome 5 in potato have no syntenic position in tomato. Novel clusters in potato may have been originated through translocation events. For example, a translocation of a segment of the ancestral cluster B of the potato chromosome 6 could have given rise to the first members of cluster C (Figure 3B). Evidence for this hypothesis includes the close relationship of StbMih33- StbMih26 and StbMih7-StbMih32 in the phylogenetic tree and the similarity of the intergenic sequences between these two pair of genes. Additional clusters of chromosome 6 of potato (clusters D and E) may have also originated by the duplication and translocation of an ancestral copy found in clusters C or A, respectively (Figure 3B). The great number of copies in cluster C was also puzzling. The increase in size of this cluster may have occurred by successive unequal crossing over events. The intimate phylogenetic relationships of some of the genes from this group (StbMih12-StbMih3-StbMih31, StbMih6-StbMih25-StbMih4, StbMih17-StbMih18, and StbMih30-StbMih8) were congruent with this hypothesis.

In contrast to the inferred evolution of the two resistance gene families, single copy genes did not suffer gene duplications in any of the genomes analyzed indicating that gene clusters are more prone to duplication and translocation through unequal crossing overs or errors in the replication or recombination processes (Krebs *et al.* 2013).

The distribution of homologous sequences in the genomes analyzed and the discovery of redundant genes provide insight into how novel pathogen-resistance genes can evolve via subsequent gene duplication events, unequal crossing over, translocation, and diversifying selection (Michelmore and Meyers 1998; Roth *et al.* 2007; Long *et al.* 2003). In conclusion, comparisons of gene arrangements between related plant genomes offer insight on their genome evolution. The complete sequencing of the tomato and potato genomes permitted an unprecedented view of *Solanum* resistance gene families, which may also impact in molecular breeding efforts.

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TABLES

Table 1. Number of gene copies in the tomato and potato genomes

Gene name	Chromosome number ^a	Number of gene copies in <i>S. lycopersicum</i>	Number of gene copies in <i>S. tuberosum</i>
<i>Mi-1.2</i> (3732 bp)	2	0	1
	4	0	1
	5	8	4
	6	7	31
	9	1	1
<i>Sw5-b</i> (3741 bp)	1	1	5
	5	0	2
	6	1	3
	7	0	1
	8	0	1
	9	6	23
	12	1	0
<i>Hero</i> (4280 bp)	3	1	1
	4	8	11
	6	1	1
	9	1	1
<i>Gpa2</i> (3208 bp)	10	0	1
	12	3	15
<i>Pto</i> (915 bp)	3	0	1
	5	5	6
	6	1	1

	11	1	1
<i>Waxy</i> (1320 bp)	8	1	1
<i>Agt-1</i> (1090 bp)	12	1	1
<i>Ufm-1</i> (283 bp)	12	1	1

^a Chromosomes that are not listed, do not contain gene copies for the corresponding gene family.

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Figure 1. Physical location of *Mi-1* and *Sw5* homologues of tomato and potato. Tomato and potato chromosomes are represented in white (T) and grey (P), respectively. *Sw5* and *Mi-1* homologues are indicated on the right and left of each chromosome, respectively. Missing chromosomes do not contain any *Mi-1* or *Sw5* homologues. The approximate location of centromeres in the potato and tomato chromosomes was estimated from Park et al. (2007) and SolGenomics Network, respectively.

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Figure 2: Analyses of Sw5 homologues. **A.** Maximum Likelihood phylogenetic tree of 71 sequences from *Capsicum annuum* (CA), *S. lycopersicum* (SlySw5h) and *S. tuberosum* (StSw5h) based on 3,741 bp. Numbers on branches correspond to bootstrap support values >50% from 100 bootstrap replicates. The chromosome location (Cn) is shown next to the gene name. **B.** Graphical representation of Sw5 homologues located in chromosome 9 of *S. lycopersicum* (above) and *S. tuberosum* (below). Well-supported evolutionary relationships are indicated by solid lines. Arrows with numbers indicate Sw5 homologues and letters represent different loci.

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Figure 3: Analyses of *Mi-1* homologues. **A.** Maximum Likelihood phylogenetic tree of 126 sequences from *Capsicum annuum* (CA), *S. lycopersicum* (SlyMih) and *S. tuberosum* (StbMih) based on 3,876 bp. Numbers on branches correspond to bootstrap support values >50% from 100 bootstrap replicates. The chromosome location (Cn) is shown next to the gene name. **B.** Graphical representation of *Mi-1* homologues from chromosome 6 from *S. lycopersicum* (above) and *S. tuberosum* (below). Well-supported evolutionary relationships are indicated by solid lines. Arrows with numbers indicate *Mi-1* homologues and letters represent different loci.

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Mostly Solanum Sw5 homologues found in Chromosome 9

A

B

Table S1. Sw5 homologues in *S. lycopersicum* and *S. tuberosum* genomes.

Gene Id	Species	Chromosome	Location	E-value	Pseudogene?	Length (bp)
SlySw5h1	<i>S. lycopersicum</i>	1	64132079-64132569	3e-116	y	490
SlySw5h2	<i>S. lycopersicum</i>	6	28770097-28769325	0	y	772
SlySw5h3	<i>S. lycopersicum</i>	9	67305412-67301675	0	n	3740
SlySw5h4	<i>S. lycopersicum</i>	9	67264887-67268567	0	y	3680
SlySw5h5	<i>S. lycopersicum</i>	9	67271867-67274964	0	y	3099
SlySw5h6	<i>S. lycopersicum</i>	9	57623293-57624987	0	y	1694
SlySw5h7	<i>S. lycopersicum</i>	9	57632879-57633525	2e-126	y	646
SlySw5h8	<i>S. lycopersicum</i>	9	60416974-60416289	4e-59	y	685
SlySw5h9	<i>S. lycopersicum</i>	12	36849257-36850871	0	y	1614
StbSw5h1	<i>S. tuberosum</i>	9	52463812-52467551	0	y	3739
StbSw5h2	<i>S. tuberosum</i>	9	52476100-52479765	0	y	3665
StbSw5h3	<i>S. tuberosum</i>	9	39437902-39434178	0	y	3724
StbSw5h4	<i>S. tuberosum</i>	9	52503565-52505756	0	y	2191
StbSw5h5	<i>S. tuberosum</i>	9	52514572-52517091	0	y	2519
StbSw5h6	<i>S. tuberosum</i>	9	52562918-52559071	0	y	3847
StbSw5h7	<i>S. tuberosum</i>	9	52303902-52307768	0	y	3866
StbSw5h8	<i>S. tuberosum</i>	9	52523818-52527160	0	y	3342
StbSw5h9	<i>S. tuberosum</i>	9	52327226-52328474	0	y	1248
StbSw5h10	<i>S. tuberosum</i>	9	52588516-52584861	0	y	3655
StbSw5h11	<i>S. tuberosum</i>	9	52277856-52281626	0	y	3770
StbSw5h12	<i>S. tuberosum</i>	9	52258466-52262124	0	y	3658
StbSw5h13	<i>S. tuberosum</i>	9	52618296-52614558	0	y	3738
StbSw5h14	<i>S. tuberosum</i>	9	52469931-52472995	0	y	3064
StbSw5h15	<i>S. tuberosum</i>	9	52272853-52275919	0	y	3066
StbSw5h16	<i>S. tuberosum</i>	9	51739970-51736787	0	y	3183
StbSw5h17	<i>S. tuberosum</i>	9	52491452-52493110	0	y	1658
StbSw5h18	<i>S. tuberosum</i>	9	22298490-22295479	0	y	3011
StbSw5h19	<i>S. tuberosum</i>	9	52315099-52317260	0	y	2161
StbSw5h20	<i>S. tuberosum</i>	9	19744467-19741900	0	y	2567
StbSw5h21	<i>S. tuberosum</i>	9	52527371-52528596	0	y	1225
StBSw5h22	<i>S. tuberosum</i>	9	39440348-39439645	2e-165	y	703
StbSw5h23	<i>S. tuberosum</i>	9	38423841-38424896	8e-85	y	1055
StbSw5h24	<i>S. tuberosum</i>	1	10828634-10833206	0	y	4572
StbSw5h25	<i>S. tuberosum</i>	1	10855462-10858705	0	y	3243
StbSw5h26	<i>S. tuberosum</i>	1	6964707-6962519	0	y	2188
StbSw5h27	<i>S. tuberosum</i>	1	66440727-66443772	0	y	3045
StbSw5h28	<i>S. tuberosum</i>	1	66711701-66713709	0	y	2008
StbSw5h29	<i>S. tuberosum</i>	5	9511029-9507974	0	y	3055
StbSw5h30	<i>S. tuberosum</i>	5	6557047-6560112	0	y	3065
StbSw5h31	<i>S. tuberosum</i>	6	5921825-5925565	0	y	3740
StbSw5h32	<i>S. tuberosum</i>	6	738971-735677	0	y	3294
StbSw5h33	<i>S. tuberosum</i>	6	5956379-5957030	2e-85	y	651

StbSw5h34	<i>S. tuberosum</i>	7	1352678-1350999	0	y	1679
StbSw5h35	<i>S. tuberosum</i>	8	40493685-40492553	0	y	1132
StbSw5h36	<i>S. tuberosum</i>	11	16500316-16503430	0	y	3115

^a The % identity was calculated by comparing to *Sw5-b* gene.

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% Identity ^a
83
86
97
82
84
77
80
86
81
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92
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83
84
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77

bioRxiv

80
80
84

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Table S2: Mi-1 homologues in *S. lycopersicum* and *S. tuberosum* genomes.

Gene Id	Species	Chromosome	E-value	pseudogene?	Exon1+Intron1	Exon2+Intron2
SlyMih1	<i>S. lycopersicum</i>	5	0	y	n	n
SlyMih2	<i>S. lycopersicum</i>	5	0	y	n	n
SlyMih3	<i>S. lycopersicum</i>	5	0	y	n	n
SlyMih4	<i>S. lycopersicum</i>	5	0	y	n	n
SlyMih5	<i>S. lycopersicum</i>	5	0	y	n	n
SlyMih6	<i>S. lycopersicum</i>	5	0	y	n	n
SlyMih7	<i>S. lycopersicum</i>	5	0	y	n	n
SlyMih8	<i>S. lycopersicum</i>	5	0	y	n	n
SlyMih9	<i>S. lycopersicum</i>	9	3 e-60	y	n	n
SlyMih10	<i>S. lycopersicum</i>	6	0	y	y	y
SlyMih11	<i>S. lycopersicum</i>	6	0	n	y	y
SlyMih12	<i>S. lycopersicum</i>	6	0	y	y	y
SlyMih13	<i>S. lycopersicum</i>	6	0	n	y	y
SlyMih14	<i>S. lycopersicum</i>	6	0	n	y	y
SlyMih15	<i>S. lycopersicum</i>	6	0	y	n	n
SlyMih16	<i>S. lycopersicum</i>	6	0	y	n	n
StbMih1	<i>S. tuberosum</i>	2	0	y	n	n
StbMih2	<i>S. tuberosum</i>	4	0	y	n	n
StbMih3	<i>S. tuberosum</i>	6	0	y	y	y
StbMih4	<i>S. tuberosum</i>	6	0	y	y	n
StbMih5	<i>S. tuberosum</i>	6	0	y	n	n
StbMih6	<i>S. tuberosum</i>	6	0	y	y	y
StbMih7	<i>S. tuberosum</i>	6	0	y	y	y
StbMih8	<i>S. tuberosum</i>	6	0	y	y	y
StbMih9	<i>S. tuberosum</i>	6	0	y	n	n
StbMih10	<i>S. tuberosum</i>	6	0	y	n	n
StbMih11	<i>S. tuberosum</i>	6	0	y	n	n
StbMih12	<i>S. tuberosum</i>	6	0	y	y	y
StbMih13	<i>S. tuberosum</i>	6	0	y	n	n
StbMih14	<i>S. tuberosum</i>	6	0	y	y	y
StbMih15	<i>S. tuberosum</i>	6	0	y	n	n
StbMih16	<i>S. tuberosum</i>	6	0	y	n	n
StbMih17	<i>S. tuberosum</i>	6	0	y	y	y
StbMih18	<i>S. tuberosum</i>	6	0	y	y	y
StbMih19	<i>S. tuberosum</i>	6	0	y	y	n
StbMih20	<i>S. tuberosum</i>	6	0	y	n	n
StbMih21	<i>S. tuberosum</i>	6	0	y	y	n
StbMih22	<i>S. tuberosum</i>	6	0	y	y	n
StbMih23	<i>S. tuberosum</i>	6	0	y	y	n
StbMih24	<i>S. tuberosum</i>	6	0	y	n	n
StbMih25	<i>S. tuberosum</i>	6	0	y	y	n
StbMih26	<i>S. tuberosum</i>	6	0	y	y	n

StbMih27	<i>S. tuberosum</i>	6	0	y	n	n
StbMih28	<i>S. tuberosum</i>	6	0	y	n	n
StbMih29	<i>S. tuberosum</i>	6	0	y	y	n
StbMih30	<i>S. tuberosum</i>	6	0	y	y	n
StbMih31	<i>S. tuberosum</i>	6	0	y	n	n
StbMih32	<i>S. tuberosum</i>	6	0	y	n	n
StbMih33	<i>S. tuberosum</i>	6	0	y	n	n
StbMih34	<i>S. tuberosum</i>	9	2.e-111	y	n	n
StbMih35	<i>S. tuberosum</i>	5	2.e-116	y	n	n
StbMih36	<i>S. tuberosum</i>	5	0	y	n	n
StbMih37	<i>S. tuberosum</i>	5	1.e-138	y	n	n
StbMih38	<i>S. tuberosum</i>	5	0	y	n	n

^a The % identity was calculated by comparing to *Mi-1.2* gene.

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Exon 3 length (bp)	Exon 3% Identity ^a	Exon 3 Location
1656	94	2968283-2969939
1130	83	54023408-54024538
1667	76	63127792-63126125
1629	76	63139824-63141453
2269	76	55466079-55463810
1659	77	58332176-58333835
1627	76	63417394-63419021
1900	75	59752284-59754184
717	74	56645512-56644795
3717	96	2746865-2750582
3714	95	2358513-2354799
3695	95	2703202-2706897
3714	94	2331182-2327468
3708	92	2722412-2726120
3399	96	2377597-2374198
4588	90	2321581-2316994
2166	76	51405914-51408080
3145	85	26212074-26215219
3755	88	4666589-4662834
3185	89	4712285-4709100
3751	86	2782962-2779211
3710	87	4595915-4592205
3063	88	4381959-4385022
3700	85	4784199-4780499
3444	84	21415084-21411640
3097	86	2774764-2771667
2800	86	9765061-9762261
5077	88	4585349-4580272
2643	86	4742038-4739395
3092	89	2830194-2827102
2795	85	9740609-9737814
3104	89	4736112-4733008
3668	92	4620521-4616853
3710	87	4812638-4808928
2346	88	4795389-4793043
2641	86	4758050-4755409
1811	86	2789861-2788050
3533	89	2816538-2813005
2107	91	4767375-4765268
1739	87	4637843-4636104
850	88	4643409-4642559
1982	85	4706085-4704103

1290	81	4800415-4799125
988	84	9768426-9767438
943	84	4615975-4615032
991	88	4745801-4744810
825	85	4764990-4764165
727	86	4680706-4679979
1556	80	4373369-4374925
1489	77	36614185-36615674
1743	76	52767845-52769588
1542	80	25586240-25584698
1551	78	58707965-58706414
1970	76	58715465-58713495

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Table S3: Sw5 homologues in the genome of *Capsicum annuum*

Gene ID	Chromosome	E-value	% Identity ^a	Length (bp)
CA03g03770	3	0	77	3650
CA10g13570	10	0	81	1013
CA03g05100	3	0	76	1505
CA07g05750	7	0	81	810
CA03g03760	3	1 e-166	77	1074
CA03g05110	3	6 e-164	85	583
CA07g16420	7	0	79	2677
CA03g03840	3	4 e-180	82	797
CA03g03380	3	0	77	2220
CA03g01330	3	0	79	1960
CA03g03360	3	0	78	2085
CA03g03350	3	9 e-63	77	459
CA03g03920	3	2 e-108	75	1013
CA03g03970	3	0	79	1537
CA03g04650	3	0	78	3098
CA03g03710	3	0	82	1571
CA03g04670	3	2 e-134	84	515
CA07g05760	7	2 e-104	80	549
CA03g10900	3	1 e-120	81	786
CA03g03730	3	0	83	2004
CA03g03790	3	0	83	1325
CA03g03940	3	0	78	1357
CA03g03800	3	0	82	3715
CA03g03930	3	8 e-168	84	611
CA03g10910	3	1 e-81	86	288
CA03g03890	3	1 e-95	88	595

^a The % identity was calculated by comparing to *Sw5-b* gene.

Table S4: *Mi-1* homologues in the genome of *Capsicum annuum*.

Gene ID	Chromosome	E-value	Exon 3% Identity ^a	Length (bp)
CA06g05130	6	0	82	1184
CA06g05120	6	0	85	832
CA02g24750	2	0	82	3044
CA06g00820	6	2 e-164	87	516
CA06g03680	6	4 e-171	74	658
CA00g30030	unknown	0	83	3135
CA06g01250	6	0	82	2123
CA06g01210	6	1 e-135	84	526
CA06g02810	6	0	85	1008
CA06g01190	6	0	82	2322
CA00g80340	unknown	0	83	3117
CA06g00980	6	0	83	1712
CA06g02200	6	0	82	1280
CA06g02160	6	0	85	1009
CA06g02100	6	0	85	816
CA06g00950	6	0	84	778
CA06g03410	6	0	86	665
CA06g02040	6	5 e-95	86	338
CA06g02030	6	0	82	1261
CA06g02620	6	1 e-76	78	801
CA06g02520	6	0	84	1896
CA06g02680	6	0	84	834
CA06g05110	6	0	84	896
CA06g03630	6	0	80	2230
CA06g01040	6	6 e-119	79	639
CA06g02180	6	3 e-176	85	631
CA00g76980	unknown	0	82	3509
CA06g01770	6	0	82	2349
CA06g02830	6	0	84	2709
CA06g02740	6	0	83	2709
CA06g00660	6	0	84	1680
CA06g01020	6	0	82	1550
CA06g01230	6	0	83	2614
CA06g01750	6	0	86	736
CA06g03650	6	0	83	2061
CA00g30020	unknown	0	83	3093
CA06g03690	6	0	82	1234
CA06g87560	6	0	82	1809
CA05g15170	5	0	82	2161
CA06g01180	6	0	83	3067
CA06g01350	6	0	85	774
CA06g02450	6	7 e-84	83	354
CA06g00910	6	2 e-109	83	441
CA06g00890	6	0	85	1368
CA06g01110	6	0	85	772

CA00g87620	unknown	0	84	953
CA06g01700	6	6 e-109	81	516
CA06g00990	6	0	82	3177
CA00g30010	unknown	0	82	2434
CA06g03420	6	0	83	1224
CA06g02070	6	0	83	1088
CA06g00530	6	0	86	1667
CA06g01130	6	0	81	1241
CA06g01220	6	8 e-118	83	472
CA06g02730	6	0	81	1247
CA06g00770	6	0	83	3108
CA06g02530	6	0	85	669
CA06g00920	6	0	81	1674
CA06g02570	6	0	83	1141
CA06g02420	6	0	83	2945
CA06g01740	6	0	81	1830
CA06g00650	6	2 e-109	86	365
CA06g00730	6	0	84	840
CA06g00750	6	0	85	851
CA06g02150	6	0	83	2240
CA06g00720	6	0	81	3661
CA06g03640	6	0	82	2147
CA06g00610	6	0	77	1923
CA06g00960	6	2 e-73	85	275
CA06g00580	6	0	84	3153
CA06g02170	6	0	78	1883

a The % identity was calculated by comparing to Mi-1.2 gene.