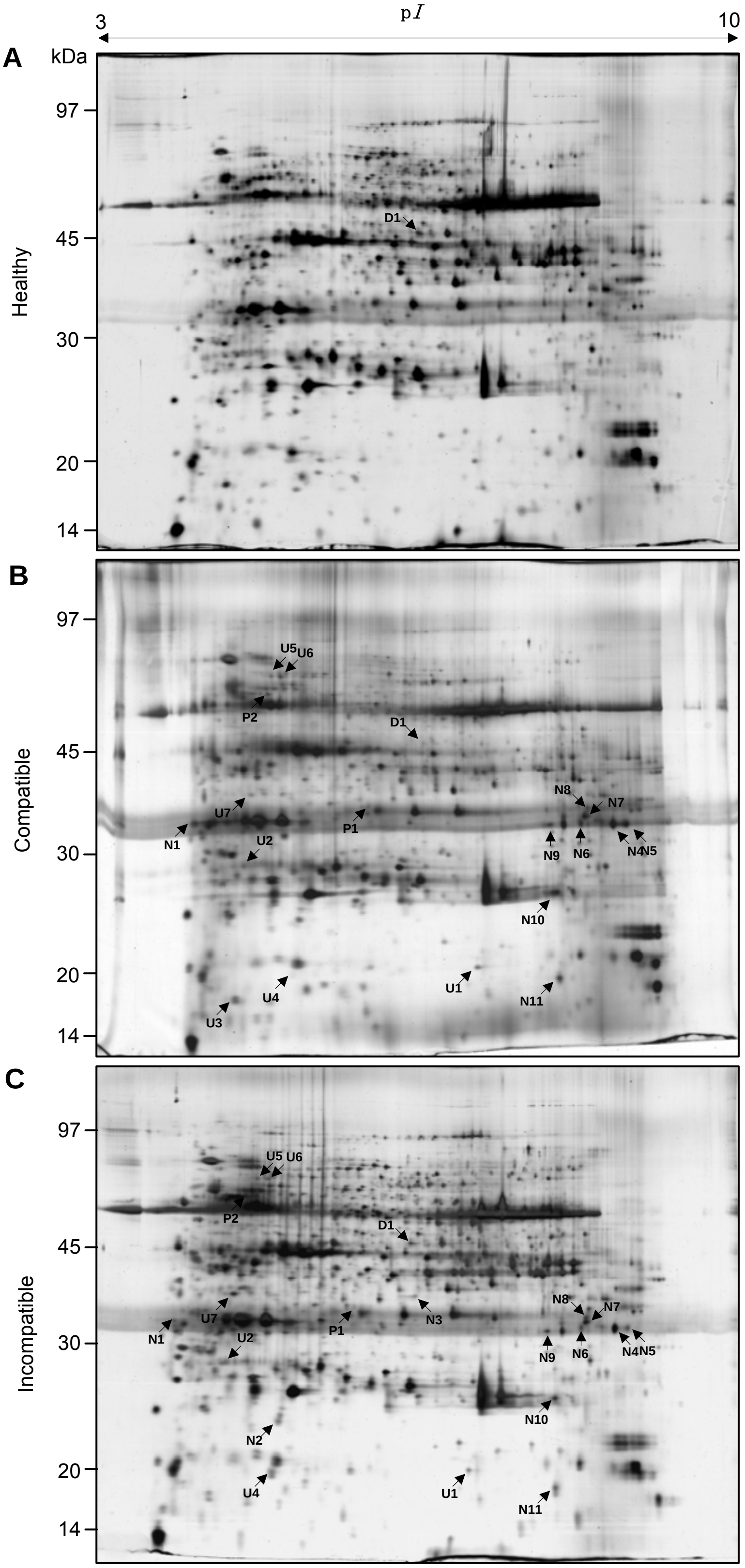
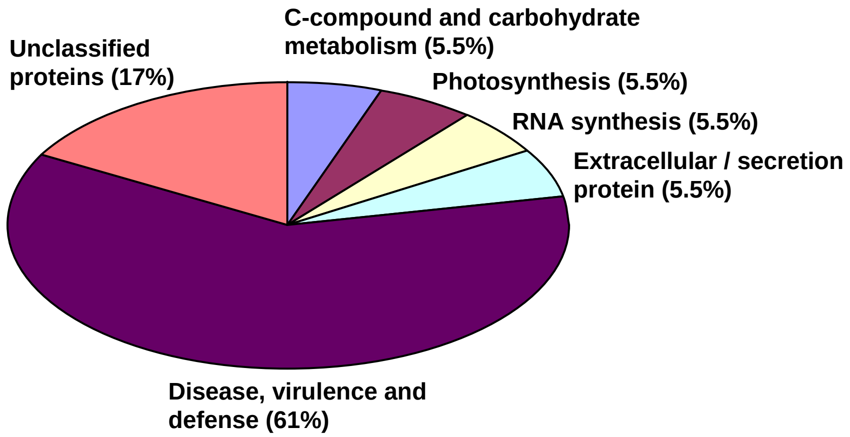


Supplemental Figure 1.

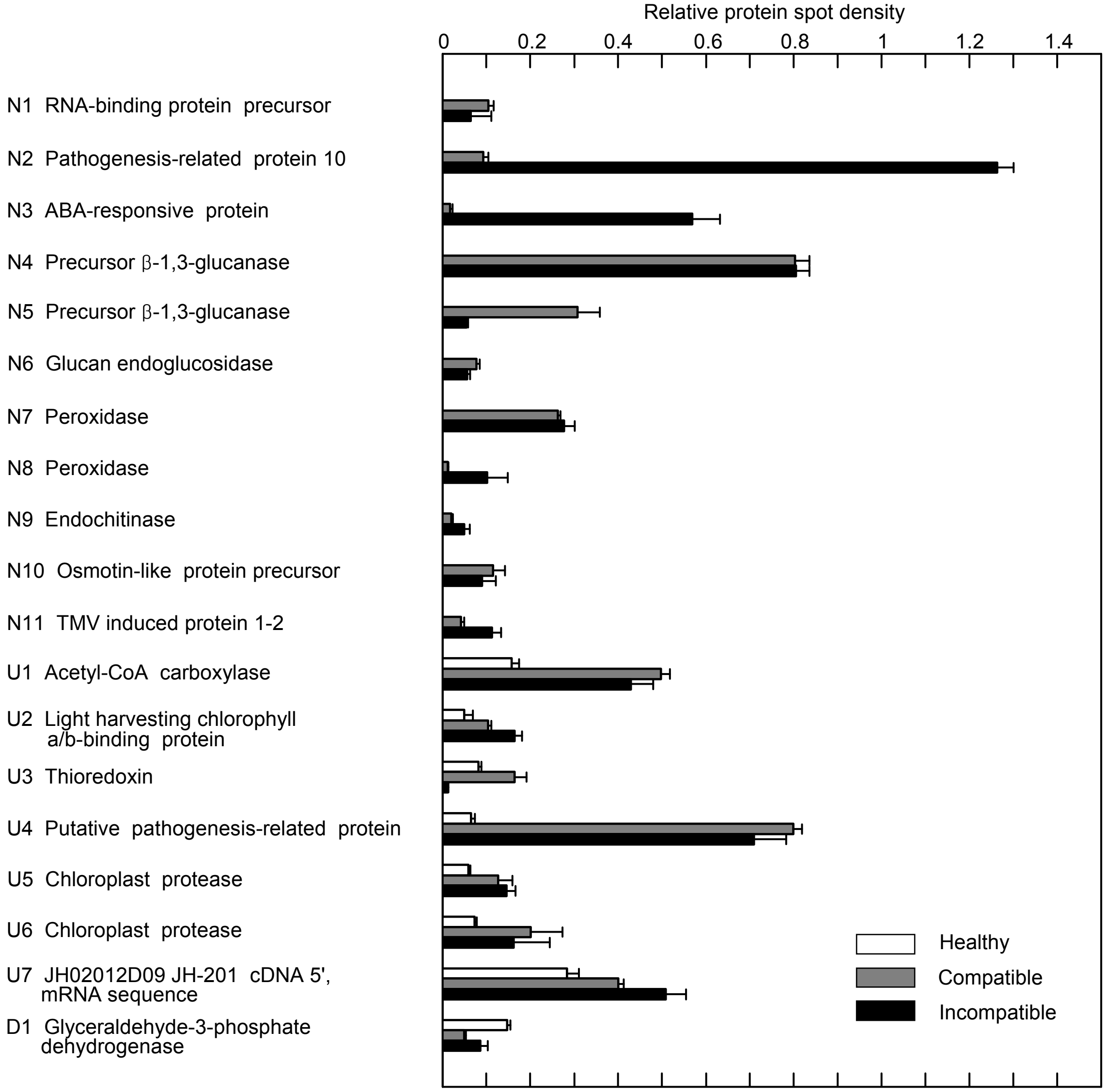
Supplemental Figure 1. 2D Gel Images of Proteins in Pepper Leaves Uninfected and Infected by *Xcv*.

Proteins were separated in the first dimension on IPG strips (24 cm, p*I* 3-10 nonlinear) and in the second dimension on a 12.5% polyacrylamide SDS gel. Differentially expressed proteins are numbered: N1-N11 for newly induced proteins, U1-U7 for upregulated proteins, and D1 for downregulated proteins. These spot numbers are assigned arbitrarily, and are shown in Table 1.
The p*I* range of the p*I* gradient strips is shown above the gel images, and the positions of protein molecular weight markers, MW (kDa), are indicated on the left.
(A) Proteins in healthy pepper leaves.
(B and C) Proteins in pepper leaves 15 h after inoculation with the virulent (compatible) Ds1 **(B)** and avirulent (incompatible) Bv5-4a **(C)** strains of *Xcv*, respectively.



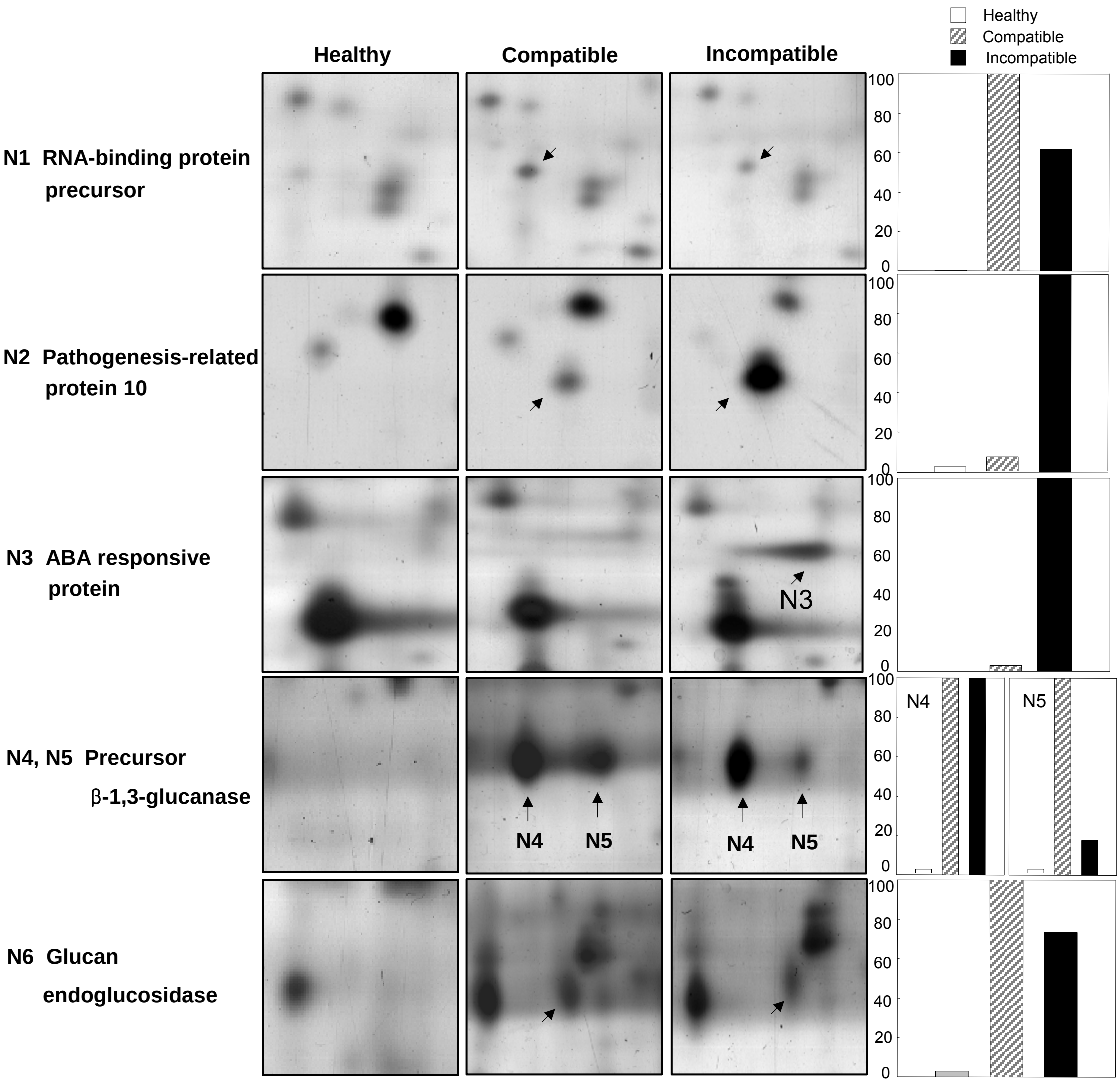
Supplemental Figure 2. The Proportion of Proteins that are Differentially Expressed in Pepper Leaves Infected by the DS1 and Bv5-4a Strains of *Xcv.*

Using *Arabidopsis* putative orthologs of identified pepper proteins, these proteins were functionally categorized based on the SOLANACEAE EST Analysis System and the MIPS *Arabidopsis thaliana* genome database (MatDB).



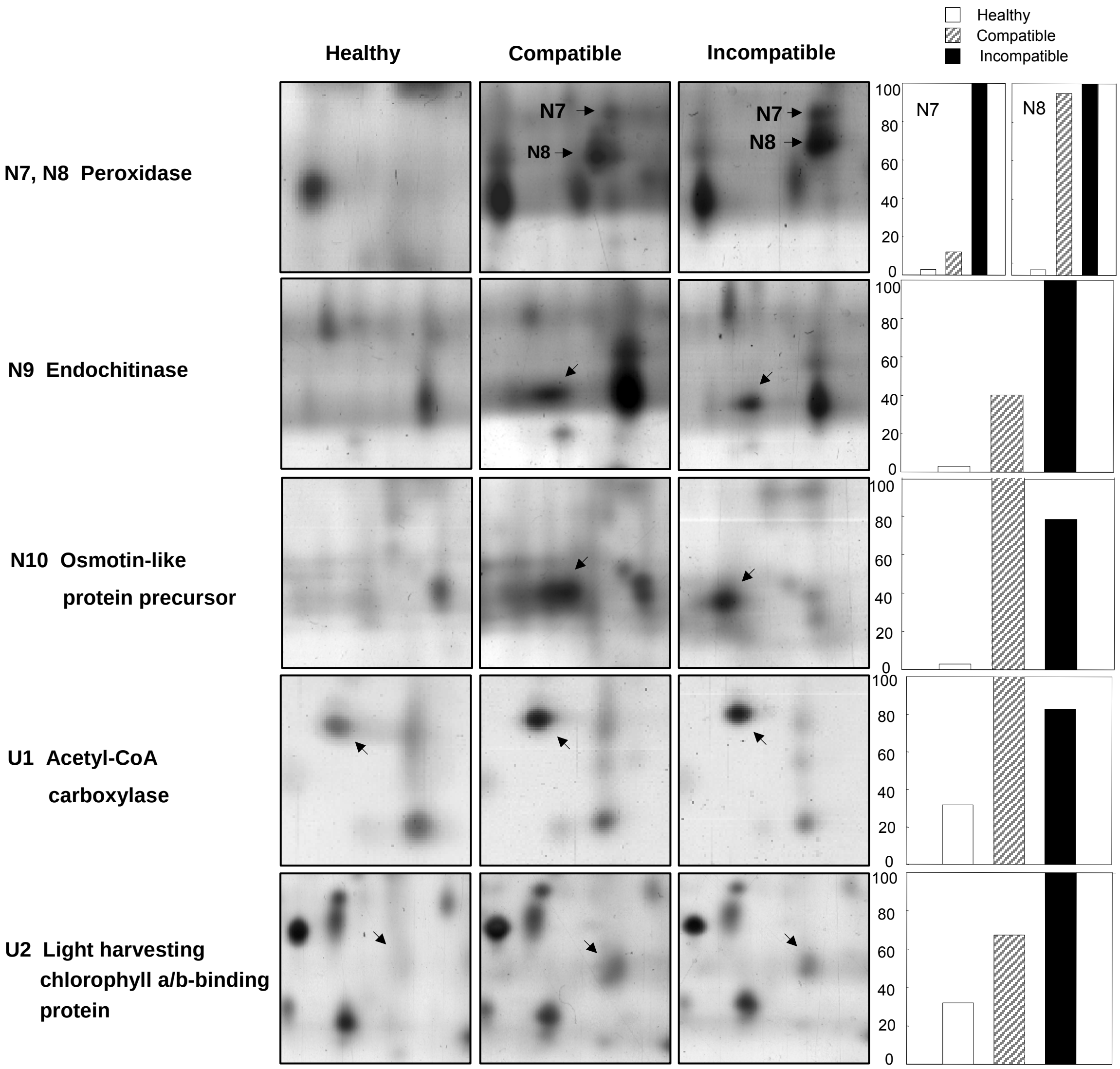
Supplemental Figure 3. Relative Protein Expression Changes in Pepper Leaves Infected by *Xcv.*

The changes in protein spots were calculated with ImageMaster^{TM} 2D Platinum 6.0 and are plotted as the relative densities of spots in Supplemental Figure 1. The values are the means ± standard deviations of percentage volumes of proteins from three independent experiments.

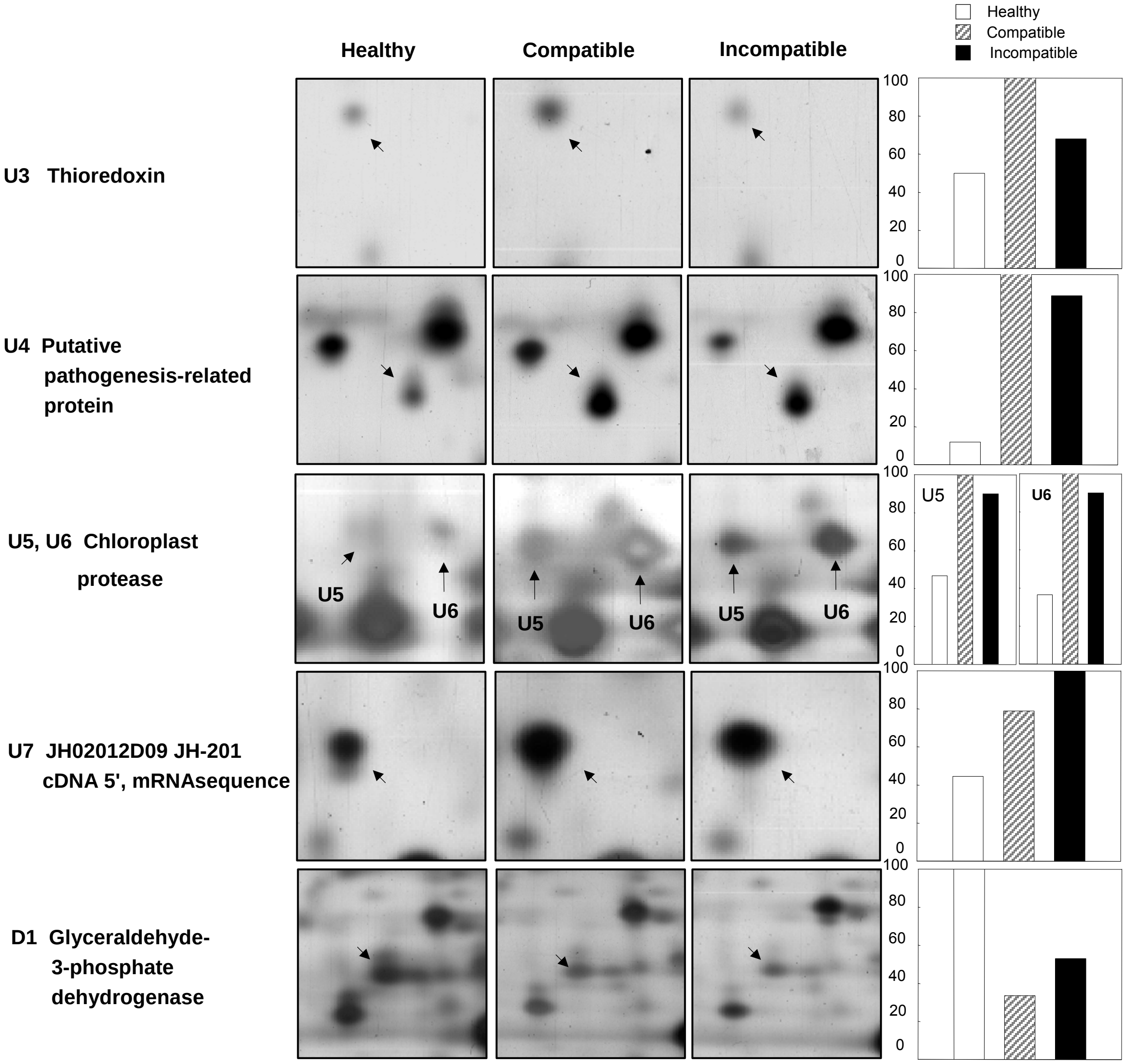


Supplemental Figure 4. Differentially Expressed Protein Spots.

The relative intensities of the protein spots are shown at the right. The highest levels are shown as 100.



Supplemental Figure 4 (continued).



Supplemental Figure 4 (continued).

A

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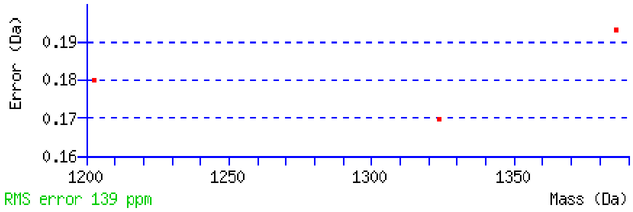
MTGTTEENQP KVQESEPQAP SIPTSSSSDE KEKQPEMDQQ KWGTHIMGPP
AVPTSHPDNQ KAAALWRAAD QKEEFHPQPY VVYTPVDHRP TNNPLESVVN
FNSWSNRAET IARNIWHNLR TGPSVTEAAW GKLNLTAKAL TEGGFEPLYK
QIFSTDPNEQ LKKTFACYLS TTTGPVAGTL YLSSTKVAFC SDRPLSFKAP
SGQEAWSYYK VAIPLTNIGT MNPIVMRENP PERYIQIVTI DGHDFWFMGF
VNFEKATHHL LDALSNFKAQ PPHVGEVPQP ASN*
```

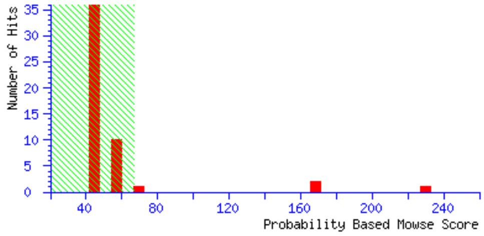
B

```
gi|25038635      Mass: 13009    Score: 230    Queries matched: 3   Frame: 2
KS12040A12 KS12 Capsicum annuum cDNA, mRNA sequence
 Start - End      Observed    Mr(expt)    Mr(calc)      Delta   Miss Sequence
     6 - 17      602.3937   1202.7729   1202.5931     0.1798      0  R.TGPSVTEAAWGK.L    (Ions score 89)
    24 - 35      662.9277   1323.8408   1323.6710     0.1698      0  K.ALTEGGFEPLYK.Q    (Ions score 49)
    84 - 95      693.9164   1385.8182   1385.6251     0.1930      0  K.APSGQEAWSYYK.V    (Ions score 95)
```



Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 67 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Supplemental Figure 5. Identification of ABR1 by LC/MS-MS.

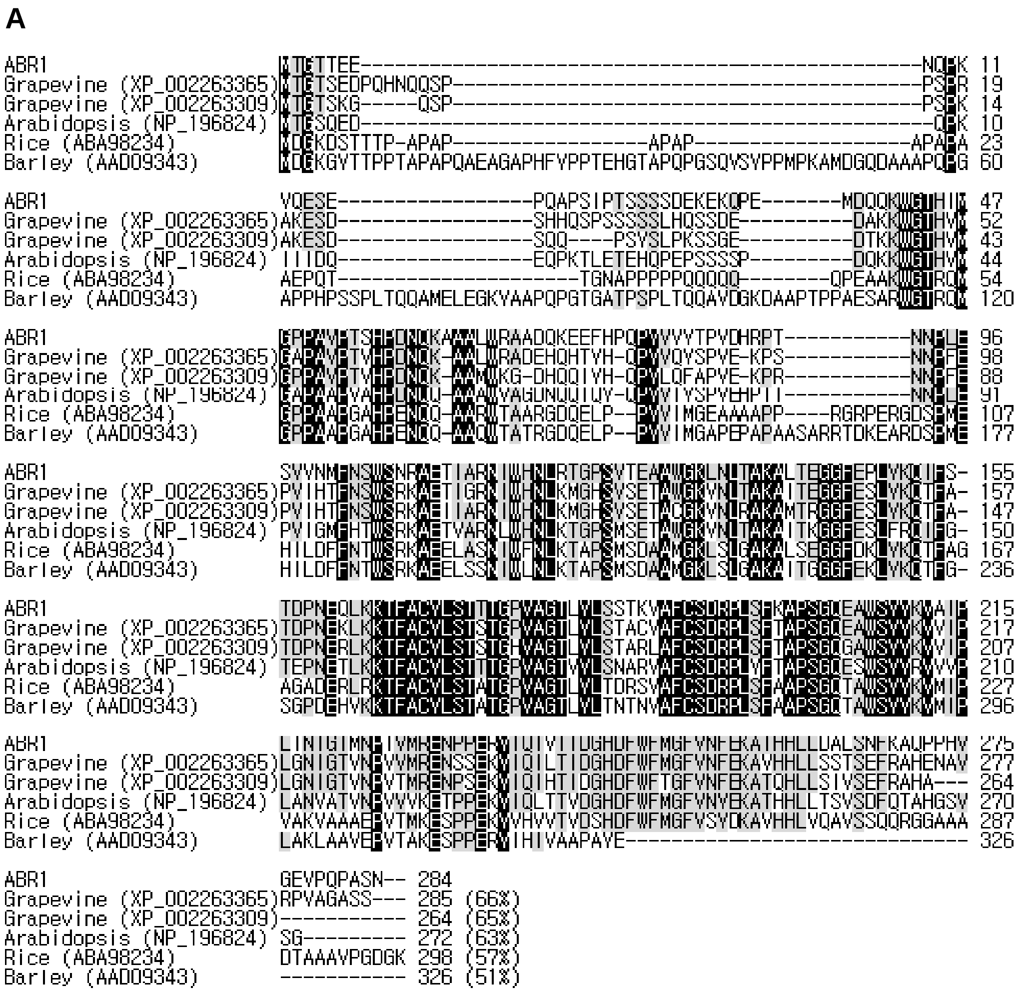
(A) The identified peptides and their positions in the ABR1 sequence are marked in yellow. Previously reported EST sequences are underlined.

(B) The corresponding peptide list, delta mass error of the observed ions, and the probability based MOWSE (for Molecular Weight Search) score by MASCOT MS/MS ion search (http://www.matrixscience.com).

```
cttgaaaatagttttccgcacttaaatcagttaatcATGACAGGCACAACAGAAGAAAAT    60
                                     M  T  G  T  T  E  E  N      8
CAACCCAAAGTTCAAGAATCAGAGCCTCAAGCACCCTCTATTCCTACATCTTCTTCTTCT   120
 Q  P  K  V  Q  E  S  E  P  Q  A  P  S  I  P  T  S  S  S  S     28
GATGAGAAAGAGAAACAACCAGAAATGGATCAACAAAAATGGGGCACACACATAATGGGT   180
 D  E  K  E  K  Q  P  E  M  D  Q  Q  K  W  G  T  H  I  M  G     48
CCACCAGCAGTTCCAACAAGTCATCCAGATAATCAGAAAGCTGCTGCGTTATGGAGAGCT   240
 P  P  A  V  P  T  S  H  P  D  N  Q  K  A  A  A  L  W  R  A     68
GCAGACCAAAAAGAAGAGTTTCACCCACAGCCTTACGTTGTTTATACTCCAGTTGATCAT   300
 A  D  Q  K  E  E  F  H  P  Q  P  Y  V  V  Y  T  P  V  D  H     88
AGGCCTACTAATAATCCACTTGAATCTGTTGTTAATATGTTTAATTCTTGGAGTAATCGA   360
 R  P  T  N  N  P  L  E  S  V  V  N  M  F  N  S  W  S  N  R    108
GCTGAGACCATCGCCCGCAACATCTGGCATAATCTGAGAACTGGACCATCAGTGACAGAA   420
 A  E  T  I  A  R  N  I  W  H  N  L  R  T  G  P  S  V  T  E    128
GCAGCGTGGGGAAAGCTTAATTTGACAGCCAAGGCCTTAACAGAAGGCGGATTCGAGCCG   480
 A  A  W  G  K  L  N  L  T  A  K  A  L  T  E  G  G  F  E  P    148
CTTTACAAGCAGATTTTCTCTACGGACCCTAATGAGCAGCTGAAGAAGACATTTGCTTGT   540
 L  Y  K  Q  I  F  S  T  D  P  N  E  Q  L  K  K  T  F  A  C    168
TATCTTTCAACAACTACTGGTCCTGTTGCTGGAACACTCTATTTGTCATCTACTAAGGTT   600
 A  F  C  S  D  R  P  L  S  F  K  A  P  S  G  Q  E  A  W  S    208
TACTACAAGGTAGCAATACCATTGACAAACATTGGGACTATGAACCCAATAGTGATGAGA   720
 Y  Y  K  V  A  I  P  L  T  N  I  G  T  M  N  P  I  V  M  R    228
GAGAATCCACCAGAGAGGTACATTCAGATAGTTACAATCGATGGTCATGACTTCTGGTTC   780
 E  N  P  P  E  R  Y  I  Q  I  V  T  I  D  G  H  D  F  W  F    248
ATGGGGTTTGTCAATTTTGAGAAAGCAACACATCATCTCCTTGATGCCTTGTCTAATTTT   840
 M  G  F  V  N  F  E  K  A  T  H  H  L  L  D  A  L  S  N  F    268
AAGGCCCAACCTCCTCATGTTGGGGAAGTGCCACAACCAGCTAGTAACTAGgaaaaaatg   900
 K  A  Q  P  P  H  V  G  E  V  P  Q  P  A  S  N  *             285
gctctgtcataacttattgggctgcacactgctttactttttctattttctttgtttgtt   960
cctgcattagatatatgtattctctgtatgtatttttattgcaacattatttgtattata  1020
cacactgctttagtttttattttctctgtttaggagattgacatatatactgtctgtatt  1080
tttattgtaacatttttgtattagactctcgtgtgtatttttattgtaacattatttata  1140
ttgtaaaaaaaaaaaaaaaaaaaaaaaaaaaa                              1172
```

Supplemental Figure 6. Nucleotide and Deduced Amino Acid Sequences of the Pepper (*Capsicum annuum*) ABA-Responsive Protein (*ABR1*) Gene cDNA.

The nucleotide and amino acid residues are numbered at the right. The initiation codon is indicated in bold and the termination codon is indicated by an asterisk (*). The gray box represents the GRAM domain present in glucosyltransferases, myotubularin and other putative membrane-associated proteins.



A

```
ABR1                    MTGTTEE-------------------------------------------------NQPK 11
Grapevine (XP_002263365)MTGTSEDPQHNQQSP-----------------------------------------PSPR 19
Grapevine (XP_002263309)MTGTSKG-----QSP-----------------------------------------PSPK 14
Arabidopsis (NP_196824) MTGSQED--------------------------------------------------QPK 10
Rice (ABA98234)         MDGKDSTTTP-APAP-----------------APAP-------------------APAPA 23
Barley (AAD09343)       MDGKGYTTPPTAPAPQAEAGAPHFVPPTEHGTAPQPGSQVSYPPMPKAMDGQDAAAPQPG 60

ABR1                    VQESE-----------------PQAPSIPTSSSSDEKEKQPE-------MDQQKWGTHIM 47
Grapevine (XP_002263365)AKESD-----------------SHHQSPSSSSSLHQSSDE----------DAKKWGTHVM 52
Grapevine (XP_002263309)AKESD-----------------SQQ----PSYSLPKSSGE----------DTKKWGTHVM 43
Arabidopsis (NP_196824) IIIDQ-----------------EQPKTLETEHQPEPSSSSP---------DQKKWGTHVM 44
Rice (ABA98234)         AEPQT---------------------TGNAPPPPPQQQQQ--------QPEAAKWGTRQM 54
Barley (AAD09343)       APPHPSSPLTQQAMELEGKYAAPQPGTGATPSPLTQQAVDGKDAAPTPPAESARWGTRQM 120

ABR1                    GPPAVFTSHPDNQKAAALWRAADQKEEFHPQPWVVYTPVDHRPT-----------NNPLE 96
Grapevine (XP_002263365)GAPAVFTVHPDNQK-AALWRADEHQHTVH-QPWVQYSPVE-KPS-----------NNPFE 98
Grapevine (XP_002263309)GPPAVFTVHPDNQK-AAMWKG-DHQQIYH-QPWLQFAPVE-KPR-----------NNPFE 88
Arabidopsis (NP_196824) GAPAAFVAHHLNQQ-AAAWVAGDNQQIWY-QPWVIYSPVEHPTI-----------NNPLE 91
Rice (ABA98234)         GPPAAFGAHPENQQ-AARWTAARGDQELP--PWVIMGEAAAAPP----RGRPERGDSPME 107
Barley (AAD09343)       GPPAAFGAHPENQQ-AAQWTATRGDQELP--PWVIMGAPEPAPAASARRTDKEARDSPME 177

ABR1                    SVYNMFNSWSNRAETIARNIWHNLRTGPSVTEAAWGKLNLTAKALTEGGFEPLYKQIFS- 155
Grapevine (XP_002263365)PVIHTFNSWSRKAETIGRNIWHNLKMGHSVSETAWGKVNLTAKAITEGGFESLYKQTFA- 157
Grapevine (XP_002263309)PVIHTFNSWSRKAEIIARNIWHNLKMGHSVSETACGKVNLRAKAMTRGGFESLYKQTFA- 147
Arabidopsis (NP_196824) PVIGMFHTWSRKAETVARNLWHNLKTGPSMSETAWGKVNLTAKAITKGGFESLFRQIFG- 150
Rice (ABA98234)         HILDFFNTWSRKAEELASNIWFNLKTAPSMSDAAMGKLSLGAKALSEGGFDKLYKQTFAG 167
Barley (AAD09343)       HILDFFNTWSRKAEELSSNIWLNLKTAPSMSDAAMGKLSLGAKAITGGGFEKLYKQTFG- 236

ABR1                    TDPNEQLKKTFACYLSTTTGPVAGTLYLSSTKVAFCSDRPLSFKAPSGQEAWSYVKVAIP 215
Grapevine (XP_002263365)TDPNEKLKKTFACYLSTSTGPVAGTLYLSTACVAFCSDRPLSFTAPSGQEAWSYVKVVIP 217
Grapevine (XP_002263309)TDPNERLKKTFACYLSTSTGHVAGTLYLSTARLAFCSDRPLSFTAPSGQGAWSYVKVVIP 207
Arabidopsis (NP_196824) TEPNETLKKTFACYLSTTTGPVAGTVYLSNARVAFCSDRPLVFTAPSGQESWSYVRVVVP 210
Rice (ABA98234)         AGADERLRKTFACYLSTATGPVAGTLYLTDRSVAFCSDRPLSFAAPSGQTAWSYVKVMIP 227
Barley (AAD09343)       SGPDEHVKKTFACYLSTATGPVAGTLYLTNTNVAFCSDRPLSFAAPSGQTAWSYVKVMIP 296

ABR1                    LTNIGIMNFIVMRENPPEKVIQIVITDGHDFWFMGFVNFEKATHHLLDALSNFKAQPPHV 275
Grapevine (XP_002263365)LGNIGTVNFVVMRENSSEKVIQILTIDGHDFWFMGFVNFEKAVHHLLSSTSEFRAHENAV 277
Grapevine (XP_002263309)LGNIGTVNFVTMRENPSEKVIQIHTIDGHDFWFTGFVNFEKATQHLLSIVSEFRAHA--- 264
Arabidopsis (NP_196824) LANVATVNFVVVKETPPEKVIQLTTVDGHDFWFMGFVNYEKATHHLLTSVSDFQTAHGSV 270
Rice (ABA98234)         VAKVAAAEFVTMKESPPEKVVHVVTVDSHDFWFMGFVSYDKAVHHLVQAVSSQQRGGAAA 287
Barley (AAD09343)       LAKLAAVEFVTAKESPPERVIHIVAAPAYE------------------------------ 326

ABR1                    GEVPQPASN-- 284
Grapevine (XP_002263365)RPVAGASS--- 285 (66%)
Grapevine (XP_002263309)----------- 264 (65%)
Arabidopsis (NP_196824) SG--------- 272 (63%)
Rice (ABA98234)         DTAAAVPGDGK 298 (57%)
Barley (AAD09343)       ----------- 326 (51%)
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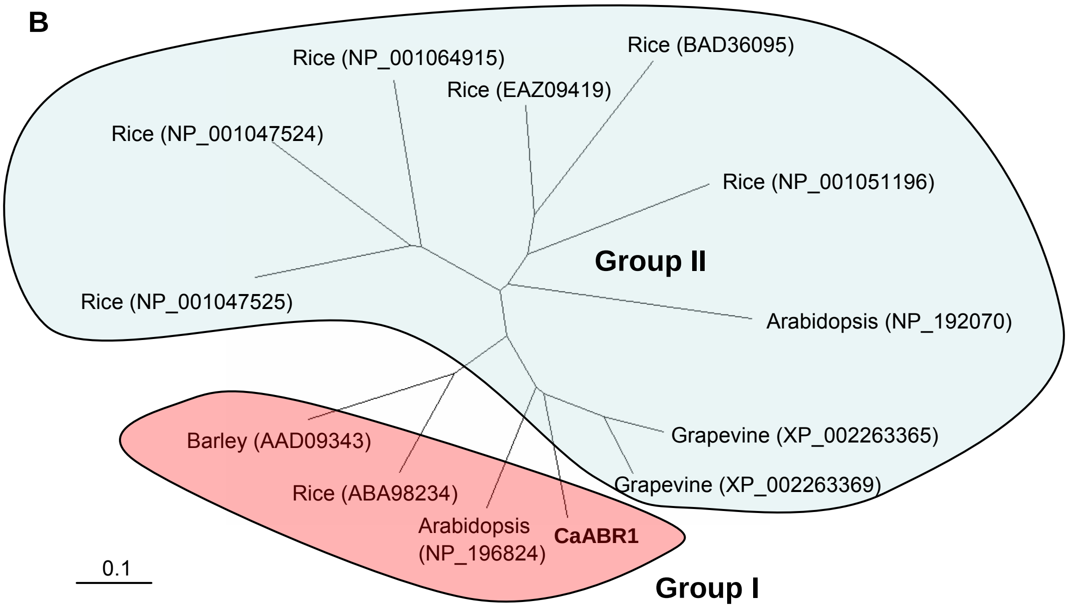
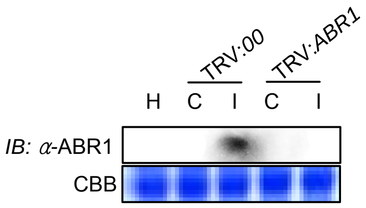


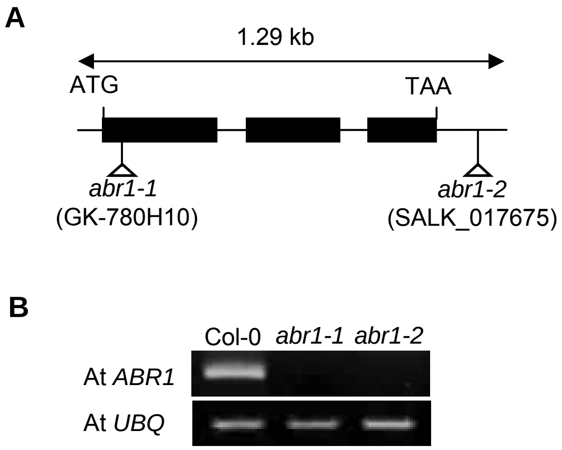
Supplemental Figure 7. Comparison of ABR1 with Other ABA-Responsive Proteins.

(A) Comparison of the deduced amino acid sequences of pepper (*Capsicum annuum*) ABA-responsive protein (ABR1) with those of grapevine unidentified protein products, *Arabidopsis* ABA-responsive protein, rice ABA-responsive protein, and barley ABA-responsive protein (Liu et al., 1999). Gaps introduced for optimal alignment are indicated by hyphens (-). The numbers at the right refer to amino acid residue positions.
(B) Phylogenetic analysis of ABR1 and related plant ABA-responsive protein homologs. The unit at the bottom of the tree indicates the number of substitution events. Group I, ABA-responsive proteins; Group II, unidentified proteins.



Supplemental Figure 8. Immunoblot analysis of Expression of ABR1 in Leaves of Empty Vector (TRV:00) and *ABR1*-Silenced (TRV:ABR1) Pepper Plants.

Total proteins were extracted 24 h after infection by *Xcv. H*: Healthy, C: Compatible, I: Incompatible, CBB: Coomassie brilliant blue.



Supplemental Figure 9. T-DNA Insertion Sites and Expression of *Arabidopsis* ABA-Responsive Protein-Like At *ABR1.*

(A) T-DNA insertion sites in At *ABR1*.
(B) RT-PCR analysis of expression of At *ABR1* in the *abr1-1* and *abr1-2* mutants.

Supplemental Table 1. Pathogen Proteins Newly Expressed in Pepper Leaves Infected by Virulent (compatible) Strain Ds1 and Avirulent (incompatible) Strain Bv5-4a of *Xanthomonas campestris* pv. *vesicatoria*

Spot number	Protein (organism)	Accession number	Experimental pI/MW(kDa)	Theoretical pI/MW(kDa)	SC (%)[a]	MS used for identification
P1	Cation/multidrug efflux pump (*Magnetospirillum magnetotacticum* MS-1)	ZP_00055164	5.77 / 38	6.4 / 93.21	13	MALDI-TOF
P2	60 kDa chaperonin (*Xanthomonas axonopodis* pv. *citri* strain 306)	AAM35431	5.04 / 66	5.0 / 57.15	33	MALDI-TOF
P3	Distinct helicase family with a unique C-terminal domain including a metal-binding cysteine cluster (*Magnetococcus* sp. MC-1)	ZP_00291359	4.71 / 42	5.7 / 187.88	10	MALDI-TOF

[a] SC: Sequence coverage.

Supplemental Table 2. Gene-Specific Primers for qRT-PCR Used in This Study

Gene	Forward and reverse primers
18S rRNA	F:5'-TATGGTGTGCACCGGTCGTCTCGT-3'
	R:5'-GCAGTTGTTCGTCTTTCATAAATCCAA-3'
CaABR1	F:5'-ATGACAGGCACAACAGAAGAAAAT-3'
	R:5'-AATAAGTTATGACAGAGCCATTTT-3'
CaBPR1	F:5'-CAGGATGCAACACTCTGGTGG-3'
	R:5'-ATCAAAGGCCGGTTGGTC-3'
CaPO2	F:5'-ATGGCAGAGAAAACCACCAGCA-3'
	R:5'-TCAAAAAAAAGTGACCTCCTTTCTGT-3'
CaSAR82	F:5'-CAGGGAGATGAATTCTGAGGC-3'
	R:5'-CATATGAACCTCTATGGATTTCTG-3'

Supplemental Table 3. Primers for Generation of GFP Fusion Constructs Used in This Study.

Gene	Forward and reverse primers
CaABR1	F:5'-TCTAGAATGACAGGCACAACAGAAGAA-3'
	R:5'GGATCCAATAAGTTATGACAGAGCC-3'
CaABR1 ^{N}	F:5'-TCTAGAATGACAGGCACAACAGAAGAA-3'
	R:5'-GGATCCCTCGAATCCGCCTTC-3'
CaABR1 ^{GRAM}	F:5'-TCTAGAATGCCGCTTTACAAGCAG-3'
	R:5'-GGATCCCACTATTGGGTTCATAGTCC-3'
CaABR1 ^{C}	F:5'-TCTAGAATGAGAGAGAATCCACCAGAG-3'
	R:5'GGATCCAATAAGTTATGACAGAGCC-3'
CaABR1 $^{\Delta C}$	F:5'-TCTAGAATGACAGGCACAACAGAAGAA-3'
	R:5'-GGATCCCACTATTGGGTTCATAGTCC-3'
CaABR1 $^{\Delta N}$	F:5'-TCTAGAATGCCGCTTTACAAGCAG-3'
	R:5'-GGATCCAATAAGTTATGACAGAGCC-3'