Supplementary data

A *Phytophthora infestans* cystatin-like protein targets a novel tomato papain-like apoplastic protease

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Fig. S1. Multiple sequence alignment of PIP1 and RCR3^{pimp} proteins. Identical amino acids are shaded in black and similar amino acids are shaded in gray. Residue numbers are indicated on the left of the sequences. The alignment was conducted using the program Clustal-X [1], and visualized with BOXSHADE [2].

1. Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG: The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Res* 1997, 25:4876-4882.
2. BOXSHADE [http://bioweb.pasteur.fr/seqanal/interfaces/boxshade.html]

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PIP1    0  MASNFFLKNITVVLLLFSILSLYPFIVTSRNLKELSMLERHENWMVHHGRVYKDDIEKEH
RCR3    0  MAMKVDLMNILIT--LFFVISMFNTQTRGRSQPKLSVSERHELWMSRHGRVYKDEVEKGE

PIP1   60  RFKTFKENVEFIESFNKNGTQRYKLAVNKYADLTTEEFTTSFMGLDTSLLSQQESTATTT
RCR3   58  RFMIFKENMKFIESVNKAGNLSYKLGMNEFADITSQEFLAKFTGLNIPNSYLSPSPMSST

PIP1  120  SFKYDSVTE--VPNSMDWRKRGSVTGVKDQGVCGCCWAFSAAAAIEGAYQIANNELISLS
RCR3  118  EFKINDLSDDYMPSNLDWRESGAVTQVKHQGRCGCCWAFSAVGSLEGAYKIATGNLMEFS

PIP1  178  EQQLLDCSTQNKGCEGGLMTVAYDFLLQNNGGGITTETNYPYEEAQNVCKT-EQPAAVTI
RCR3  178  EQELLDCTTNNYGCNGGLMTNAFDFIIEN--GGISRESDYEYLGEQYTCRSREKTAAVQI

PIP1  237  NGYEVVPSDESSLLKAVVNQPISVGIAANDEFHMYGSGIYDGSCNSRLNHAVTVIGYGTS
RCR3  236  SSYKVVPEGETSLLQAVTKQPVSIGIAASQDLQFYAGGTYDGNCADQINHAVTAIGYGTD

PIP1  297  EEDGTKYWIVKNSWGSDWGEEGYMRIARDVGVDGGHCGIAKVASFPTA-
RCR3  296  EE-GQKYWLLKNSWGTSWGENGFMKIIRDSGDPSGLCDIAKMSSYPNIA
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