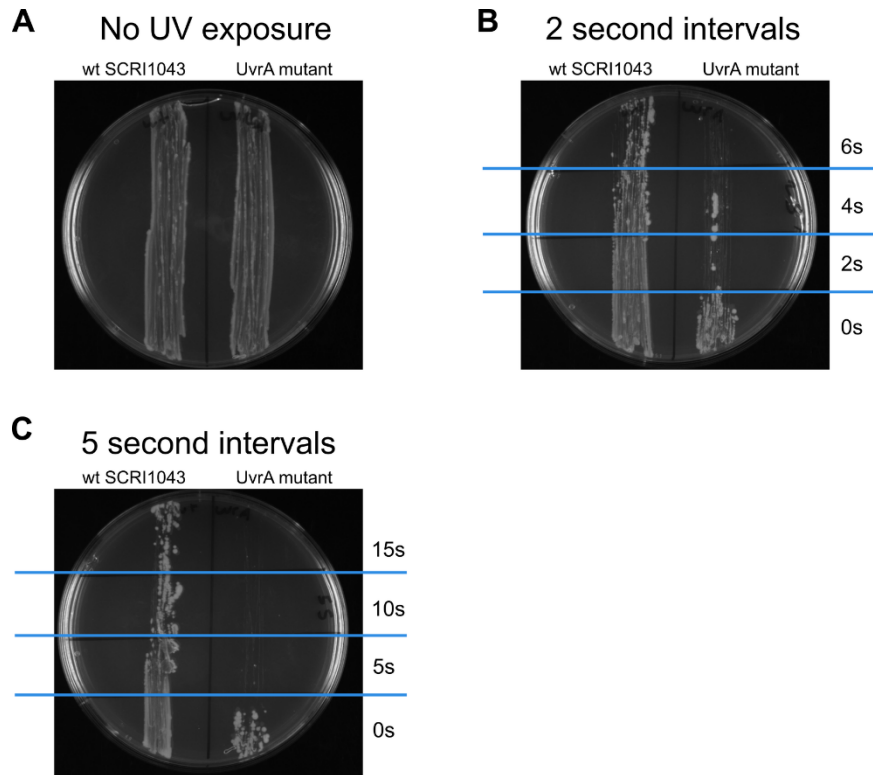


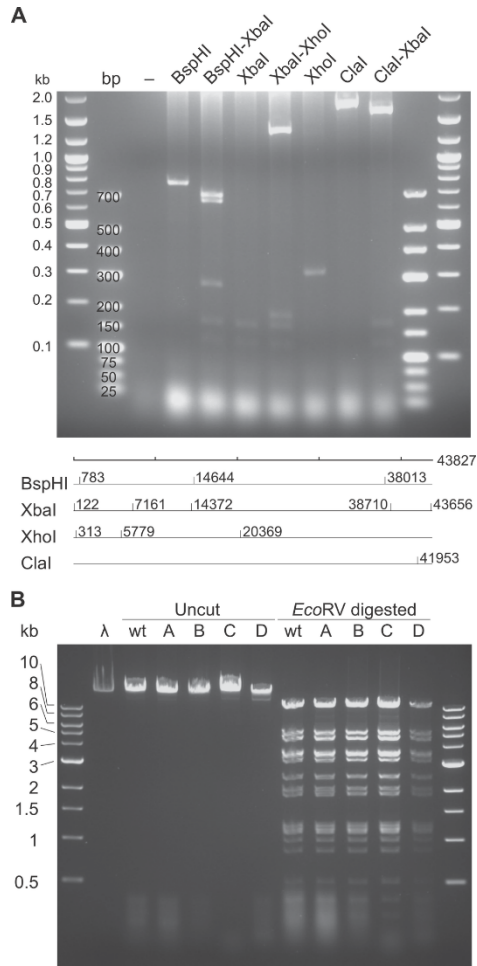
1 **Supplemental material**

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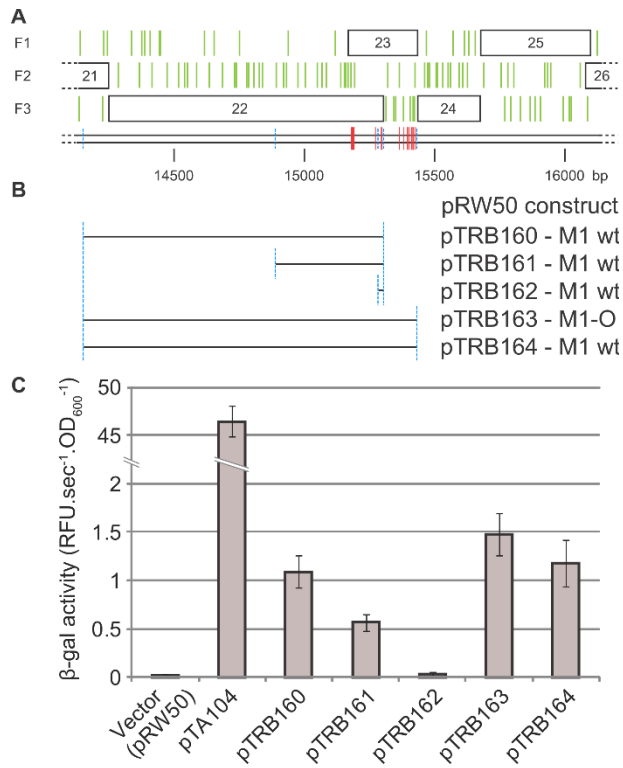
4 FIG S1 UV sensitivity test against *P. atrosepticum* and the *uvrA* mutant. (A) Without exposure to
5 UV light there is no observable difference in growth between wt SCRI1043 and the *uvrA* mutant.
6 (B), and (C) show different UV exposures at two and five seconds intervals respectively. The
7 growth of the *uvrA* mutant is significantly reduced in these conditions while the wt strain shows
8 a less dramatic effect.



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10 FIG S2 Restriction digest analysis of Φ M1 wt and escape phages. (A) Φ M1 wt contains DTRs of
 11 approximately 293 bp. Fourteen μ g of Φ M1 wt genomic DNA was digested with the indicated
 12 enzymes for 3 h, then separated by gel electrophoresis within a 2% agarose gel. The restriction
 13 pattern matched the predicted digest from the finalised Φ M1 wt genomic sequence, as indicated
 14 below the gel image. An uncut sample lane is shown in "-". (B) There are no gross genetic
 15 changes between Φ M1 wt and the selected escape phages Φ M1 A, B, C and D. Genomic DNA
 16 from each phage was digested with *EcoRV* for 3 hours then separated by gel electrophoresis
 17 within a 1% agarose gel. Genomic DNA from phage λ (48,502 bp) was used as a high molecular
 18 weight marker for genomic DNA sizing.

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21 FIG S3 *phiM1-23* has a weak promoter upstream. (A) and (B) Sections of the Φ M1 escape locus
 22 were cloned into the LacZ reporter plasmid pRW50. Blue dotted lines in (A) reflect the construct
 23 boundaries in (B). The figure is drawn to scale. (C) These constructs were tested for LacZ
 24 activity in liquid assays. There is a promoter immediately upstream of *phiM1-23*, though the
 25 activity is weak compared to the positive control, pTA104, which contains the constitutive
 26 ToxIN_{Pa} promoter.

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TABLE S1 Details of ORFs and tRNA within the Φ M1 wild type genome

Gene	Start position (bp)	End position (bp)	Length (bp)	Size (aa)	E value	*Significant BLAST hit (Organism)	Accession No.
<i>phiM1-01</i>	785	940	156	52	1 x 10 ⁻⁷	Hypothetical protein SMR0164 (<i>Serratia marcescens</i> plasmid R478)	NP_941234
<i>phiM1-02</i>	1348	1542	195	65	N/A	No significant homologue	-
<i>phiM1-03</i>	1542	1730	189	63	N/A	No significant homologue	-
<i>phiM1-04</i>	1868	2434	567	189	2 x 10 ⁻¹⁶	Hypothetical protein, gp2 (<i>Vibrio</i> phage VP93)	ACP44073
<i>phiM1-05</i>	2501	2761	261	87	N/A	No significant homologue	-
<i>phiM1-06</i>	2841	2948	108	36	N/A	No significant homologue	-
<i>phiM1-07</i>	3105	3281	177	59	N/A	No significant homologue	-
<i>phiM1-08</i>	3281	3622	342	114	1 x 10 ⁻⁴	Hypothetical protein, gp5 (<i>Vibrio</i> phage VP93)	ACP44076
<i>phiM1-09</i>	3643	5373	1731	577	N/A	No significant homologues	-
<i>phiM1-10</i>	5366	6334	969	323	4 x 10 ⁻³¹	Putative peptidase, gp7 (<i>Vibrio</i> phage VP93)	ACP44078
<i>phiM1-11</i>	6324	6755	432	144	N/A	No significant homolog	-
<i>phiM1-12</i>	6888	7730	843	281	4 x 10 ⁻²⁷	Putative primase DnaG, gp10 (<i>Vibrio</i> phage VP93)	ACP44081
<i>phiM1-13</i>	7821	8054	234	78	N/A	No significant homolog	-
<i>phiM1-14</i>	8058	9317	1260	420	2 x 10 ⁻¹¹⁷	DnaB, putative DNA helicase, gp23 (<i>Pseudomonas</i> phage LKA1)	CAK24991
<i>phiM1-15</i>	9586	9792	207	69	N/A	No significant homolog	-
<i>phiM1-16</i>	9827	10051	225	75	N/A	No significant homolog	-
<i>phiM1-17</i>	10047	10343	297	99	N/A	No significant homolog	-
<i>phiM1-18</i>	10339	10518	180	60	N/A	No significant homolog	-
<i>phiM1-19</i>	10588	11070	483	161	2 x 10 ⁻²³	Hypothetical protein, Orf78 (<i>Pseudomonas</i> phage D3)	AAF80834
<i>phiM1-20</i>	11045	13384	2340	780	0.0	Putative DNA polymerase, gp14 (<i>Vibrio</i> phage VP93)	ACP44085
<i>phiM1-21</i>	13406	14239	834	278	2 x 10 ⁻³¹	Hypothetical protein, gp31 (<i>Pseudomonas</i> phage LKA1)	CAK24999
<i>phiM1-22</i>	14256	15299	1044	348	1 x 10 ⁻⁶⁹	Putative DNA exonuclease, gp32 (<i>Pseudomonas</i> phage LKA1)	CAK25000
<i>phiM1-23</i>	15169	15423	255	85	N/A	No significant homolog	-
<i>phiM1-24</i>	15423	15665	243	81	N/A	No significant homolog	-
<i>phiM1-25</i>	15661	16083	423	141	8 x 10 ⁻³⁴	Putative DNA endonuclease, gp33 (<i>Pseudomonas</i> phage LKA1)	CAK25001
<i>phiM1-26</i>	16067	16285	219	73	N/A	No significant homolog	-
<i>phiM1-27</i>	16450	17421	972	324	3 x 10 ⁻⁷²	Hypothetical phosphatase, gp23 (<i>Enterobacteria</i> phage SP6)	AAP48762
<i>phiM1-28</i>	17535	17900	366	122	8 x 10 ⁻²⁶	PseT polynucleotide kinase, gp27 (<i>Erwinia amylovora</i> phage Era 103)	ABM63417
<i>phiM1-29</i>	17900	18199	300	100	1 x 10 ⁻¹³	Hypothetical protein, gp35 (<i>Pseudomonas</i> phage LKA1)	CAK25003
<i>phiM1-30</i>	18317	18496	180	60	N/A	No significant homolog	-
<i>phiM1-31</i>	18506	20947	2442	814	9 x 10 ⁻¹⁰¹	T3/T7-like RNA polymerase, gp37 (<i>Pseudomonas</i> phage LKA1)	CAK25005
<i>phiM1-32</i>	21043	21237	195	65	N/A	No significant homolog	-

*BLAST searches performed 2012

TABLE S1 continued. Details of ORFs and tRNA within the Φ M1 wild type genome

Gene	Start position (bp)	End position (bp)	Length (bp)	Size (aa)	E value	*Significant BLAST hit (Organism)	Accession No.
<i>phiM1-33</i>	21215	21625	411	137	N/A	No significant homolog	-
<i>phiM1-34</i>	21645	21944	300	100	N/A	No significant homolog	-
<i>phiM1-35</i>	21950	23458	1509	503	4×10^{-120}	Putative head-tail connector protein, gp27 (<i>Vibrio</i> phage VP93)	ACP44098
<i>phiM1-36</i>	23461	24327	867	289	2×10^{-15}	Putative scaffolding protein, gp28 (<i>Vibrio</i> phage VP93)	ACP44099
<i>phiM1-37</i>	24344	24799	456	152	1×10^{-7}	Putative HNH endonuclease, gp21 (<i>Enterobacteria</i> phage T7)	AAP33928
<i>phiM1-38</i>	24799	25779	981	327	8×10^{-82}	Putative capsid protein, gp29 (<i>Vibrio</i> phage VP93)	ACP44100
<i>tRNA^{lle}</i>	25840	25937	98	N/A		Detected de novo using tRNAScan	-
<i>phiM1-39</i>	259555	26509	555	185	3×10^{-29}	Putative tail tubular protein A, gp30 (<i>Vibrio</i> phage VP93)	ACP44101
<i>phiM1-40</i>	26522	28849	2328	776	2×10^{-145}	Putative tail tubular protein B, gp31 (<i>Vibrio</i> phage VP93)	ACP44102
<i>phiM1-41</i>	28849	29460	612	204	7×10^{-6}	Hypothetical protein, gp32 (<i>Vibrio</i> phage VP93)	ACP44103
<i>phiM1-42</i>	29473	32184	2712	904	5×10^{-9}	Putative injection needle component, gp33 (<i>Vibrio</i> phage VP93)	ACP44104
<i>phiM1-43</i>	32197	35985	3789	1263	1×10^{-80}	Putative internal core protein, gp34 (<i>Vibrio</i> phage VP93)	ACP44105
<i>phiM1-44</i>	35998	37599	1602	534	2×10^{-22}	Putative tail-fibre protein, gp35 (<i>Vibrio</i> phage VP93)	ACP44106
<i>phiM1-45</i>	37611	37895	285	95	1×10^{-12}	Putative DNA maturase A, gp37 (<i>Vibrio</i> phage VP93)	ACP44108
<i>phiM1-46</i>	37907	39721	1815	605	0.0	Putative DNA maturase B, gp38 (<i>Vibrio</i> phage VP93)	ACP44109
<i>phiM1-47</i>	39733	39918	186	62	N/A	No significant homolog	
<i>phiM1-48</i>	39932	40468	537	179	5×10^{-5}	Putative structural protein, gp56 (<i>Pseudomonas</i> phage LKA1)	CAK25024
<i>phiM1-49</i>	40481	40864	384	128	2×10^{-10}	Hypothetical protein, gp65 (<i>Enterobacteria</i> phage RTP)	CAJ42269
<i>phiM1-50</i>	40860	41123	264	88	2.8	Hol, putative holing protein, Orf28 (<i>Pasteurelia</i> phage F108)	AAZ93663
<i>phiM1-51</i>	41110	41712	603	201	1×10^{-9}	Putative lysozyme-like endolysin, gp37 (<i>Erwinia</i> phage Φ Ea21-4)	ACH88950
<i>phiM1-52</i>	41730	43487	1758	586	3×10^{-36}	Tailspike protein (<i>Salmonella</i> phage Det7)	CA078738

35 *BLAST searches performed 2012

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TABLE S2 M1-23 mutations

Phages	Mutation relative to Φ M1 wt	Location relative to <i>phiM1-23</i>	Effect on M1-23	Effect on exonuclease	Number of phages
Φ M1-E1	15169 A to C	A1C	Met to Leu	Tyr to Ser	4
Φ M1-E2					
Φ M1-E3					
Φ M1-E4					
Φ M1-C					
Φ M1-E5					
Φ M1-E6					
Φ M1-E7					
Φ M1-E8					
Φ M1-E9					
Φ M1-U4					
Φ M1-U5					
Φ M1-U6					
Φ M1-U9					
Φ M1-E10	15171 G to A	G3A	Met to Ile	Asp to Asn	1
Φ M1-E11	15175 A to T	A7T	Lys to Stop	Gln to Leu	1
Φ M1-E12	15256 A to T	A88T	Lys to Stop	Glu to Val	1
Φ M1-X	15288 AA to A	AA120A	FS to Stop after 9aa	FS to Stop after 45aa	4
Φ M1-E13					
Φ M1-E14					
Φ M1-E15					
Φ M1-B					
Φ M1-E16					
Φ M1-E17					
Φ M1-E18					
Φ M1-E19					
Φ M1-E20					
Φ M1-E21	15292 C to T	C124T	Arg to Stop	Pro to Leu	6
Φ M1-E16					
Φ M1-E17					
Φ M1-E18					
Φ M1-E19					
Φ M1-E20					
Φ M1-E21					
Φ M1-E22					
Φ M1-E23					
Φ M1-Y					
Φ M1-E21	15359 T to C	T191C	Leu to Pro	-	1
Φ M1-E22					
Φ M1-E23					
Φ M1-Y					
Φ M1-W					
Φ M1-E24					
Φ M1-E25					
Φ M1-U7					
Φ M1-O					
Φ M1-Q					
Φ M1-E26	15384 T to G	T216G	Tyr to Stop	-	2
Φ M1-E27					
Φ M1-D					
Φ M1-E					
Φ M1-E28					
Φ M1-V					
Φ M1-E29					
Φ M1-A					
Φ M1-E30					
Φ M1-E21	15397 G to A	G229A	Asp to Asn	-	1
Φ M1-W					
Φ M1-E24					
Φ M1-E25					
Φ M1-U7					
Φ M1-O					
Φ M1-Q					
Φ M1-E26					
Φ M1-E27					
Φ M1-E21	15398 A to T	A230T	Asp to Val	-	1
Φ M1-W					
Φ M1-E24					
Φ M1-E25					
Φ M1-U7					
Φ M1-O					
Φ M1-Q					
Φ M1-E26					
Φ M1-E27					
Φ M1-E24	15398 A to C	A230C	Asp to Ala	-	2
Φ M1-E25					
Φ M1-U7					
Φ M1-O					
Φ M1-Q					
Φ M1-E26					
Φ M1-E27					
Φ M1-D					
Φ M1-E					
Φ M1-E21	15398 A to G	A230G	Asp to Gly	-	1
Φ M1-U7					
Φ M1-O					
Φ M1-Q					
Φ M1-E26					
Φ M1-E27					
Φ M1-D					
Φ M1-E					
Φ M1-E28					
Φ M1-E21	15407 A to C	A239C	Gln to Pro	-	4
Φ M1-U7					
Φ M1-O					
Φ M1-Q					
Φ M1-E26					
Φ M1-E27					
Φ M1-D					
Φ M1-E					
Φ M1-E28					
Φ M1-E21	15410 T to C	T242C	Met to Thr	-	2
Φ M1-D					
Φ M1-E					
Φ M1-E28					
Φ M1-V					
Φ M1-E29					
Φ M1-A					
Φ M1-E30					
Φ M1-E30					
Φ M1-E21	15410 T to G	T242G	Met to Arg	-	1
Φ M1-E28					
Φ M1-V					
Φ M1-E29					
Φ M1-A					
Φ M1-E30					
Φ M1-E30					
Φ M1-E30					
Φ M1-E30					
Φ M1-E21	15415 T to G	T247G	Tyr to Asp	-	2
Φ M1-V					
Φ M1-E29					
Φ M1-A					
Φ M1-E30					
Φ M1-E30					
Φ M1-E30					
Φ M1-E30					
Φ M1-E30					
Φ M1-E21	15416 A to C	A248C	Tyr to Ser	-	2
Φ M1-A					
Φ M1-E30					
Φ M1-E30					
Φ M1-E30					
Φ M1-E30					
Φ M1-E30					
Φ M1-E30					
Φ M1-E30					

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TABLE S2 continued. M1-23 mutations

Phages	Mutation relative to Φ M1 wt	Location relative to <i>phiM1-23</i>	Effect on M123	Effect on exonuclease	Number of phages
Φ M1-Z	15416 A to G	A248G	Tyr to Cys	-	21
Φ M1-E31					
Φ M1-E32					
Φ M1-E33					
Φ M1-E34					
Φ M1-E35					
Φ M1-E36					
Φ M1-E37					
Φ M1-E38					
Φ M1-E39					
Φ M1-E40					
Φ M1-E41					
Φ M1-E42					
Φ M1-E43					
Φ M1-E44					
Φ M1-E45					
Φ M1-E46					
Φ M1-U1					
Φ M1-U2					
Φ M1-U8					
Φ M1-U10					
Φ M1-E47	15419 T to C	T251C	Leu to Pro	-	1
Φ M1-E48	15424 T to C	T256C	Stop to Arg	-	2
Φ M1-E49			(extension of 10 aa)		
Different mutations: 21			Total mutations: 70		