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Supplemental Information

Intra- and inter-generic transfer of pathogenicity island-encoded virulence genes by *cos* phages

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Inventory of Supplemental Information

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Supplementary Table 1. Bacterial strains used in this study.

Strains	Description	Reference
RN4220	Restriction-defective derivative of RN450	(Kreiswirth <i>et al.</i> 1983)
JP10435	RN4220 lysogenic for ϕ 12	(Quiles-Puchalt <i>et al.</i> 2014)
JP11010	JP10435 SaPIbov5 <i>tetM</i>	(Quiles-Puchalt <i>et al.</i> 2014)
JP11229	JP10435 SaPIbov5 <i>tetM</i> Δ cos site	(Quiles-Puchalt <i>et al.</i> 2014)
JP10924	RN4220 lysogenic for ϕ 12 Δ <i>terS</i>	This work
JP11012	JP10924 SaPIbov5 <i>tetM</i>	This work
LUG1170	SH1000 ϕ SLT	(Labandeira-Rey <i>et al.</i> 2007)
JP11194	LUG1170 SaPIbov5 <i>tetM</i>	(Quiles-Puchalt <i>et al.</i> 2014)
JP11230	LUG1170 SaPIbov5 <i>tetM</i> Δ cos site	(Quiles-Puchalt <i>et al.</i> 2014)
JP830	<i>S. epidermidis</i>	(Maiques <i>et al.</i> 2007)
JP831	<i>S. epidermidis</i>	(Maiques <i>et al.</i> 2007)
JP7422	<i>L. monocytogenes</i> SK1351	(Chen & Novick 2009)
JP7432	<i>L. monocytogenes</i> EGDe	(Chen & Novick 2009)
JP1220	<i>S. xylosus</i> C2a	(Maiques <i>et al.</i> 2007)
JP4226	DU298 (<i>S. aureus</i> RN4220 <i>coa::ermC</i>)	(Viana <i>et al.</i> 2010)
JP11545	JP829 (SaPIbov5 <i>tst::tetM</i>)	This work
JP11553	JP830 (SaPIbov5 <i>tst::tetM</i>)	This work
JP11543	JP7422 (SaPIbov5 <i>tst::tetM</i>)	This work
JP11544	JP7432 (SaPIbov5 <i>tst::tetM</i>)	This work
JP11542	JP1220 (SaPIbov5 <i>tst::tetM</i>)	This work
JP11554	JP4226 (SaPIbov5 <i>tst::tetM</i>)	This work
JP10812	<i>E. coli</i> DH5 α (pJP1511)	This work

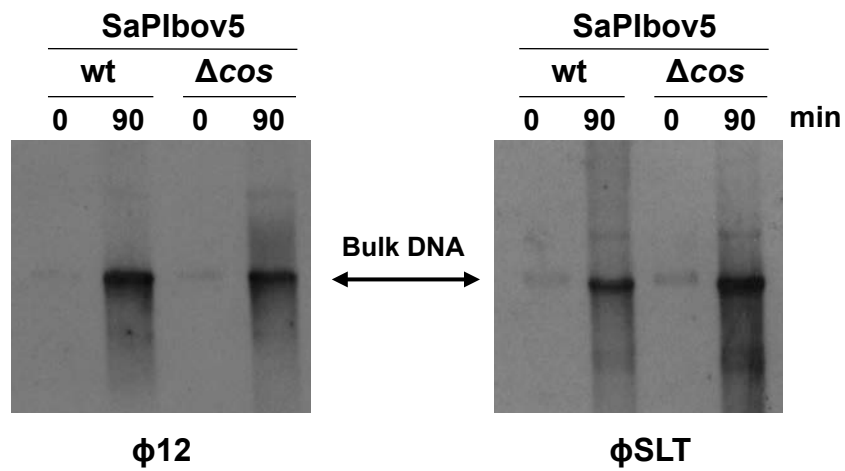
Supplementary Table 2. Primers used in this study.

PCR	Oligonucleotides	Sequence (5'-3')
Integration	lpr-13mP	AA <u>ACTGCAGGA</u> AGTTCAAGACAGATTAGGTCACGG
	lpr-2c	TTGGTGGATTACCAGAAGACATGG
<i>Stl</i>	SaPIbov att-9cE	CC <u>GGAATTC</u> ATTGAGTGGGAATAATTATATATAGC
	SaPIbov1-203mB	CGCGGATCCCATGGAAGGAGCTGGTCAAATGGC
<i>Pri</i>	SaPIbov1-215cB	CGCGGATCCAATTGTGCCGTAATGTGTTGG
	SaPIhor2-12c	CTTCATCAAATTGATACATAGC
<i>Ori</i>	SaPIhor2-7m	ATAGTATTAATGGTTACAGAGC
	SaPIbov5-22c	ATACCCAAATTGTTCTTTAAACTC
<i>Cos</i>	SaPIbov5-54mB	CGCGGATCCTTTCTTCATAACATTTGTTCTATGA
	SaPIbov5-14c	TGTCATAATTATTCTCCTATC
<i>scin</i>	SaPIbov5-28mB	CGCGGATCCAGATAAGCATGATATTAACGGG
	SaPIbov5-38cS	ACGCGT <u>CGACAT</u> TTTTTCATTACCATTAATAAATTTATATACCTG
<i>vwb</i>	SaPIbov5-18m	ATAGGAGAATAATTATGACATACTAAAAACACCCATTTGGG
	SaPIbov att-8mH	CC <u>CAAGCTT</u> TATATATAATTATTCCCACTCAATG
Plasmid	Oligonucleotides	Sequence (5'-3')
pJP1511	phi12p29-1mB	CGCGGATCCGGACCGTTGCAAAAAGG
	phiSLTp29-2c	CCTCTATATATTCTTTCAGCTGTTT
	phi12p29-3m	AAACAGCTGAAAGAATATATAGAGGAGAAGAAGGTGGATTCCG
	phi12p29-4cS	ACGCGT <u>CGACAT</u> GAATTTTCATCAAAAATGCCC

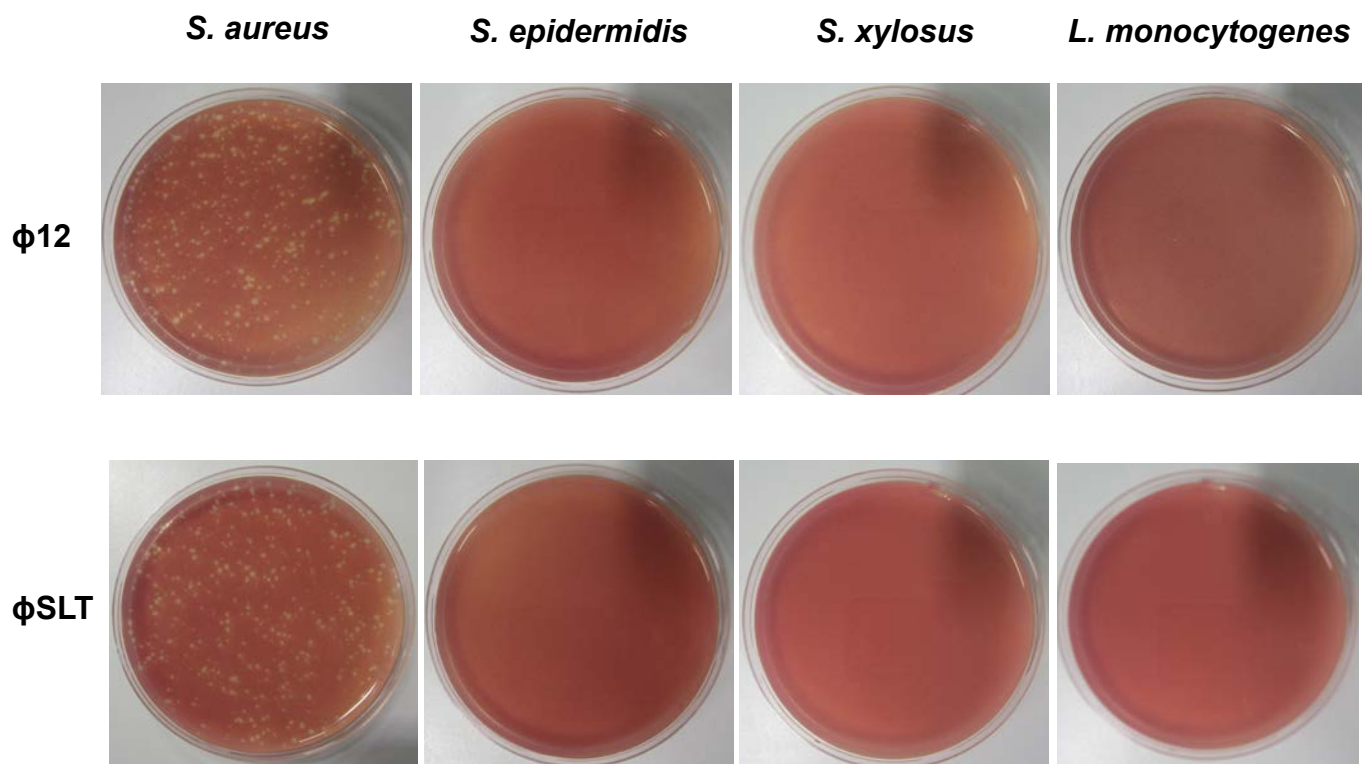
*Underlined is shown the sequence recognized by the restriction enzymes used.

References

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- Viana D, Blanco J, Tormo-Más MÁ, Selva L, Guinane CM, Baselga R, et al. (2010). Adaptation of *Staphylococcus aureus* to ruminant and equine hosts involves SaPI-carried variants of von Willebrand factor-binding protein. *Mol Microbiol* **77**: 1583–1594.



Supplementary Figure 1 Replication analysis of SaPIbov5 Δcos . Southern blot of $\phi 12$ and ϕSLT lysates, from strains carrying SaPIbov5 or SaPIbov5 Δcos , as indicated. Samples were isolated 0 or 90 min after induction with mitomycin C, separated on agarose and blotted with a SaPIbov5-specific probe. Upper band is 'bulk' DNA, and represents replicating SaPIbov5.



SupplementaryFigure 2 Efficiency of plating of cos-phages $\phi 12$ and ϕSLT against various bacterial species. Approximately 10^8 bacteria were infected with 500 p.f.u. of phage $\phi 12$ (upper panel) or ϕSLT (lower panel), plated on phage bottom agar, and incubated 24 h at 32 °C. Plates were stained with 0.1% TTC in TSB and photographed.