

Table S1. Primers used for PCR amplification and Sanger sequencing to verify the mutations of evolved strains: SeSCar (by cyclic exposure to prolonged sublethal treatments of carvacrol) and SeLCar (by cyclic exposure to short lethal treatments of carvacrol),

SeSCar mutations	Forward primer (5' → 3')	Reverse primer (5' → 3')
<i>rrsH</i>	AAGAAGCACCGGCTAACTCC	CCTTTGATTCGTTTCCGGGC
<i>lon</i>	GCGCGTAGCAAGGTCAAAAA	ACCGTCAGTTCGCCTTTCTT
<i>fepA</i>	GGCATGGTGCGGATGATTTC	CGCCAGTGATGTAGACCCAG
<i>yfhP</i>	TTCATCCTTCAGACGACCGC	GTCAATATCGCACGGAACG
<i>nirC</i>	CAGCCAACAAAGAGGCAGTG	ATAAACGCCAGCAGACACCA
SeLCar mutations	Forward primer (5' → 3')	Reverse primer (5' → 3')
TetR regulator	ATCGTTGAGTAGCGAGACGG	TCGATCCATTACCGATGCCA
<i>fliG</i>	CAACGCCAACGAATACCTGC	GACATAGGTATCCTCGCCGC
<i>trkA</i>	GCGCCAAGAAAGTGATGGTG	ACCCACTGCCAAATCCACAA
<i>nirB</i>	AAAAGCCTGACAATTCCGCC	CGCCCATGCTTTCGATCTTG
<i>bigA</i>	CGCAAACTCTCACCGACCT	G TTCAGCGTTTTACCGTCCG
<i>soxR</i>	CTCGGTCGTTCTAGCTCAA	GTCTAACTCTTCGCGCCACT

Table S2. Genomic background of *S. Typhimurium* LT2: a) antibiotic resistant genes and b) pathogenicity islands.

A)

Antibiotic resistance			
Resistance gene	Position	Predicted phenotype	Accession number
aac(6')-Iaa	1707352..1707789	Aminoglycoside resistance	NC_003197

B)

Pathogenic islands			
Gene	Origin	Position	Insertion location
SPI-5	<i>Salmonella</i> Typhimurium LT2	1175309..1184377	tRNA-serT
SPI-2	<i>Salmonella</i> Typhimurium LT2	1461731..1501801	tRNA-valV
C63PI	<i>Salmonella</i> Typhimurium SL1344	2627012..2652253	fhlA
SPI-1	<i>Salmonella</i> Typhimurium LT2	3005849..3050127	fhlA-mutS
SPI-13	<i>Salmonella</i> Gallinarum SGA-10	3277144..3277484	tRNA-pheV
SPI-13	<i>Salmonella</i> Gallinarum SGG-1	3278852..3279255	tRNA-pheV
SPI-13	<i>Salmonella</i> Gallinarum SGD-3	3279563..3279900	tRNA-pheV
SPI-3	<i>Salmonella</i> Typhimurium LT2	3948588..3965203	tRNA-selC
SPI-4	<i>Salmonella</i> Choleraesuis str SC-B67	4477300..4503998	ssb-soxSR
SPI-14	<i>Salmonella</i> Gallinarum SGA-8	926728..927228	Not published
SPI-14	<i>Salmonella</i> Gallinarum SGC-8	932304..932744	Not published

Table S3. A (maximum OD₅₉₅), μ_m (maximum specific growth rate; h⁻¹) and λ (lag time; h) values and error standard of the modified Gompertz model obtained from 3 independently growth curves of *Salmonella enterica* subsp. *enterica* serovar Typhimurium LT2 wild type (SeWT) (A) and evolved strains: SeSCar (B; by cyclic exposure to prolonged sublethal treatments of carvacrol) and SeLCar (C; by cyclic exposure to short lethal treatments of carvacrol), at different concentrations of carvacrol. The goodness of the fit is shown by R^2 and adjusted R^2 values and the root mean square error ($RMSE$).

A) SeWT

Carvacrol ($\mu\text{L/L}$)	Values			Standard error			Goodness of fit		
	A	$\mu_{\max}$	λ	A	$\mu_{\max}$	λ	R^2	Adj. R^2	$RMSE$
0	0.7174	0.4642	3.576	0.0163	0.1491	0.248	0.9348	0.9285	0.0663
0	0.7565	0.4687	3.574	0.0119	0.1005	0.175	0.9680	0.9650	0.0483
0	0.7145	0.5069	3.755	0.0150	0.1361	0.192	0.9454	0.9402	0.0613
50	0.7117	0.3141	3.503	0.0239	0.1197	0.467	0.8756	0.8637	0.0940
50	0.7080	0.3523	3.660	0.0177	0.1014	0.313	0.9298	0.9231	0.0703
50	0.6070	0.3090	3.770	0.0098	0.0570	0.200	0.9701	0.9672	0.0389
100	0.6665	0.2116	5.279	0.0124	0.0348	0.282	0.9753	0.9730	0.0438
100	0.6502	0.1912	5.182	0.0133	0.0327	0.317	0.9697	0.9668	0.0463
100	0.5708	0.2344	5.105	0.0152	0.0663	0.379	0.9397	0.9340	0.0564
150	0.6429	0.0236	12.080	0.0305	0.0022	0.785	0.9719	0.9695	0.0309
150	0.6660	0.0242	12.610	0.0196	0.0014	0.473	0.9894	0.9885	0.0192
150	0.6431	0.0253	13.740	0.0314	0.0026	0.787	0.9680	0.9653	0.0321

B) SeSCar

Carvacrol ($\mu\text{L/L}$)	Values			Standard error			Godness of fit		
	A	$\mu_{\max}$	λ	A	$\mu_{\max}$	λ	R^2	Adj. R^2	RMSE
0	0.7584	0.4321	3.826	0.0092	0.0616	0.140	0.9832	0.9816	0.0368
0	0.6869	0.4195	3.873	0.0304	0.2237	0.499	0.8053	0.7868	0.1228
0	0.7559	0.3776	3.720	0.0171	0.0973	0.282	0.9403	0.9346	0.0678
50	0.6893	0.3474	3.866	0.0196	0.1144	0.366	0.9154	0.9073	0.0775
50	0.7099	0.3282	3.640	0.0222	0.1154	0.413	0.8954	0.8854	0.0876
50	0.6906	0.3787	3.691	0.0098	0.0633	0.164	0.9749	0.9725	0.0392
100	0.7091	0.2958	3.653	0.0062	0.0278	0.123	0.9911	0.9902	0.0242
100	0.7235	0.3016	3.659	0.0198	0.0883	0.383	0.9209	0.9134	0.0769
100	0.7601	0.3072	3.931	0.0170	0.0729	0.324	0.9486	0.9437	0.0653
150	0.5753	0.2336	6.227	0.0105	0.0434	0.250	0.9780	0.9759	0.0373
150	0.6400	0.2927	4.665	0.0134	0.0664	0.270	0.9599	0.9561	0.0512
150	0.6998	0.2590	4.736	0.0083	0.0300	0.171	0.9877	0.9865	0.0307
200	0.5247	0.0179	6.560	0.0549	0.0021	1.254	0.9132	0.9053	0.0386
200	0.4917	0.0142	8.567	0.0393	0.0011	0.822	0.9600	0.9564	0.0204
200	0.5439	0.0203	10.370	0.0293	0.0015	0.638	0.9752	0.9729	0.0204
250	0.4508	0.0190	13.860	0.0329	0.0024	0.862	0.9501	0.9456	0.0230
250	0.6351	0.0139	11.970	0.0768	0.0008	0.681	0.9712	0.9686	0.0165
250	0.4577	0.0179	10.930	0.0242	0.0013	0.631	0.9746	0.9723	0.0173

C) SeLCar

Carvacrol ($\mu\text{L/L}$)	Values			Standard error			Godness of fit		
	A	$\mu_{\max}$	λ	A	$\mu_{\max}$	λ	R^2	Adj. R^2	RMSE
0	0.6850	0.4468	3.634	0.0094	0.0826	0.142	0.9754	0.9731	0.0384
0	0.7017	0.4447	3.758	0.0103	0.0789	0.149	0.9736	0.9711	0.0416
0	0.7078	0.4684	3.750	0.0105	0.0861	0.145	0.9723	0.9696	0.0427
50	0.6647	0.4112	3.612	0.0161	0.1312	0.262	0.9284	0.9216	0.0654
50	0.6495	0.3180	3.668	0.0038	0.0213	0.074	0.9958	0.9954	0.0151
50	0.6570	0.3720	3.746	0.0120	0.0800	0.206	0.9598	0.9560	0.0481
100	0.6404	0.2889	3.612	0.0156	0.0788	0.328	0.9324	0.9259	0.0615
100	0.7275	0.2374	3.527	0.0064	0.0197	0.139	0.9919	0.9911	0.0241
100	0.7105	0.2528	3.634	0.0096	0.0338	0.205	0.9801	0.9782	0.0366
150	0.4898	0.0718	6.324	0.0188	0.0129	0.640	0.9462	0.9413	0.0485
150	0.5975	0.0789	6.054	0.0202	0.0114	0.561	0.9603	0.9567	0.0490
150	0.5034	0.1147	5.776	0.0104	0.0167	0.344	0.9746	0.9723	0.0342
200	0.6030	0.0198	5.405	0.0279	0.0010	0.558	0.9810	0.9793	0.0193
200	0.5818	0.0249	6.972	0.0180	0.0009	0.368	0.9908	0.9900	0.0152
200	0.6212	0.0254	7.036	0.0220	0.0011	0.425	0.9875	0.9863	0.0180
250	0.4497	0.0266	6.115	0.0297	0.0026	0.769	0.9573	0.9535	0.0320
250	0.6529	0.0140	9.497	0.0731	0.0009	0.725	0.9666	0.9636	0.0191
250	0.5375	0.0240	6.870	0.0262	0.0014	0.577	0.9769	0.9748	0.0229
300	0.4733	0.0188	7.425	0.0401	0.0019	1.020	0.9382	0.9326	0.0318
300	0.5541	0.0143	7.466	0.0435	0.0010	0.752	0.9669	0.9639	0.0197
300	0.5077	0.0169	7.158	0.0329	0.0012	0.765	0.9651	0.9619	0.0221
350	0.4467	0.0175	12.860	0.0360	0.0022	0.931	0.9463	0.9415	0.0240
350	0.5054	0.0136	12.840	0.0665	0.0014	0.875	0.9414	0.9361	0.0217
350	0.5336	0.0114	12.260	0.1156	0.0011	1.201	0.9227	0.9157	0.0228

Table S4. Genetic variations detected by whole genome sequencing (WGS) between SeWT and the reference genome of *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. LT2 (NCBI accession: NC_003197.2). Single nucleotide variation (SNV), insertion (Ins) and deletion (Del).

Genome position	Genes	Locus tag	Mutation*	Change	Information
290,718	<i>rrsH</i>	STM0249	SNV: C1529A	No coding	RNA 16S ribosomal
364,623	<i>crl</i>	STM0319	Del: -T 104	Frame shift	Sigma factor-binding protein
416,555	<i>prpR</i>	STM0367	SNV: C1159T	Leu387Phe	Operon regulator
453,939	<i>brnQ</i>	STM0399	SNV: C681T	Silent mutation (Tyr227)	Branched-chain amino acid transport system carrier protein
509,118	<i>cypD</i>	STM0452	SNV: T450A	Asp150Glu	Peptidylprolyl isomerase
608,859	<i>fimH</i>	STM0547	SNV: G182C	Gly61Ala	Adhesin
1,205,933	Intergenic <i>wraB - ycdF</i>	STM1119 STM1120	SNV: G → A	No coding	-
1,778,104	<i>ycjF</i>	STM1684	SNV: T821C	Leu274Pro	UPF0283 membrane protein
1,841,398	-	STM1747	SNV: G98A	Arg33Gln	Hypothetical protein
1,849,642	<i>hnr</i>	STM1753	SNV: T305G	Val102Gly	Regulator of RpoS
3,469,143	<i>dacB</i>	STM3300	SNV: C483T	Silent mutation (Ser161)	Transpeptidase
3,673,628	<i>malQ</i>	STM3513	SNV: T287G	Leu96Arg	4-Alpha-glucanotransferase
3,675,952	<i>malP</i>	STM3514	Del: -GCCGCCTG 358	Frame shift	Alpha-1,4 phosphorylase
3,819,815	-	STM3633	SNV: T562C	Silent mutation (Leu188)	LacI family transcriptional regulator
4,122,937	<i>gppA</i>	STM3913	SNV: G385T	Gly129Cys	Pyrophosphatase
4,122,950	<i>gppA</i> <i>rhlB</i>	STM3913 STM3914	Del: -1,179 pb	Knock-out (<i>gppA</i> , <i>rhlB</i>)	Pyrophosphatase ATP-dependent RNA helicase RhlB
4,291,432	<i>yjiQ</i>	STM4082	SNV: G323A	Stop-gain	Hypothetical protein
4,294,693	<i>glpK</i>	STM4086	SNV: G1171A	Asp391Asn	Glycerol kinase
4,697,694	<i>treB</i>	STM4454	Ins: + A 543	Frame shift	Pseudogene (trehalose metabolism)

*Position respect to the start of the coding region.