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Diagram illustrating the genomic organization and regulatory elements of the *rstA* and *rstR* genes. The DNA sequence is shown with various regulatory motifs and coding regions highlighted.

Regulatory Elements:

- 10 and -35 regions:** Conserved promoter elements (Shine-Dalgarno sequence) for both genes, located upstream of the *rstA* and *rstR* coding regions.
- Operator sites (O_1 , O_2 , O_3):** Specific DNA sequences (indicated by green bars) that serve as binding sites for regulatory proteins, located downstream of the *rstA* and *rstR* coding regions.

Gene Structure:

- rstA* gene:** The coding region is indicated by a red arrow labeled *rstA*. The sequence is shown as GAGTGA...CAT...CTGTCAAG...TTCA-ATTTATAGTGA.
- rstR* gene:** The coding region is indicated by a red arrow labeled *rstR*. The sequence is shown as TGTTC...ATGTTTAGTTCA...ATTAGG-GA...T-AGAAATAAATCAAGCTAAAGGGGATTG-TTATGAAGATAAAAGAAAGGCTAGCC.

The diagram shows the relative positions of these elements, with the *rstA* gene located upstream of the *rstR* gene. The *rstA* gene is transcribed from left to right, and the *rstR* gene is transcribed from right to left. The *rstA* gene is flanked by O_1 and O_2 operator sites, while the *rstR* gene is flanked by O_3 operator sites.

Half-site operator sequences	known predicted	RstR operators	
Promoter elements (-10, -35)	known predicted	LexA-binding site	CTGT...

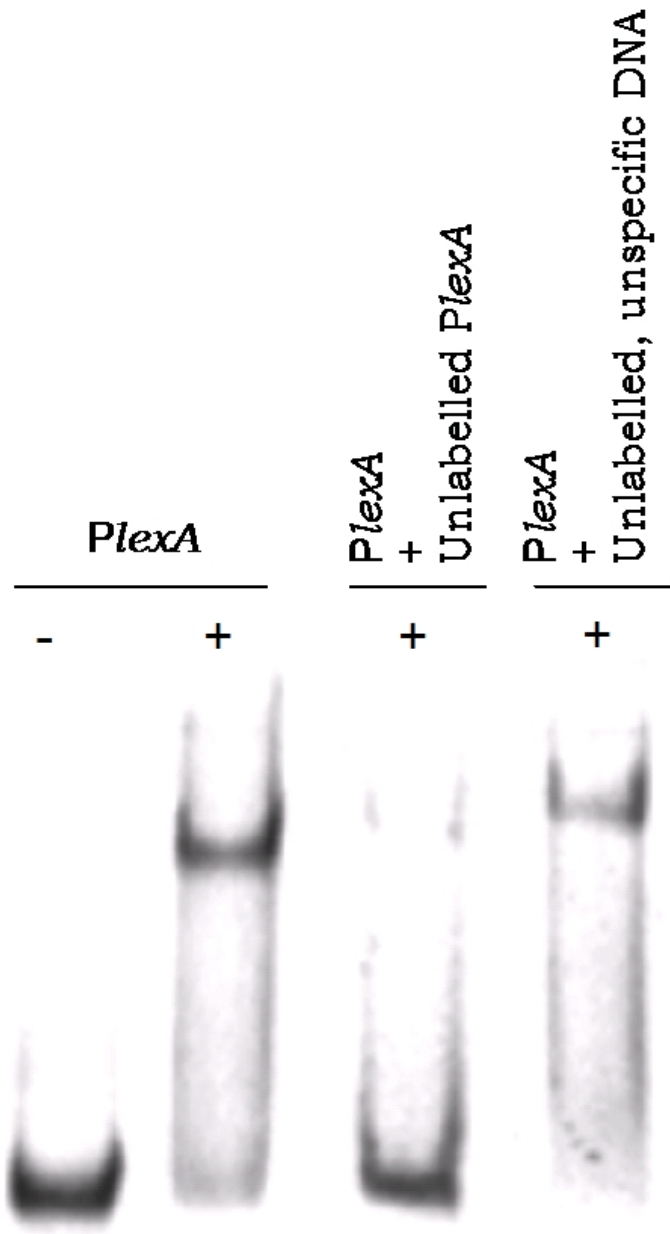
HCUF01
 HC-43A1
 HC-61A1
 N16961
2010EL-1786
 O395
 MJ-1236
 BX_330286
 v51
 Consensus

Sequence logos for the LexA-binding site. The top sequence is the consensus sequence: AATGCGCAGTTTCAAGACTAATGTACAAAAAACAGCC-TTACAAT-AGAAATAAATCAAGCTAAAG. Below it are six experimental sequences, with the first one highlighted in red. The sequences are: 1. AATGCGCAGTTTCAAGACTAATGTACAAAAAACAGCC-TTACAAT-AGAAATAAATCAAGCTAAAG (red), 2. TATTGGGATTGTAA--CAGCTGTCAAAAAACAGGATTATAATGTTCAAAAATAAGCACAACTATAG, 3. TATTGGGATTGTAA--CAGCTGTCAAAAAACAGGATTATAATGTTCAAAAATAAGCACAACTATAG, 4. TATTGGGATTGTAA--CGACTGTCAAAAAACAGGATTATAATGTTCAAAAATAAGCACAACTATAG, 5. AATTGTGATTGTAA--CGACTGTCAAAAAACAGGATTATAATGTTCAAAAATAAGCACAACTATAG, 6. AATTGTGATTGTAA--CGACTGTCAAAAAACAGGATTATAATGTTCAAAAATAAGCACAACTATAG. The LexA-binding site is indicated by a blue box around the sequence AATGTACAAAAAACAGCC. The El Tor sequence is indicated by a red line under the first sequence. The Classical sequence is indicated by a green line under the last sequence.

Ind5	TGGCACGGCGGAGATGTTTTTGTGTTGTGTTGAACACTTCCATACCGTCTCCTGTT	ACAATAATAACTGT
HFU-02	TGGCACGGCGGAGATGTTTTTGTGTTGTGTTGAACACTTCCATACCGTCTCCTGTT	ACAATAATAACTGT
HC-48A1	TGGCACGGCGGAGATGTTTTTGTGTTGTGTTGAACACTTCCATACCGTCTCCTGTT	ACAATAATAACTGT
MO10	TGGCACGGCGGAGATGTTTTTGTGTTGTGTTGAACACTTCCATACCGTCTCCTGTT	ACAATAATAACTGT
HC-28A1	TGGCACGGCGGAGATGTTTTTGTGTTGTGTTGAACACTTCCATACCGTCTCCTGTT	ACAATAATAACTGT
B33	TGGCACGGCGGAGATGTTTTTGTGTTGTGTTGAACACTTCCATACCGTCTCCTGTT	ACAATAATAACTGT
MZO-3	TGGCACGGCGGAGATGTTTTTGTGTT	CGTGTTGAACACTTCCATACCGTCTCCTGTTACAATAATAACTGT

Ind5	TACAAGATTGAATGTTACAGTTTAAACTGT	AGATTAGTCAACAGTTAAAATTGTTGAAA	GGCTACAGTTT
HFU-02	TACAAGATTGAATGTTACAGTTTAAACTGT	AGATTAGTCAACAGTTAAAATTGTTGAAA	GGCTACAGTTT
HC-48A1	TACAAGATTGAATGTTACAGTTTAAACTGT	AGATTAGTCAACAGTTAAAATTGTTGAAA	GGCTACAGTTT
MO10	TACAAGATTGAATGTTACAGTTTAAACTGT	AGATTAGTCAACAGTTAAAATTGTTGAAA	GGCTACAGTTT
HC-28A1	TACAAGATTGAATGTTACAGTTTAAACTGT	AGATTAGTCAACAGTTAAAATTGTTGAAA	GGCTACAGTTT
B33	TACAAGATTGAATGTTACAGTTTAAACTGT	AGATTAGTCAACAGTTAAAATTGTTGAAA	GGCTACAGTTT
MZO-3	TACAAGATTGAATA	ATTACAGTTTAAACTGTAGATGAGTCAACAGTTAAAATTGTTGAAA	GA

Ind5	TATTTGTAGAAT	ACGGGCTTATG	AAAACCTTTATCCGAACGACTAAACCATGCCTTGCAGCTTACTGGGGT
HFU-02	TATTTGTAGAAT	ACGGGCTTATG	AAAACCTTTATCCGAACGACTAAACCATGCCTTGCAGCTTACTGGGGT
HC-48A1	TATTTGTAGAAT	ACGGGCTTATG	AAAACCTTTATCCGAACGACTAAACCATGCCTTGCAGCTTACTGGGGT
MO10	TATTTGTAGAAT	ACGGGCTTATG	AAAACCTTTATCCGAACGACTAAACCATGCCTTGCAGCTTACTGGGGT
HC-28A1	TATTTGTAGAAT	ACGGGCTTATG	AAAACCTTTATCCGAACGACTAAACCATGCCTTGCAGCTTACTGGGGT
B33	TATTTGTAGAAT	ACGGGCTTATG	AAAACCTTTATCCGAACGACTAAACCATGCCTTGCAGCTTACTGGGGT
MZO-3	TATTTGTAGAAT	ACGGGCTTATG	AAAACCTTTATCCGAACGACTAAACCATGCCTTGCAGCTTACTGGGGT



Oligonucleotides used in this work		
Name	Application	Sequence (5'→3')
NdelexAVpa	Upper primer for cloning the <i>V.parahaemolyticus</i> <i>lexA</i> gen in pET15b overexpression vector.	CATATGAAGCCGTTAACGCCACGCC ^a
XholexAVpa	Lower primer for cloning the <i>V.parahaemolyticus</i> <i>lexA</i> gen in pET15b overexpression vector	CTCGAGTTACATCCAATCGGTATTG ^a
recAVpaF	Synthetic oligo to obtain the RecA EMSA probe.	TCATACAGGTATAGACACTGTATGAATCAACAGTATAATGACTTTC ATTGCTGAGCAGAAA
recAVpaR	Synthetic oligo to obtain the RecA EMSA probe.	CAATGAAAGTCATTATACTGTTGATTCATACAGTGTCTATACCTGT ATGAAAAAATTTGA
lexAVpaF	Synthetic oligo to obtain the LexA EMSA probe.	GATATACTCACAGTTAACTGTATAAAAAAGACAGGTGAGACATGAA GCCGTTAACGCCACGA
lexAVpaR	Synthetic oligo to obtain the LexA EMSA probe.	CGTGGCGTTAACGGCTTCATGTCTCACCTGTCTTTTATACAGTTA ACTGTGAGTATATCA
recGVpaF	Synthetic oligo to obtain the RecG EMSA probe.	TTTCTACGCCACTTCTTATAGTTTTTCCTGTACAAAAACACAGCTCA ATGGTTAACATACTGCTATGTAA
recGpaR	Synthetic oligo to obtain the RecG EMSA probe.	TAACATAGCAGTATGTTAACCATTGAGCTGTGTTTTGTACAGGAA AAACTATAAGAAGTGGCGTAGAAAA
mutHVpaF	Synthetic oligo to obtain the MutH EMSA probe.	GCCTAAAAACGTTTCAAAACCCCTGTTTATTCATCCAGCCCATCAG TAGATCCACTTATAA
mutHVpaR	Synthetic oligo to obtain the MutH EMSA probe.	TATAAGTGGATCTACTGATGGGCTGGATGAATAAACAGGGGTTTT GAAACGTTTTTAGGCA
imuAVpaF	Synthetic oligo to obtain the ImuA EMSA probe.	GTGTTTTTCATCATAGAAATATACTGTATTTATATACAGGTATTTTAT TTATGCAAGACATA
imuAVpaR	Synthetic oligo to obtain the ImuA EMSA probe.	ATGTCTTGCATAAATAAAATACCTGTATATAAATACAGTATATTTCT ATGATGAAAACACA
topBVpaF	Synthetic oligo to obtain the TopB EMSA probe.	ATACATACCTAGATAACGCTTACTGTTCATTTATACAGTTTTTCTT GATTTCTTAGGGCA
topBVpaR	Synthetic oligo to obtain the TopB EMSA probe.	GCCCTAAGAAATCAAGAAAAAACTGTATAAATGAACAGTAAGCGTT ATCTAGGTATGTATA
unfAVpaF	Synthetic oligo to obtain the UnfA EMSA probe.	ATCAGATACCCAAAAACAACTACTGTATACACATACAGCATGTATA AAGGAACAGTAAGAA
unfAVpaR	Synthetic oligo to obtain the UnfA EMSA probe.	TCTTACTGTTCCTTTATACATGCTGTATGTGTATACAGTAGTTTGTT TTGGGTATCTGATA
unfBVpaF	Synthetic oligo to obtain the UnfB EMSA probe.	TAGGAGGAAATTATAAACAATACTGTTTTTATATACAGTATCTAGTT TGGAGGTGAAGTAA
unfBVpaR	Synthetic oligo to obtain the UnfB EMSA probe.	TACTTCACCTCCAACTAGATACTGTATATAAAAAACAGTATTGTTTA TAATTCCTCCTAA

M13F/pUC	Universal upper primer of pGEMT vector to obtain the EMSA probe labeled with Digoxigenin (DIG).	DIG/GTTTTCCTCAGTCACGAC
M13R/pUC	Universal lower primer of pGEMT vector to obtain the EMSA probe labeled with Digoxigenin (DIG).	CAGGAAACAGCTATGAC

Strains and plasmids used in this work		
Name	Relevant characteristics genotype	Reference
Strains		
ATCC17802	<i>V. parahaemolyticus</i> ATCC17802 soca salvatge	From ATCC collection
K12	<i>E. coli</i> K12 soca salvatge	From DSMZ collection
Plasmids		
pET15b	Overexpression vector that carries an N-terminal His-Tag to allow purification of the <i>V.parahaemolyticus lexA</i> gen.	Novagen (Cat. No. 69661-3)
pGEMT	Cloning vector pGEM-T System I used to obtain the EMSA probes labeled with Digoxigenin.	Promega (Cat. No. A3600)