

## Nucleotide sequence of the *Salmonella serC* gene

Hugh G.Griffin

Division of Molecular Biology, Institute for Animal Health, Houghton Laboratory, Houghton, Huntingdon, Cambs PE17 2DA, UK

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The *serC* and *aroA* genes of *Salmonella typhimurium* constitute an operon (1). Strains harbouring stable mutations in this operon are attenuated and make excellent oral vaccines in mice and other animals (2, 3, 4). A similarly attenuated strain of *S. gallinarum* may be useful as a carrier of heterologous antigens to the chicken immune system as well as providing protection against fowl typhoid.

The nucleotide sequence of the *aroA* gene from *S. typhimurium* and the *serC* and *aroA* genes from *Escherichia coli* have been reported previously (5, 6). Below is shown the nucleotide sequence of the *serC* gene from *S. gallinarum*. The *serC* gene encodes a 362 amino acid protein and is very similar to its homolog in *E. coli*: the DNA sequences are 79% identical, the amino acid sequences are 90% identical.

M A Q V F N F S S G P A M L P A E V L K L A Q Q E L

1 CAGGCAGGAACAATGCAGCGTGGTGAAGGGAATGGCTCAGGCTTTAATTTTAAAGTTCCAGGTCGGCGATGCTCCGGCGGAAGTACTTAAACTGGCAACAGGAACT 110

R D W H G L G T S V M E I S H R G K E F I Q V A E E A E Q D F R D L L N I

111 GCSTGACTGGCAGCGTCTTGGTACGTCGGTAATGGAAATAGCCATCGAGGCAAGAGTTTATCCAGGTCGCTGAAGAGGCGGAGCAGGATTTCCGCGATCTCCTTAATA 220

P S N Y K V L F C H G G G R G Q F A G V P L N L L G D K T T A D Y V D A

221 TCCCCTCAACTATAAAGTTTTATTGTGACGGCGGGCTGCGGGCAGTTTGTGCGGTGCCCTCAATCTGCTGGGCGATAAAACCGCGGATTATGTCGATGCT 330

G Y W A A S A I K E A K K Y C A P Q I I D A K I T V D G K R A V K P M R E

331 GGTACTGGGCGGCGGCCATCAAGAGGCAAAAATACTGTGCGCCGAGATTATCGACGCCAAATCACCCTTGGCGGCAACGTCGCCGTAACCGATGCGCGA 440

M Q L S D N A A Y L H Y C P N E T I D G I A I D E T P D F G P E V V V T A

441 GTGGCAGCTTCCGATAACGCCGCTTATTACACTATTGCCCGAATGAGACCATTGACGGCATGCCATCGATGAAACGCCGGATTTGGCCCGGAAGTGGTGGTACCGG 550

D F S S T I L S A P L D V S R Y G V I Y A G A Q K N I G P A B L T L V I

551 CGGATTTTCTTACCATCTGTGTCGCCGCTGGACGCTCTGCTATGGCGTAATTTATGCTGGCGCGAGAAGAATATCGGTCGGCAGGACTGACGCTGGTTATC 660

V R E D L L G K A H E S C P S I L D Y T V L N D N D S M F N T P P T F A W

661 GTCCGGAGGATCTGTTAGGCAAGGCGCATGAGAGCTGCCCGTCCATCCTCGACTACACCGTCTGAAATGATAACGACTCGATGTTAATACGCCCGGACTTTCCGCTG 770

Y L S G L V F K W L K A Q G G V A A M H K I N Q Q K A E L L Y G V I D N S

771 GTATCTTCCGGTCTGGTGTCAAATGGTTGAAAGCGCAGGGCGGGTGGCGGATGACAAAATCAATCAGCAAAAAGCGGAGTTGCTGTACGGTGTGATTGATAACA 880

D F Y R N D V A Q A N R S R M N V P F Q L A D N A L D K V F L E E S F A

881 GCATTTCTACCGTAACGATGTGCGACAGGCCAACCGTTCGCGGATGAAATGTTCCGTTCCAGTTAGCGGCAATGCGCTGGACAAGGCTTTCTGGAAAGGCTTTCCGCG 990

A G L H A L K G H R V V G G M R A S I Y N A M P I E G V K A L T D F M I D

991 GCCGGTCTGCAGCCTTAAAGGGGACCGTGTGTTGTTGGCGGATGCGCGCTCTATCTATAACGCCATGCCGATTGAAAGGGTAAAAGCGCTAACCGATTTTCATGATCGA 1100

F E R R H G \*

1101 TTTTGAAGCTGCCACGGCTAATTCGTTTCTTTTTCATCCCGACGGCCA 1150

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