Legend

Figure1 ; Predicted structures of the RNAs used in the gel retardation experiments. The RNA sequences were folded with *mfold* (http://www.bioinfo.rpi.edu/applications/mfold). The secondary structure of the 3'*rpsO*-A18 mRNA fragment was experimentally determined (1). Enzymatic probing of a slightly longer *hfq* mRNA fragment revealed that most of the secondary structures predicted by *mfold* are not stable in solution (2).

Table 1 : Primers used to perform mutagenesis

Resulting plasmid	Template	Primer sequence
pTE607D40A	pTE607	For:GCTGCAAGGGCAAATCGAGTCTTTTGCTCA GTTCGTGATCCTGTTGAAAAACAC Rev:GTGTTTTTCAACAGGATCACGAACTGAGCA AAAGACTCGATTTGCCCTTGCAGC
pTE607F42A	pTE607	For:GGCAAATCGAGTCTTTTGATCAGGCTGTGAT CCTGTTGAAAAACACGGTC Rev:GACCGTGTTTTTCAACAGGATCACAGCCTG ATCAAAAGACTCGATTTGCC
pTE607K56A	pTE607	For:CACGGTCAGCCAGATGGTTTACGCTCACGC GATTTCTACTGTTGTCCCGTC Rev:GACGGGACAACAGTAGAAATCGCGTGAGC GTAAACCATCTGGCTGACCGTG
pTE607D40A-F42A	pTE607-F42A	For:GGCAAATCGAGTCTTTTGCTCAGGCTGTGAT CCTGTTGAAAAACACGGTC Rev;GACCGTGTTTTTCAACAGGATCACAGCCTG AGCAAAAGACTCGATTTGCC
pTE607V43C	pTE607	For:GGCAAATCGAGTCTTTTGATCAGTTCTGTAT CCTGTTGAAAAACACGGT Rev;GACCGTGTTTTTCAACAGGATACAGAACTG ATCAAAAGACTCGATTTGCC
pTE607V43R	pTE607	For:GGCAAATCGAGTCTTTTGATCAGTTCCGCAT CCTGTTGAAAAACACGGTC Rev;GACCGTGTTTTTCAACAGGATGCGGAACTG ATCAAAAGACTCGATTTGCC
pTX381V43C	pTX381	For:GGCAAATCGAGTCTTTTGATCAGTTCTGTAT CCTGTTGAAAAACACGGT Rev;GACCGTGTTTTTCAACAGGATACAGAACTG ATCAAAAGACTCGATTTGCC
pTX381V43R	pTX381	For:GGCAAATCGAGTCTTTTGATCAGTTCCGCAT CCTGTTGAAAAACACGGTC Rev;GACCGTGTTTTTCAACAGGATGCGGAACTG ATCAAAAGACTCGATTTGCC

Table 2 ; E. coli strains used in this work.

Strain	Relevant Genotype	Source or Reference
TX2808	JC7623 *hfq1*::Ω (kan^R)	(3)
HAT10	*hfq10*::cat (cm^R)	(4)
RO91	*rpoS742*::*lacZ*	(5)
MCM11	RO91 *hfq10*::cat (cm^R)	M. Springer
BL21 λDE3*hfq1*	BL21 λDE3 *hfq1*::Ω □□□□	This study
N3433	*HfrH lacZ43 relA1 spoT1 thi-1*	D. Apirion
CAG12073	*cycA30::Tn10* (tet^R)	(6)
MA261*oppA*::Km		(7)
IBPC937	TX2808 *hfq*V43R (kan^S)	This study
IBPC946	TX2808 *hfq*Δ22-294 (kan^S)	This study
IBPC929	N3433 *hfq1*::Ω(kan^R, *Bcl*I)	This study
IBPC941	N3433 *hfq*V43R *cycA30::Tn10* (tet^R)	This study
IBPC953	N3433 *hfq*Δ22-294 *cycA30::Tn10* (tet^R)	This study
IBPC959	IBPC953 *oppA* ::km (kan^R)	This study
ENSO	former name HfrG6Δ12	(8)
IBhfq95	ENSO *hfq::lacZ*	This study
IBhfq95-*hfq*V43R	ENSO *hfq::lacZ hfq*V43R	This study

Table 3; Statistics of 1HK9 (wt, V43C, V43R)

Simulation	α-helix ± σ_α%	β-strand ± σ_β%	H	B1	B2	B3	B4	B5
Initial structure	16.2	46.4	100	100	100	100	100	100
wt	16.2 ± 0.4	45.5 ± 1.4	92.1	95.9	89.4	92.8	89.8	93.1
V43C	15.8 ± 0.3	46.3 ± 1.2	90.2	96.2	91.2	95.7	90.9	94.3
V43R	15.1 ± 0.4	41.7 ± 1.6	90.5	96.0	84.4	85.9	74.6	92.1

The mean and standard deviation (σ) of α-helix and β-strand are given for the minimized (initial) structure and for the time-averaged wt, V43C and V43R structures. The mean percentage of helix (H) and β-strands (B1 to B5) are shown to the right.

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