

Supplementary Table S1. Nucleotide polymorphisms detected in the sequence of the *groEL* gene 571 bp fragment and predicted amino-acid changes in the samples analysed in this study. Nucleotide position refers to the position in the amplified fragment once primers were removed; reference base represent the base identified as the most common in the overall alignment and called base represent the nucleotide substitution observed in the same position; number of sequences indicates the number of the sequences with the reference base; SNP indicates number of sequences showing base change at that specific position; Underlined are the base changes in each codon.

Nucleotide position	Ref base	Called base	Possible codons modified		Coded amino-acid	Type of mutation	Number of sequences showing SNPs
1 (588)	C	Y	CG <u>C</u>	CG <u>T</u>	Arg	Synonymous	1/72
10 (597)	T	A	CT <u>T</u>	CT <u>A</u>	Leu	Synonymous	1/72
73 (660)	C	T	TTC	TT <u>T</u>	Phe	Synonymous	1/72
145 (732)	A	G	AG <u>A</u>	AG <u>G</u>	Arg	Synonymous	36/72
187 (774)	G	T	CT <u>G</u>	CT <u>T</u>	Leu	Synonymous	30/72
193 (780)	G	A	AC <u>A</u>	AC <u>G</u>	Thr	Synonymous	6/72
253 (840)	T	C	TT <u>T</u>	TT <u>C</u>	Phe	Synonymous	20/72
262 (849)	G	R	AG <u>G</u>	AG <u>A</u>	Arg	Synonymous	1/72
346 (933)	T	C	GG <u>T</u>	GG <u>C</u>	Gly	Synonymous	33/72
415 (1002)	T	C	GG <u>T</u>	GG <u>C</u>	Gly	Synonymous	22/72
526 (1113)	G	A	GCC	GCA	Ade	Synonymous	23/72
535 (1122)	C	T	TCC	TC <u>T</u>	Ser	Synonymous	10/72
541 (1128)	C	T	GGC	GG <u>T</u>	Gly	Synonymous	22/72