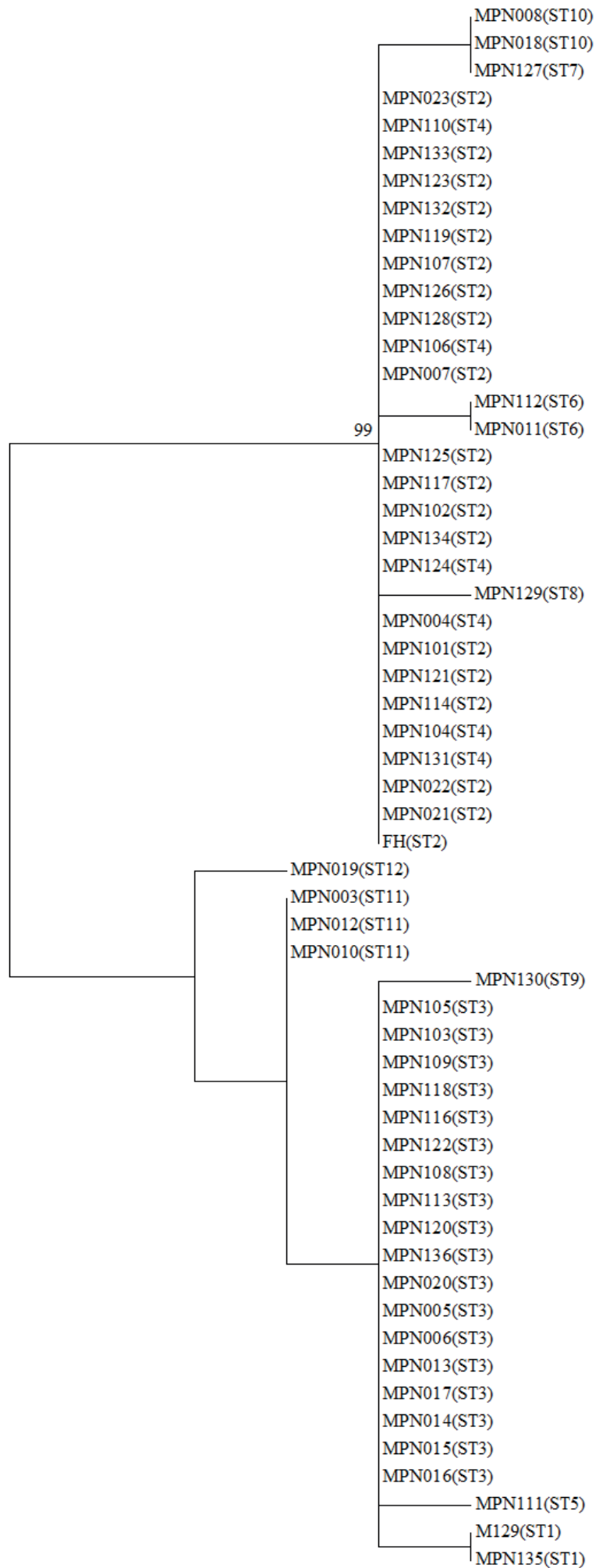
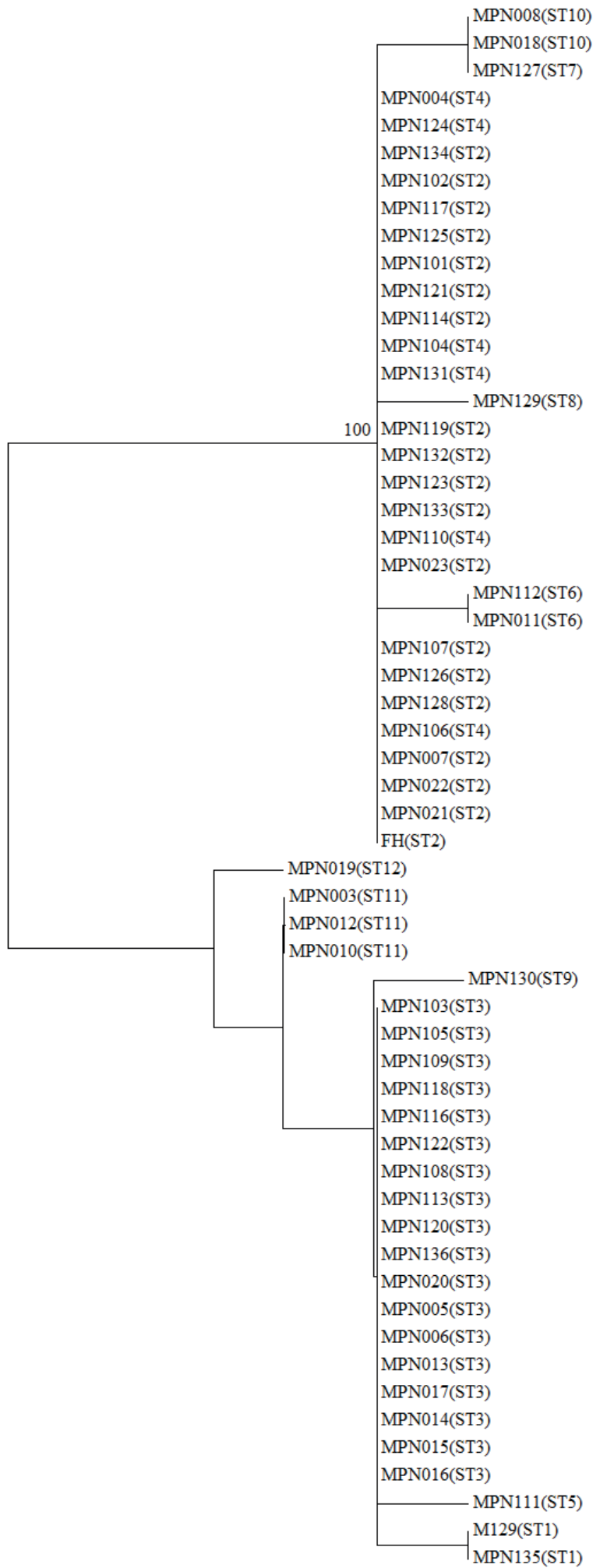


A.



0.0002

B.



0.0002

**Figure A1. Phylogenetic trees based on concatenated sequences of eight MLST loci.**

Phylogenetic trees were constructed based on concatenated sequences of eight housekeeping loci for 12 unique STs using Maximum-likelihood (A) and Neighbour-joining (B) methods. Individual strains and STs can be identified in the traditional rectangular branch style. Bootstrap support values of over 70% are shown.

A.

ADK-4 VANTTGLFHLSTGDIFR<sup>T</sup>VMQEQGALSQTLAHYMNQGLYVPDELTNQTFWHFVTTHQNEL  
ADK-3 VANTTGLFHLSTGDIFRSVMQEQGALSQTLAHYMNQGLYVPDELTNQTFWHFVTTHQNEL  
ADK-1 VANTTGLFHLSTGDIFRSVMQEQGALSQTLAHYMNQGLYVPDELTNQTFWHFVTTHQNEL  
ADK-2 VANTTGLFHLSTGDIFRSVMQEQGALSQTLAHYMNQGLYVPDELTNQTFWHFVTTHQNEL  
\*\*\*\*\*.\*\*\*\*\*

ADK-4 HKGFILDGYPRTLNLQLEFLQSKLQLDQVFHLKLSDPQVLVARILNRLVCPSCGSVYNKQS  
ADK-3 HKGFILDGYPRTLNLQLEFLQSKLQLDQVFHLKLSDPQVLVARILNRLVCPSCGSVYNKQS  
ADK-1 HKGFILDGYPRTLNLQLEFLQSKLQLDQVFHLKLSDPQVLVARILNRLVCPSCGSVYNKQS  
ADK-2 HKGFILDGYPRTLNLQLEFLQSKLQLDQVFHLKLSDPQVLVARILNRLVCPSCGSVYNKQS  
\*\*\*\*\*

ADK-4 KPPLKANQCDCRCHATLQARNDDTEAVILKRLTLYEDT 157  
ADK-3 KPPLKANQCD<sup>I</sup>CHATLQARNDDTEAVILKRLTLYEDT 157  
ADK-1 KPPLKANQCDCRCHATLQARNDDTEAVILKRLTLYEDT 157  
ADK-2 KPPLKANQCDCRCHAM<sup>L</sup>LQARNDDTEAVILKRLTLYEDT 157  
\*\*\*\*\* \*\*

B.

ARCC-1 PHQAVYFLTQTLVEASDPAFQNPKNKPVGPFYNTTEETARSANPNSTVVEDAGRGRKVVAS  
ARCC-2 PHQAVYFLTQTLVEASDPAFQNPKNKPVGPFYNTTEETARSANPNSTVVEDAGRGRKVVAS  
\*\*\*\*\*

ARCC-1 PKPVDVLGIDAIAKSSFNQGNLVIVGGGGVPTIKTKSGYATVDGVIDKDLALSEIAIKVE  
ARCC-2 PKPVDVLGIDAIAKSSFNQGNLVIVGGGGVPTIKTKSGYATVDGVIDKDLALSEIAIKVE  
\*\*\*\*\*

ARCC-1 ADL FVILTAVDFVYINYGQPNEQKLCINTKEAKTLMAANQFAKGSMLPKVEACLNFVQS  
ARCC-2 ADL FVILTAVDFVYINYGQPNEQKLCINTKEAKTLMAANQFAKGSMLPKVEACLNFVQS  
\*\*\*\*\*

ARCC-1 GTNKTAIIAQ 190  
ARCC-2 GTNKTAIIAQ 190  
\*\*\*\*\*

C.

GLYA-1 ENYVSRDILEVTGSILTNKYAEGYPTRRFYEGCEVVDESESLAINTCKELFGAKWANVQP  
GLYA-3 ENYVSRDILEVTGSILTNKYAEGYPTRRFYEGCEVVDESESLAINTCKELFGAKWANVQP  
GLYA-2 ENYVSRDILEVTGSILTNKYAEGYPTRRFYEGCEVVDESESLAINTCKELFGAKWANVQP  
\*\*\*\*\*

GLYA-1 HSGSSANYAVYLALLKPGDAILGLDLNCGGHLTHGNKFNFSGKQYQPYSY TINPETEMLD  
GLYA-3 HSGSSANYAVYLALLKPGDAILGLDLNCGGHLTHGNKFNFSGKQYQPYSY TINPETEMLD  
GLYA-2 HSGSSANYAVYLALLKPGDAILGLDLNCGGHLTHGNKFNFSGKQYQPYSY TINPETEMLD  
\*\*\*\*\*

GLYA-1 YDEVLRVAREVKPKLIICGFSNYSRTVDFERFSAIAKEVGAYLLADIAHIAGLVAAGLHP  
GLYA-3 YDEVLRVAREVKPKLIICGFSNYSRTVDFERFSAIAKEVGAYLLADIAHIAGLVAAGLHP  
GLYA-2 YDEVLRVAREVKPKLIICGFSNYSRTVDFERFSAIAKEVGAYLLADIAHIAGLVAAGLHP  
\*\*\*\*\*

GLYA-1 NPLPYTDVVTSTTHKTLRGPRGGLIMSNNEAIRKLD SGVFPGC 224  
GLYA-3 NPLPYTDVVTSTTHKTLRGPRGGLIMSNNEAIRKLD SGVFPGC 224  
GLYA-2 NPLPY<sup>A</sup> DVVTSTTHKTLRGPRGGLIMSNNEAIRKLD SGVFPGC 224  
\*\*\*\*\*.

D.

ATPA-1 VADGIAKVSGLLENALLNELIEFENNVQGIALNLEQNTVGVALFGDYSKIREGSTAKRTHN  
 ATPA-4 VADGIAKVSGLLENALLNELIEFENNVQGIALNLEQNTVGVALFGDYSKIREGSTAKRTHN  
 ATPA-2 VADGIAKVSGLLENALLNELIEFENNVQGIALNLEQNTVGVALFGDYSKIREGSTAKRTHN  
 ATPA-3 VADGIAKVSGLLENALLNELIEFENNVQGIALNLEQNTVGVALFGDYSKIREGSTAKRTHN  
 \*\*\*\*\*

ATPA-1 VMQTPVGDVMLGRIVNALGEPVDGRGPIKAEEFDQVEKIAPGVMTRKTVNQPLETGILTI  
 ATPA-4 VMQTPVGDVMLGRIVNALGEPVDGRGPIKAEEFDQVEKIAPGVMTRKTVNQPLETGILTI  
 ATPA-2 VMQTPVGDVMLGRIVNALGEPVDGRGPIKAEEFDQVEKIAPGVMTRKTVNQPLETGILTI  
 ATPA-3 VMQTPVGDVMLGRIVNALGEPVDGRGPIKAEEFDQVEKIAPGVMTRKTVNQPLETGILTI  
 \*\*\*\*\*

ATPA-1 DALFPIGKGQRELIVGDRQTGKTSIAIDTIINQRGKDVYCVYVAMGQKNSSVAQIVHOLE  
 ATPA-4 DALFPIGKGQRELIVGDRQTGKTSIAIDTIINQRGKDVYCVYVAMGQKNSSVAQIVHOLE  
 ATPA-2 DALFPIGKGQRELIVGDRQTGKTSIAIDTIINQRGKDVYCVYVAMGQKNSSVAQIVHOLE  
 ATPA-3 DALFPIGKGQRELIVGDRQTGKTSIAIDTIINQRGKDVYCVYVAMGQKNSSVAQIVHOLE  
 \*\*\*\*\*

ATPA-1 VTDSMKYTTVVCATASNPASMIYLTPTFTGITIAEYWLKQKGDVLIVFDDLSKHAIAYRTL  
 ATPA-4 VTDSMKYTTVVCATASNPASMIYLTPTFTFTGITIAEYWLKQKGDVLIVFDDLSKHAIAYRTL  
 ATPA-2 VTDSMKYTTVVCATASDPASMIYLTPTFTFTGITIAEYWLKQKGDVLIVFDDLSKHAIAYRTL  
 ATPA-3 VTDSMKYTTVVCATASDPASMIYLTPTFTFTGITIAEYWLKQKGDVLIVFDDLSKHAIAYRTL  
 \*\*\*\*\*

ATPA-1 SLLLRPPGREAFPGDVFYLSRLL 265  
 ATPA-4 SLLLRPPGREAFPGDVFYLSRLL 265  
 ATPA-2 SLLLRPPGREAFPGDVFYLSRLL 265  
 ATPA-3 SLLLRPPGREAFPGDVFYLSRLL 265  
 \*\*\*\*\*

E.

GMK-1 SGVGKSSLVRCLIDHFKDKLRYISATTRKMRNSETEGVDYFFKDKAEFEKLI AADAFVE  
 GMK-2 SGVGKSSLVRCLIDHFKDKLRYISATTRKMRNSETEGVDYFFKDKAEFEKLI AADAFVE  
 \*\*\*\*\*

GMK-1 WAMYNDNYYGTLKSQAEQIIHNGGNLVLEIEYQGALQVKQKYPNDVVLIFIKPPSMEELL  
 GMK-2 WAMYNDNYYGTLKSQAEQIIHNGGNLVLEIEYQGALQVKQKYPNDVVLIFIKPPSMEELL  
 \*\*\*\*\*

GMK-1 VRLKKRNDEDA 131  
 GMK-2 VRLKKRNDEDA 131  
 \*\*\*\*\*

F.

GYRB-1 VPDFTVMEKSDYKQTVIASRLQQLAFLNKGIIQIDFVDERRQNPQSFSWKYDGGLVQYIHH  
 GYRB-2 VPDFTVMEKSDYKQTVIASRLQQLAFLNKGIIQIDFVDERRQNPQSFSWKYDGGLVQYIHH  
 \*\*\*\*\*

GYRB-1 LNNEKEPLFEDIIFGEKTDTVKSVSRDES YTIKVEVAFQYNKTYNQSIF SFCNNINTTEG  
 GYRB-2 LNNEKEPLFEDIIFGEKTDTVKSVSRDES YTIKVEVAFQYNKTYNQSIF SFCNNINTTEG  
 \*\*\*\*\*

GYRB-1 GTHVEGFRNALVKI INRFAVEN 142  
 GYRB-2 GTHVEGFRNALVKI INRFAVEN 142  
 \*\*\*\*\*

G.

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PGM-1 APCTMKSdleafmvflkdyhnviiGTLGGRYYGMDRDQRWDREEIAYNAILGNSKASFTD
PGM-2 APCTMKSdleafmvflkdyhnviiGTLGGRYYGMDRDQRWDREEIAYNAILGNSKASFTD
PGM-3 APCTMKSdleafmvflkdyhnviiGTLGGRYYGMDRDQRWDREEIAYNAILGNSKASFTD
*****

PGM-1 PVAYVQSAYDQKVTDEFLYPVAVNGNVDKEQFALKDHDSVIFFNFRPDRARQMSHMLFQTD
PGM-2 PVAYVQSAYDQKVTDEFLYPVAVNGNVDKEQFALKDHDSVIFFNFRPDRARQMSHMLFQTD
PGM-3 PVAYVQSAYDQKVTDEFLYPVAVNGNVDKEQFALKDHDSVIFFNFRPDRARQMSHMLFQTD
*****

PGM-1 YYDYTPKAGRKHNLFFVTMMNYEGIKPSAVVFPPETIPNTFGEVIAHNKLGKQLRIAETEK
PGM-2 YYDYTPKAGRKHNLFFVTMMNYEGIKPSAVVFPPETIPNTFGEVIAHNKLGKQLRIAETEK
PGM-3 YYDYTPKAGRKHNLFFVTMMNYEGIKPSAVVFPPETIPNTFGEVIAHNKLGKQLRIAETEK
*****.*****

PGM-1 YAHVTTTTDGGVEVDLPNETKCMVPSLKVATYDLAPEMACKGITDQLLNQINQFDLTVLN
PGM-2 YAHVTTTTDGGVEVDLPNETKCMVPSLKVATYDLAPEMACKGITDQLLNQINQFDLTVLN
PGM-3 YAHVTTTTDGGVEVDLPNETKCMVPSLKVATYDLAPEMACKGITDQLLNQINQFDLTVLN
*****

PGM-1 FANPDMVGHTGNYAACVQGLEALDVQIQRIIDFCKANHITLFLTADHGNAEEMIDSNNNP
PGM-2 FANPDMVGHTGNYAACVQGLEALDVQIQRIIDFCKANHITLFLTADHGNAEEMIDSNNNP
PGM-3 FANPDMVGHTGNYAACVQGLEALDVQIQRIIDFCKANHITLFLTADHGNAEEMIDSNNNP
*****

PGM-1 VTKHTVNKVPFVCTDTNIDLQQDSASLANIAPTILAYLGLKQPAEMTANSLLYKKV 356
PGM-2 VTKHTVNKVPFVCTDTNIDLQQDSASLANIAPTILAYLGLKQPAEMTANSLLISSK 356
PGM-3 VTKHTVNKVPFVCTDTNIDLQQDSASLANIAPTILAYLGLKQPAEMTANSLLISSK 356
*****.*

H.

PPA-1 IFADQAFPLPGVVVPTRIVGALEMVDDGELDTKLLGVIDCDPRYKEINSVNDLPKHRVDEI
PPA-2 IFADQAFPLPGVVVPTRIVGALEMVDDGELDTKLLGVIDCDPRYKEINSVNDLPKHRVDEI
*****

PPA-1 IGFLKTYKLLQKKEVIIKGVQSLEW 85
PPA-2 IGFFKTYKLLQKKEVIIKGVQSLEW 85
***.*****

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**Figure A2. Alignments of amino acid sequences of each allelic type at each of the eight MLST loci.** Amino acid sequence alignments were generated for each of the eight loci based on nucleotide sequence of each allelic type. Synonymous changes in amino acid sequence are highlighted in yellow. \* (asterisk) indicates positions which have a single, fully conserved residue; : (colon) indicates conservation between groups of strongly similar properties - scoring > 0.5 in the Gonnet PAM 250 matrix; . (period) indicates conservation between groups of weakly similar properties - scoring < 0.5 in the Gonnet PAM 250 matrix.