

Supplementary Materials for

Characterization of spotted fever group *Rickettsiae* in ticks from a city park of Rome, Italy

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Figures 1-4: enlarged version.

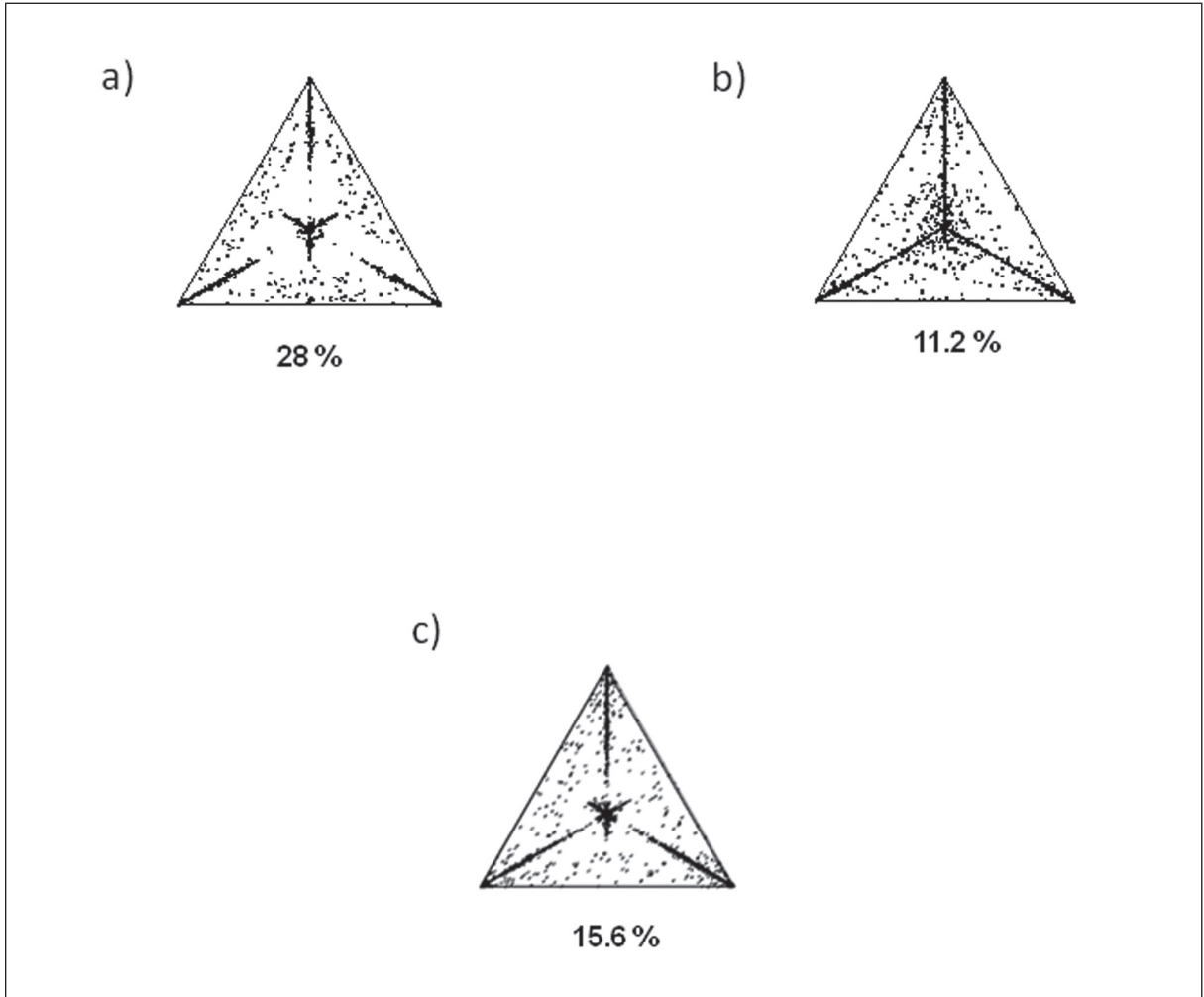


Figure 1

Likelihood mapping of rickettsia sequences using the *gtIA* dataset (a), the *ompA* dataset (b) and the 17-kDa dataset (c). The dots inside the triangles represent the posterior probabilities of the possible unrooted topologies for each quartet. Numbers in the centre of the triangles indicate the percentage of dots in the centre of the triangle corresponding to phylogenetic noise (star-like trees).

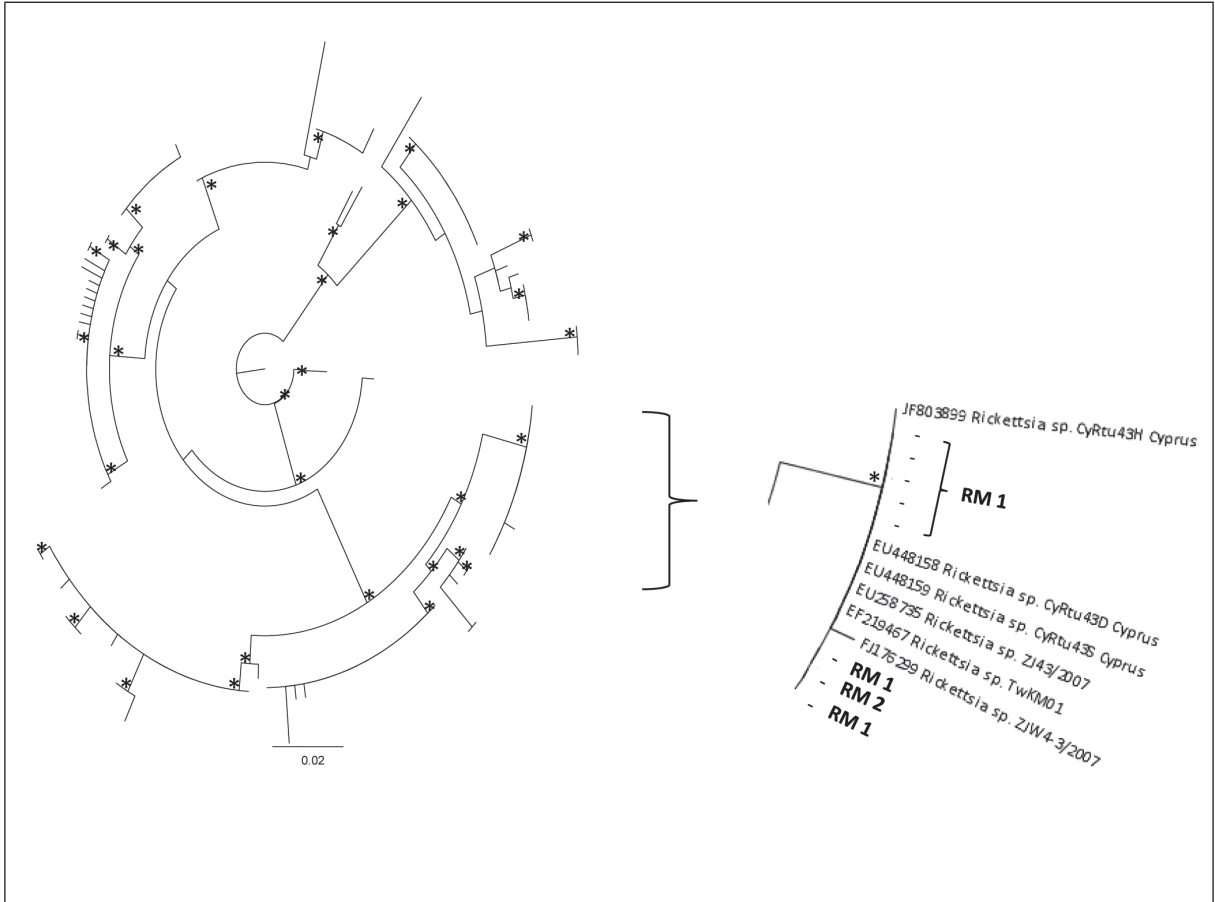


Figure 2 Maximum likelihood phylogenetic analysis of rickettsia partial *ompA* gene sequences (second dataset). Branch lengths were estimated with the best fitting nucleotide substitution model according to a hierarchical likelihood ratio test and were drawn in scale with the bar at the bottom indicating 0.02 nucleotide substitutions per site. The * along the branch represents significant statistical support for the clade subtending that branch (bootstrap support > 75%). The tree is midpoint rooted. The Italian isolates (collected in Rome) are shown in bold.

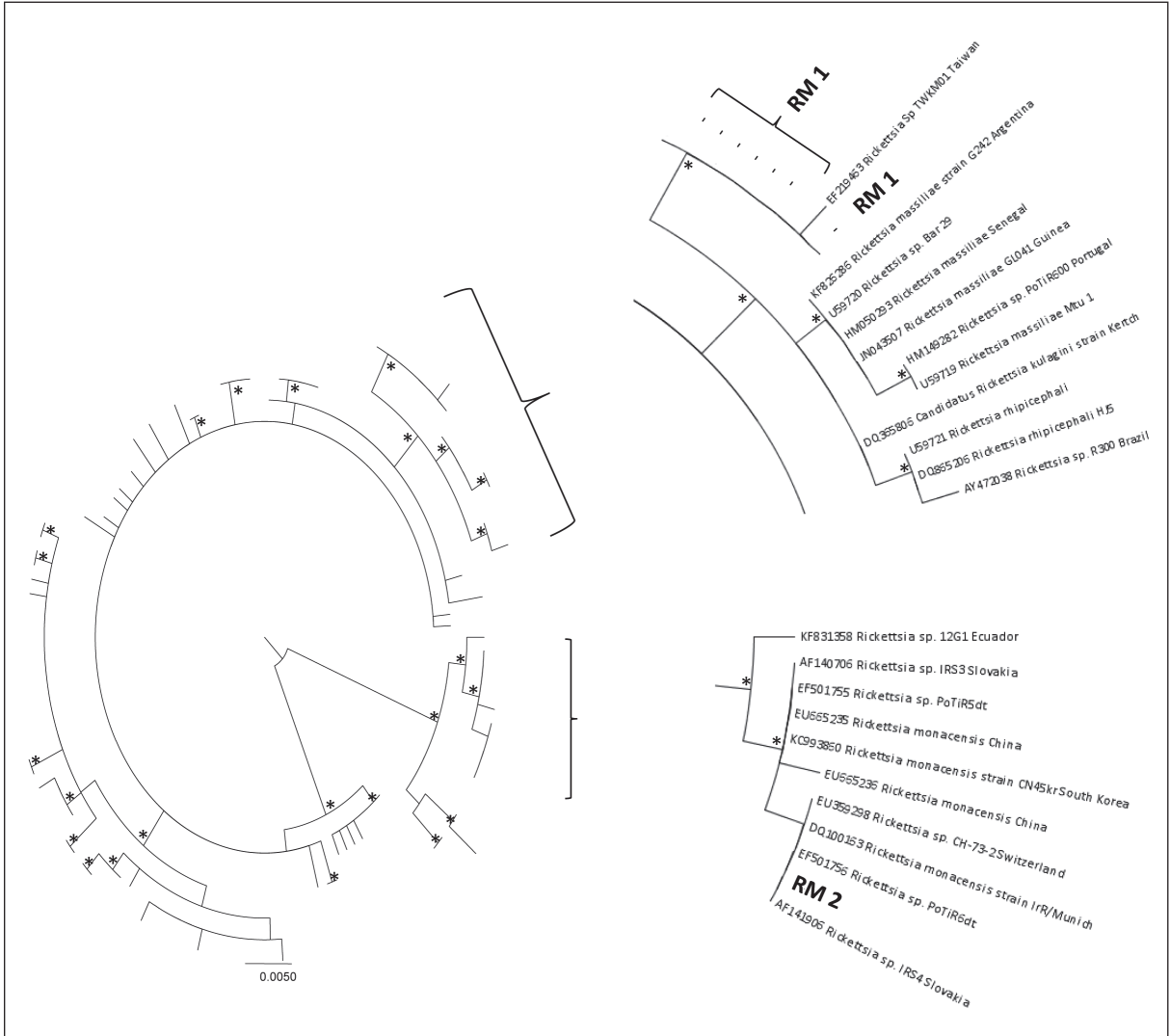


Figure 3

Maximum likelihood phylogenetic analysis of *Rickettsia* partial *gltA* gene sequences (second dataset). Branch lengths were estimated with the best fitting nucleotide substitution model according to a hierarchical likelihood ratio test and were drawn in scale with the bar at the bottom indicating 0.0050 nucleotide substitutions per site. The * along the branch represents significant statistical support for the clade subtending that branch (bootstrap support > 75%). The tree is midpoint rooted. The Italian isolates (collected in Rome) are shown in bold.

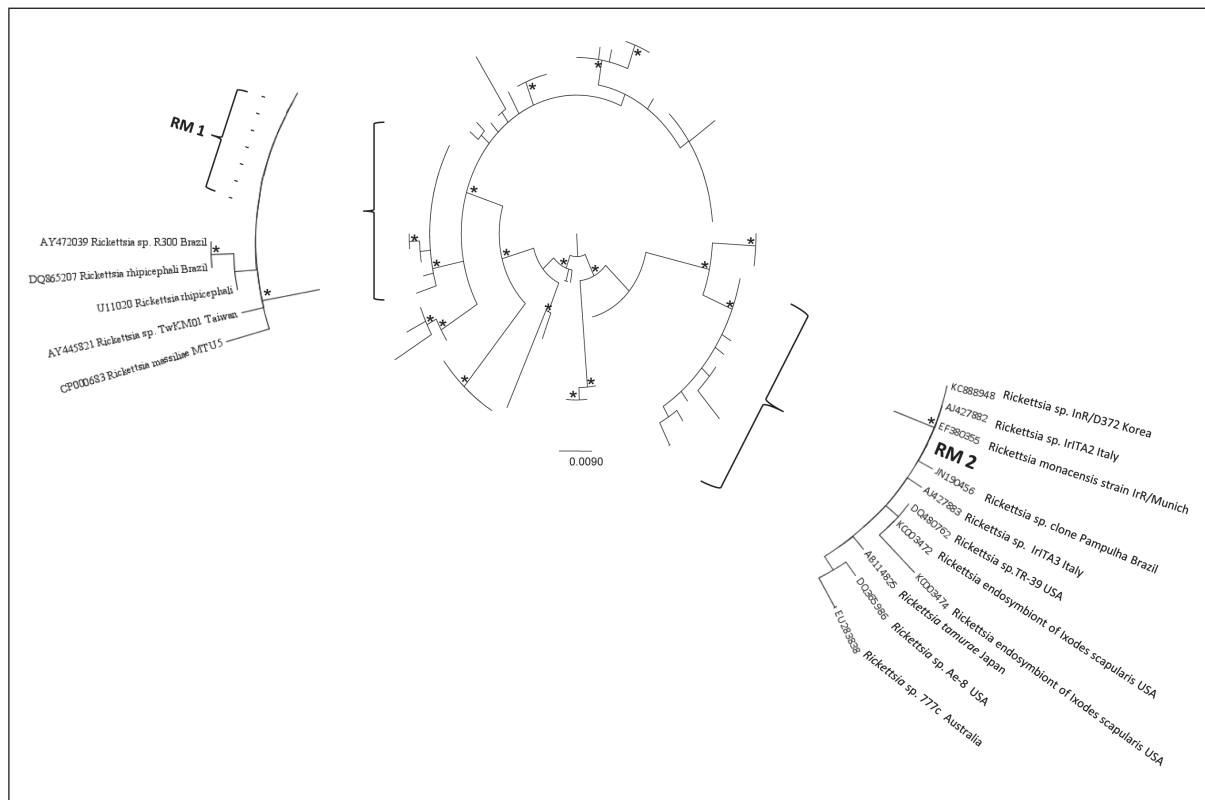


Figure 4
 Maximum likelihood phylogenetic analysis of rickettsia partial 17-kDa gene sequences (third dataset). Branch lengths were estimated with the best fitting nucleotide substitution model according to a hierarchical likelihood ratio test and were drawn in scale with the bar at the bottom indicating 0.0090 nucleotide substitutions per site. The * along the branch represents significant statistical support for the clade subtending that branch (bootstrap support > 75%). The tree is midpoint rooted. The Italian isolates (collected in Rome) are shown in bold.