Supplementary File

Molecular Characterisation using 16S rRNA and COI Gene Sequences in Hard Ticks of Gwalior, India

Pooja Ghosh[#], S.N. Tikar[#,*], Mahendra K. Gupta[@], and D. Sukumaran[#]

[#]DRDO-Defence Research and Development Establishment, Gwalior - 474 002, India
[@]Jiwaji University, Gwalior - 474 001, India
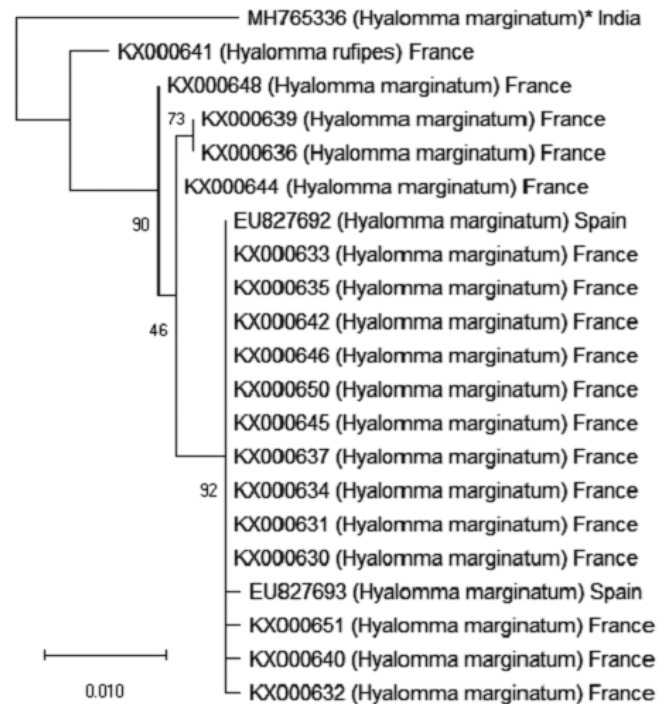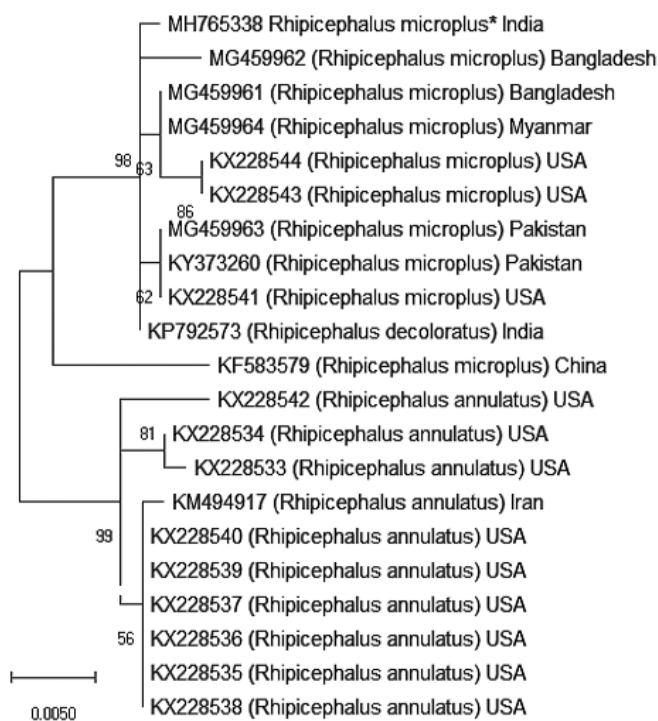[*]E-mail: sachin.tikar@drde.drdo.in

Figure S1. Maximum likelihood (ML) tree inferred from COI partial sequences of *Rh. microplus* tick specimens collected in the present study (*) and sequences from GenBank.

Figure S2. Maximum likelihood (ML) tree inferred from COI partial sequences of *Hy. marginatum* tick specimens collected in the present study (*) and sequences from GenBank.
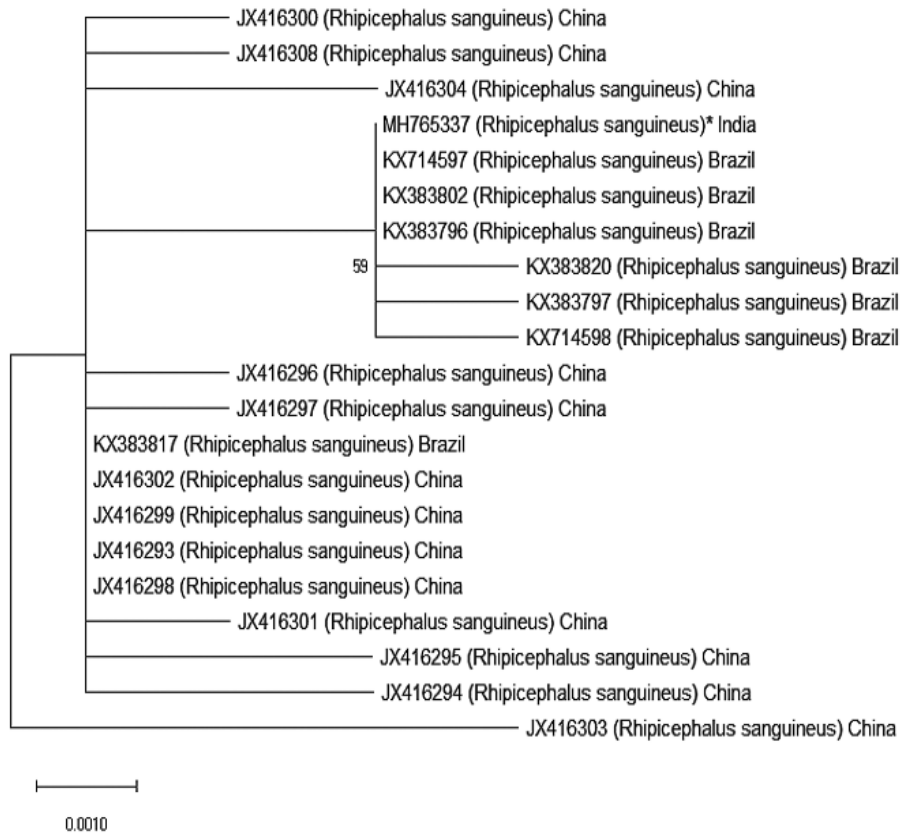
Figure S3. Maximum likelihood (ML) tree inferred from COI partial sequences of *Rh. sanguineus* tick specimens collected in the present study (*) and sequences from GenBank.
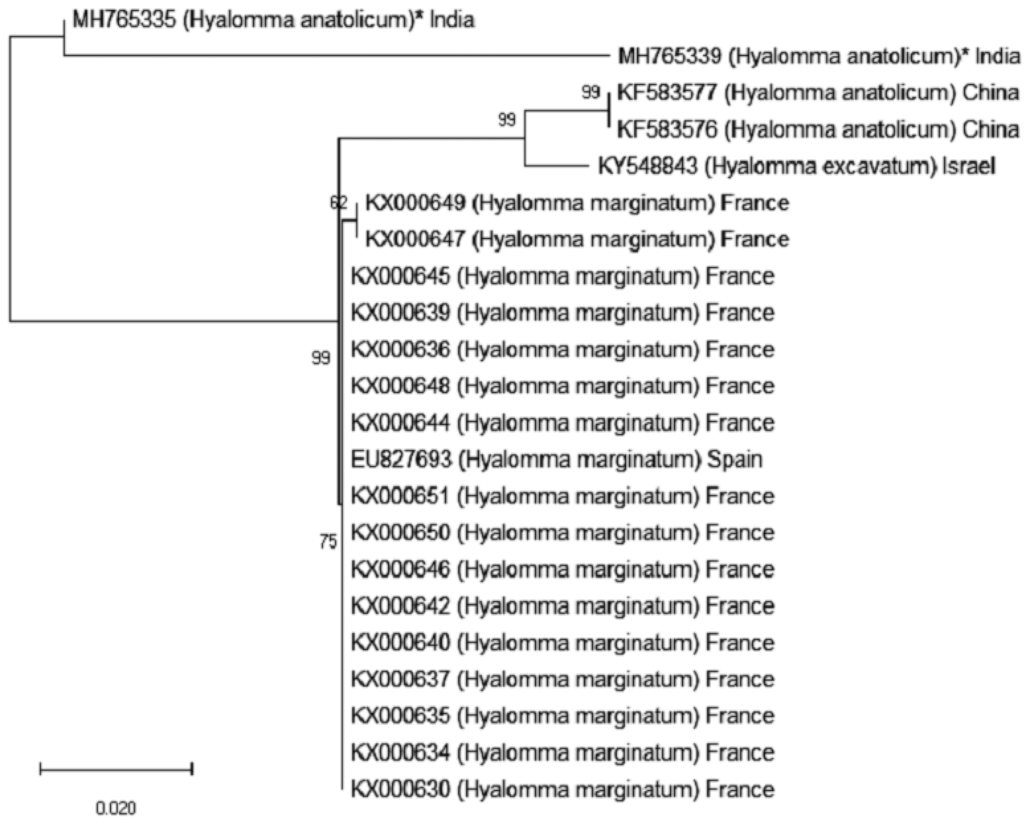

Figure S4. Maximum likelihood (ML) tree inferred from COI partial sequences of *Hy. anatolicum* tick specimens collected in the present study (*) and sequences from GenBank.