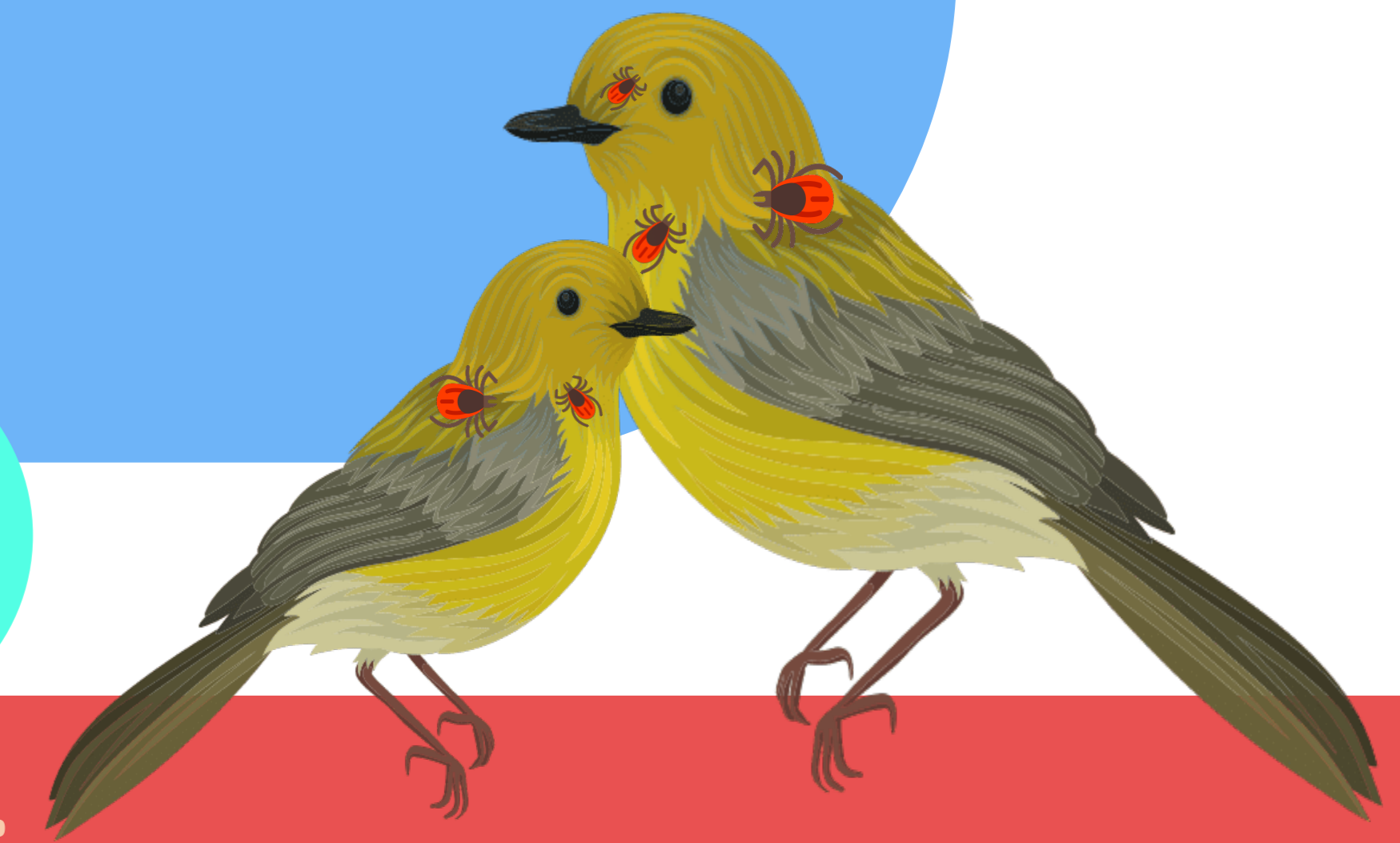
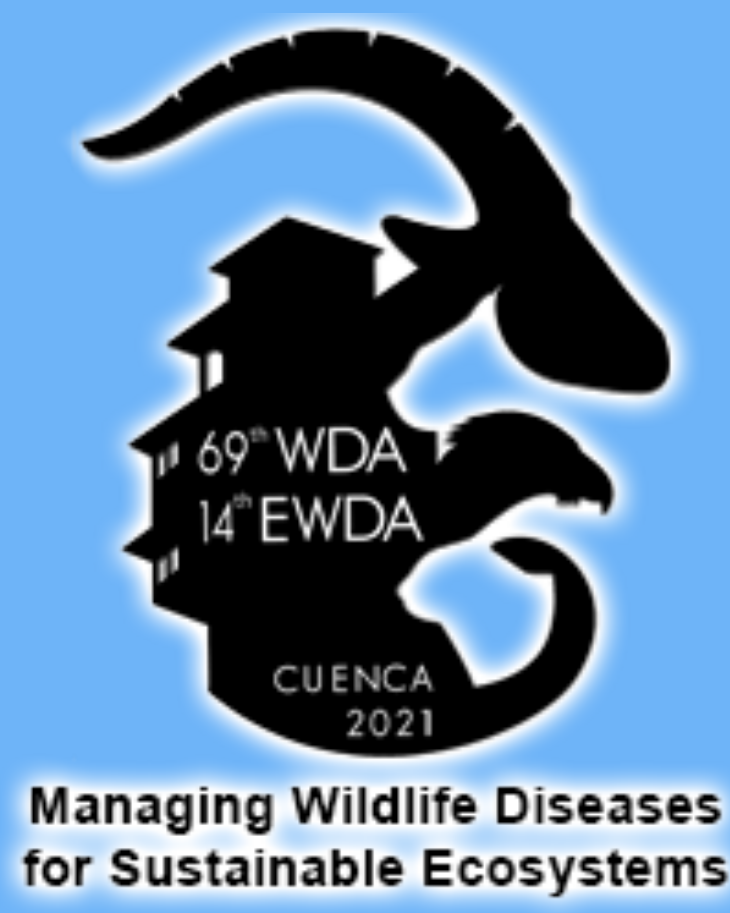


Rickettsia aeschlimannii in *Hyalomma marginatum* and *H. rufipes* ticks from trans-Saharan migratory passerines in Spain

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Introduction

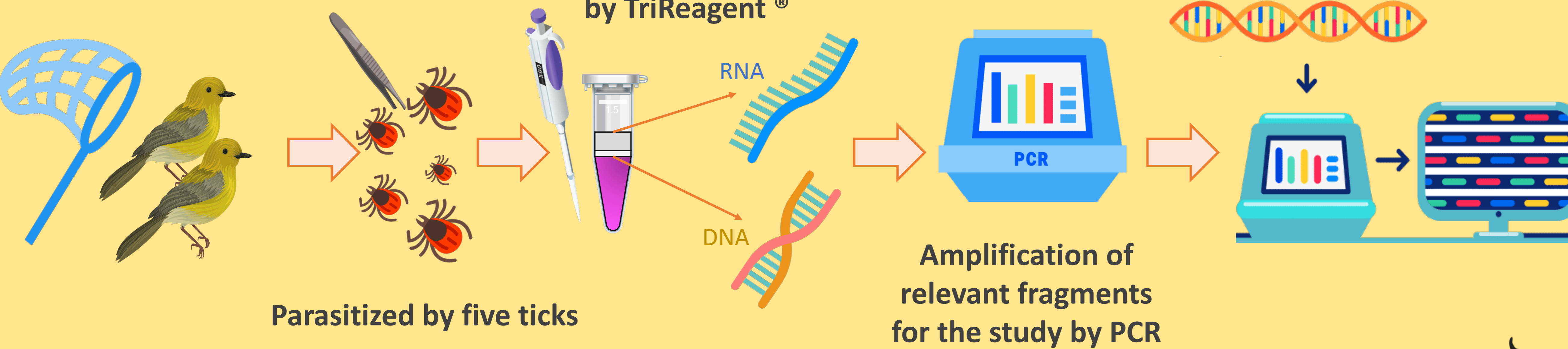
During the spring and autumn around two billion birds of a range of species migrate across the Mediterranean Sea between Africa and Eurasia. Along their journeys these birds can be vehicles to the dispersal of plant seeds, invertebrates and the infectious pathogens these carry at very long distances. Migratory birds aid in the spread of ticks and their pathogens as well (1).

Material and methods

Two birds captured

DNA/RNA Extraction by TriReagent®

Sequencing



Results

- ✓ Tick 16S rDNA gene for molecular identification:
 - Three nymphs *Hyalomma marginatum*
 - One nymph and a larva *H. rufipes*
- ✓ *Rickettsia* 16S rRNA, OmpA, OmpB, AtpA, RecA genes
 - *Rickettsia aeschlimannii*
- ✗ *Anaplasma* 16S rRNA gene
- ✗ *Babesia/Theileria* 18S rRNA gene
- ✗ CCHFv S-segment
- ✗ Flavivirus RdRp gene

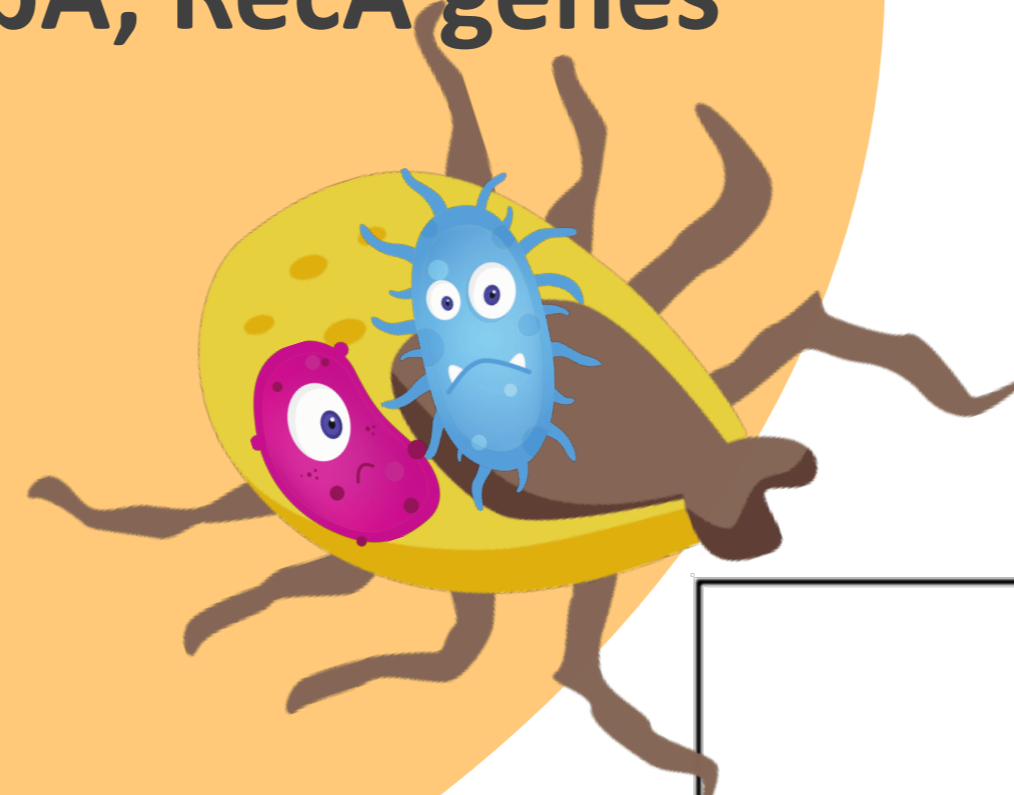
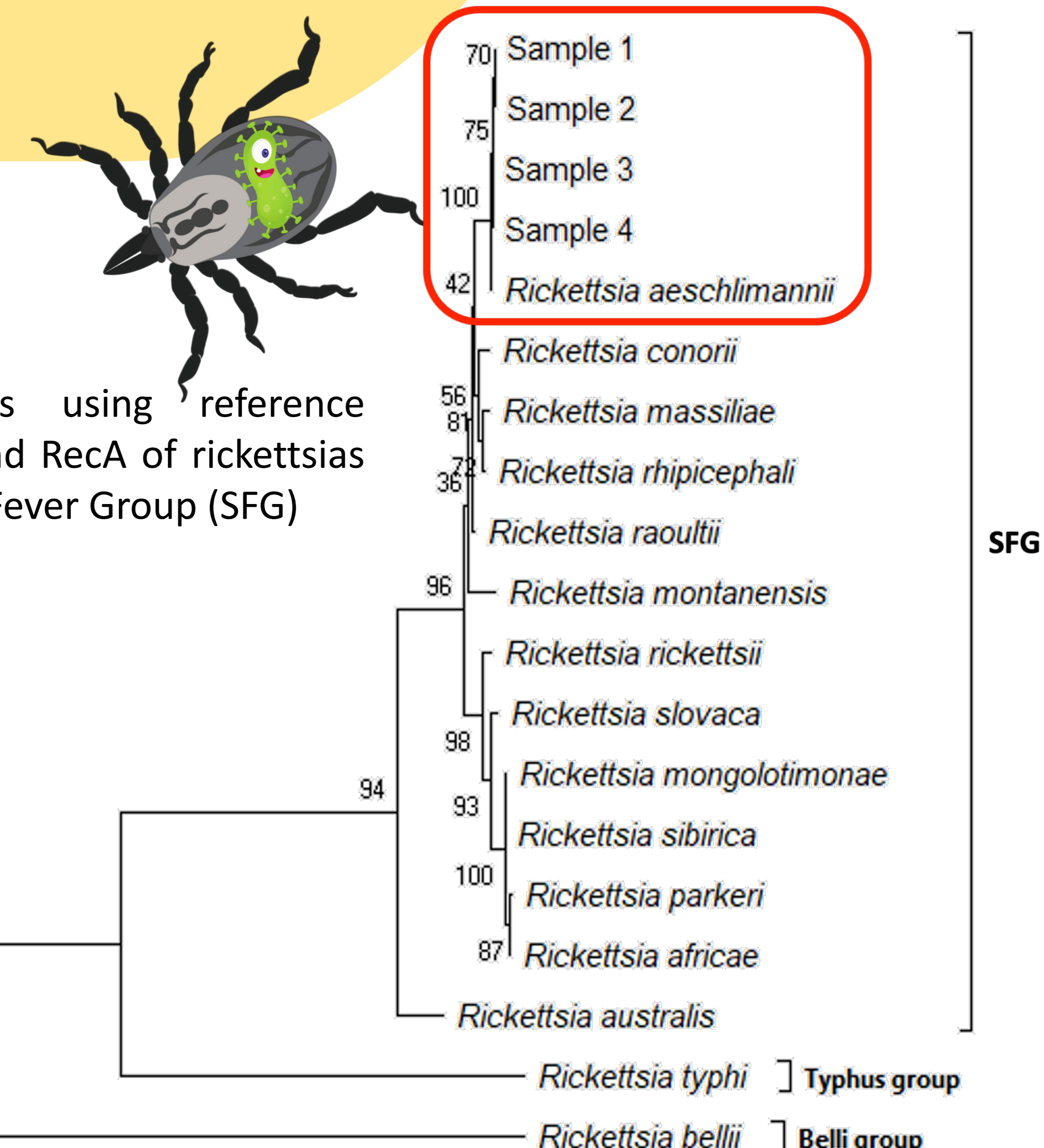
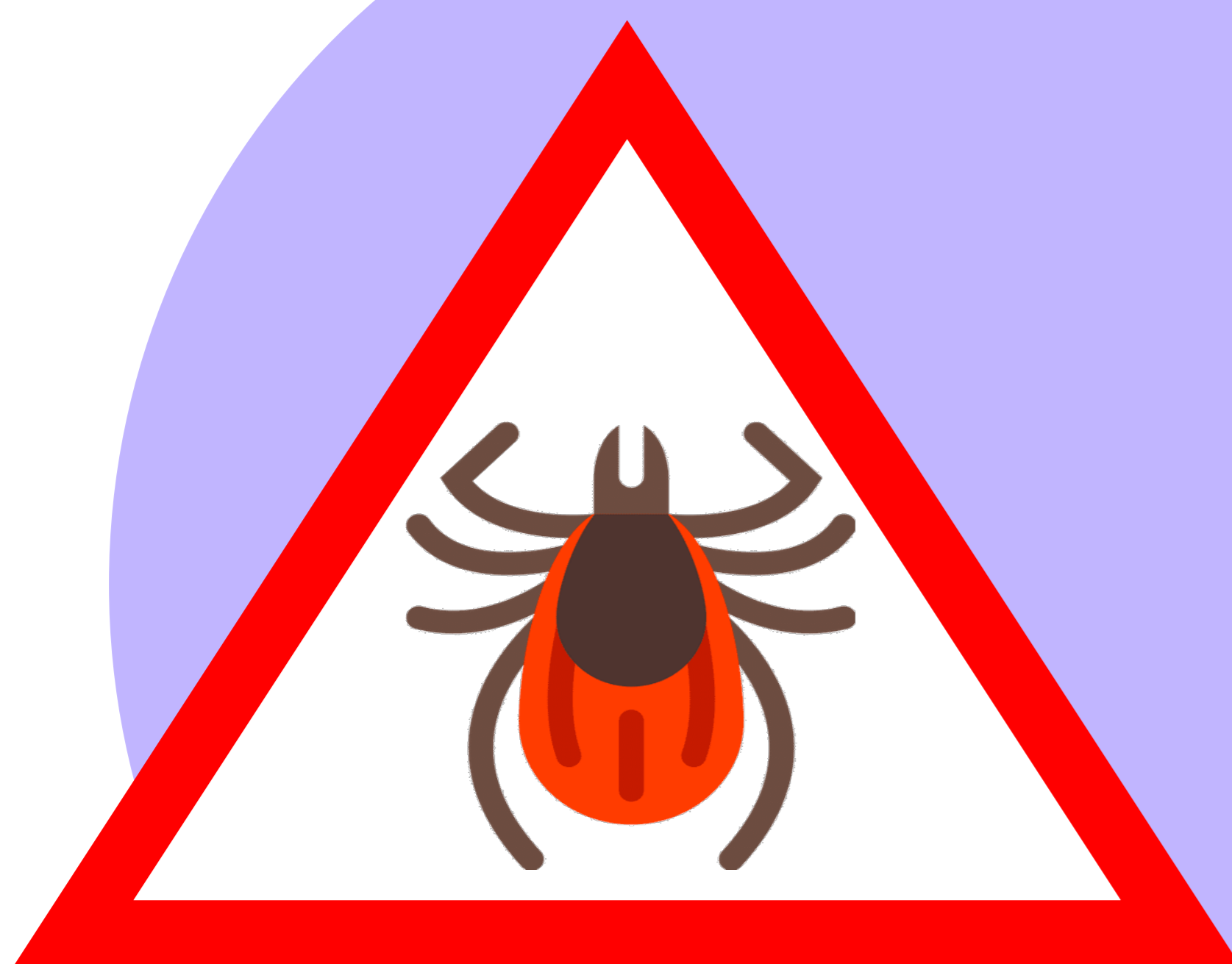


Figure 1: Phylogenetic analysis using reference genes AtpA, OmpB and RecA of rickettsias belonging to Spotted Fever Group (SFG)



Discussion and conclusions

- ❖ The presence of *H. rufipes* immatures on the reed warbler sampled shows that it was migrating from Africa because *H. rufipes* has not stable populations in Europe.
- ❖ These results corroborate that migratory birds act as vehicles whereby ticks and their pathogens are spread out between Europe and Africa (2).
- ❖ *Rickettsia aeschlimannii* has not yet widely colonized Europe as suggested by the scarce reports in European tick species (3) and the few human cases of rickettsiosis attributed to *R. aeschlimannii* (4).
- ❖ The constant flow of infected ticks on migratory birds may however change the future scenario (5).
- ❖ The reasons behind the current scenario merit further attention to understand *R. aeschlimannii*'s ecology and prevent it becoming enzootic in Europe.



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Acknowledgements

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