



Key

- Geographical clustering of *A. phagocytophilum* ecotypes I reported (this study) from sheep, cattle and *I. ricinus* with previously reported European ecotype I from humans (e.g., AF033101: Austria; AF033101: Slovenia), horses, hedgehog, brown bear, polecat, cattle, sheep, roe deer, dogs, wild goat, fox and dogs
- Distinct geographical clustering of American NCBI reference *A. phagocytophilum* ecotypes I obtained from horses, rodents, rabbit, dogs, cat and human patients
- Ecotype I *A. phagocytophilum* sequences reported from Great Britain cattle

Note: Ecotype I subclade without a specific rectangular bar signifies geographical clustering of the additional *A. phagocytophilum* ecotype I obtained from cattle, sheep and ticks in this study, with previously reported European ecotype I from wild ruminants, cattle, sheep horse and dog.

Additional file 1: Fig S1. A full polar cladogram displayed following maximum likelihood phylogenetic tree constructed at 10,000 bootstrap approximations using *A. phagocytophilum* groEL gene nucleotide sequences (48) generated from this study and representative ecotypes (328) reported in previous literature (Jahfara et al., 2005; Bianchessi et al., 2023). Clades in black text represents ecotype I, red represents ecotype II, green represents ecotype III, and blue represents ecotype IV. While taxa in magenta under ecotypes I and II represent Nucleotide sequences reported from GB livestock, *I. ricinus* and deer species. Branch tips in gray represents ecotypes I reported from Great Britain cattle. The phylogeny is rooted at midpoint and drawn to display circular node shapes at bootstrap support values $\geq 90\%$. Nucleotide sequences obtained from this study were name using pathogen (*A. phagocytophilum*) name, sequence source/host and the year samples were collected etc. as below: A.pha. (*A. phagocytophilum*); h1 or h2.B.tau (heifer1 or 2, *Bos taurus*); f.B.tau (female, *Bos taurus*); f.l.ric (female, *Ixodes ricinus*); O.ari (*Ovis aries*); n1 or n2/l.ric (nymph, *Ixodes ricinus*); C.ela. (*Cervus elaphus*); n = x means pooled samples, C.cap (*Capreolus capreolus*).