CORRECTION

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Correction to: The absence of the *drhm* gene is not a marker for human-pathogenicity in European *Anaplasma phagocytophilum* strains

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Correction to: Parasites Vectors (2020) 13:238
https://doi.org/10.1186/s13071-020-04116-z

Following publication of the original article [1], the author flagged that unfortunately there are errors in some of the figures and additional files.

The color-coding in Figs. 1 and 2, and in Additional file 3: Figure S1 and Additional file 4: Figure S2 is wrong: Bison samples are displayed in dark blue instead of light blue.

In addition, some numbers for the *atpA* alleles in Additional file 1: Table S1 are wrong.

The corrected versions of Figs. 1 and 2, and Additional files 1, 3 and 4 are provided in this correction.

The authors apologize for the inconvenience caused.

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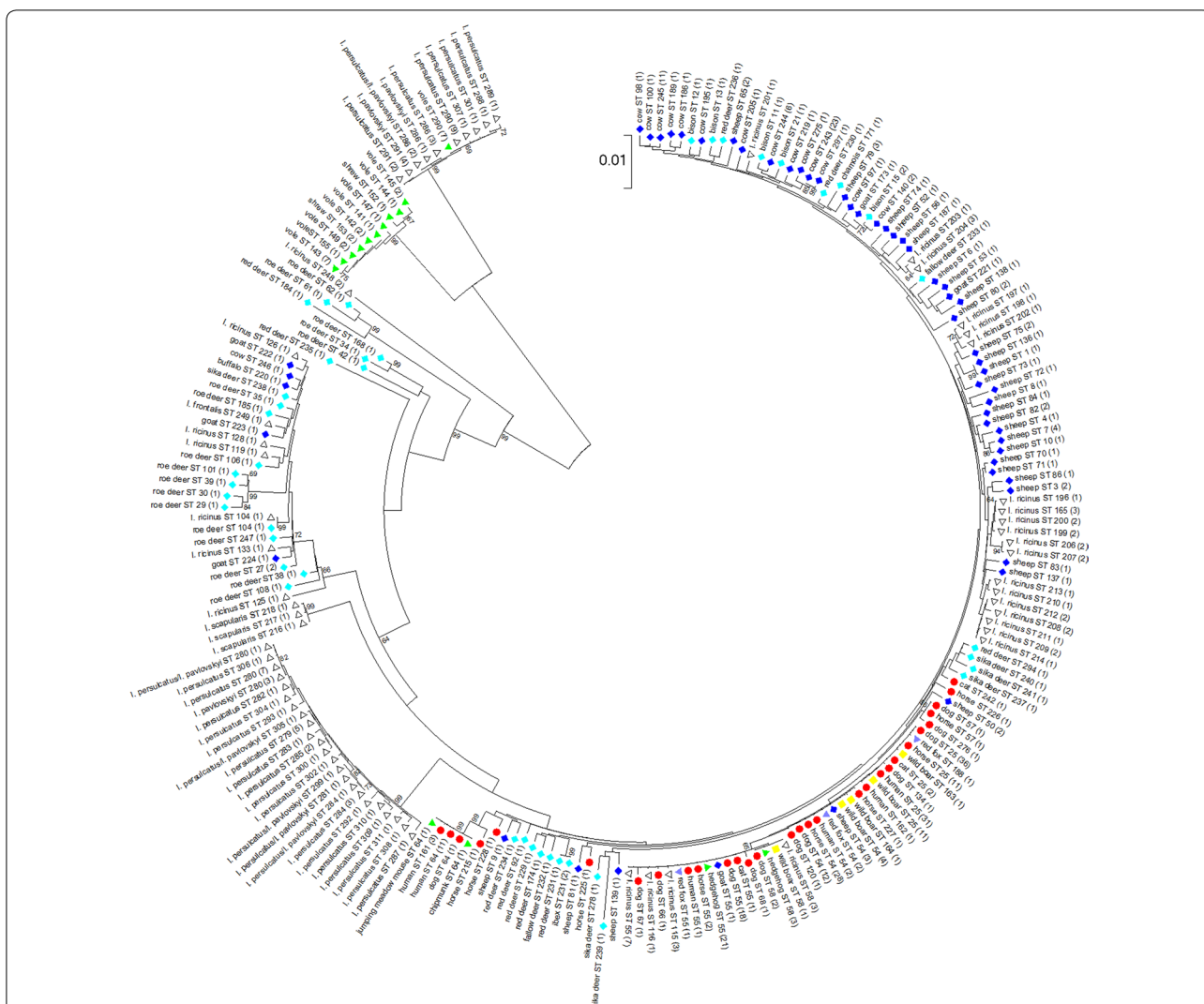Full list of author information is available at the end of the article

Fig. 1 Phylogenetic tree calculated from the concatenated housekeeping gene sequences of 520 samples without ambiguous nucleotides. Tree construction was achieved by the NJ method using the Jukes-Cantor matrix with the complete deletion option. Bootstrap values $\geq$ 64% are shown next to the branches. The scale-bar indicates the number of nucleotide substitutions per site. The final data set contained 2877 positions. Identical ST are displayed only once per species. The number in parenthesis indicates the frequency with which the respective ST was found. *Key*: red circles, sequences from humans, dogs, horses and cats; dark blue diamonds, sequences from domestic ruminants (cattle, sheep, goats and water buffalo); light blue diamonds, sequences from wild ruminants (roe deer, red deer, sika deer, fallow deer, European bison, mouflon, chamois and ibex); green triangles, sequences from small mammals (hedgehogs, voles, shrews, chipmunk and jumping meadow mouse); yellow squares, sequences from wild boars; purple triangles, sequences from red foxes; white triangles, sequences from ticks
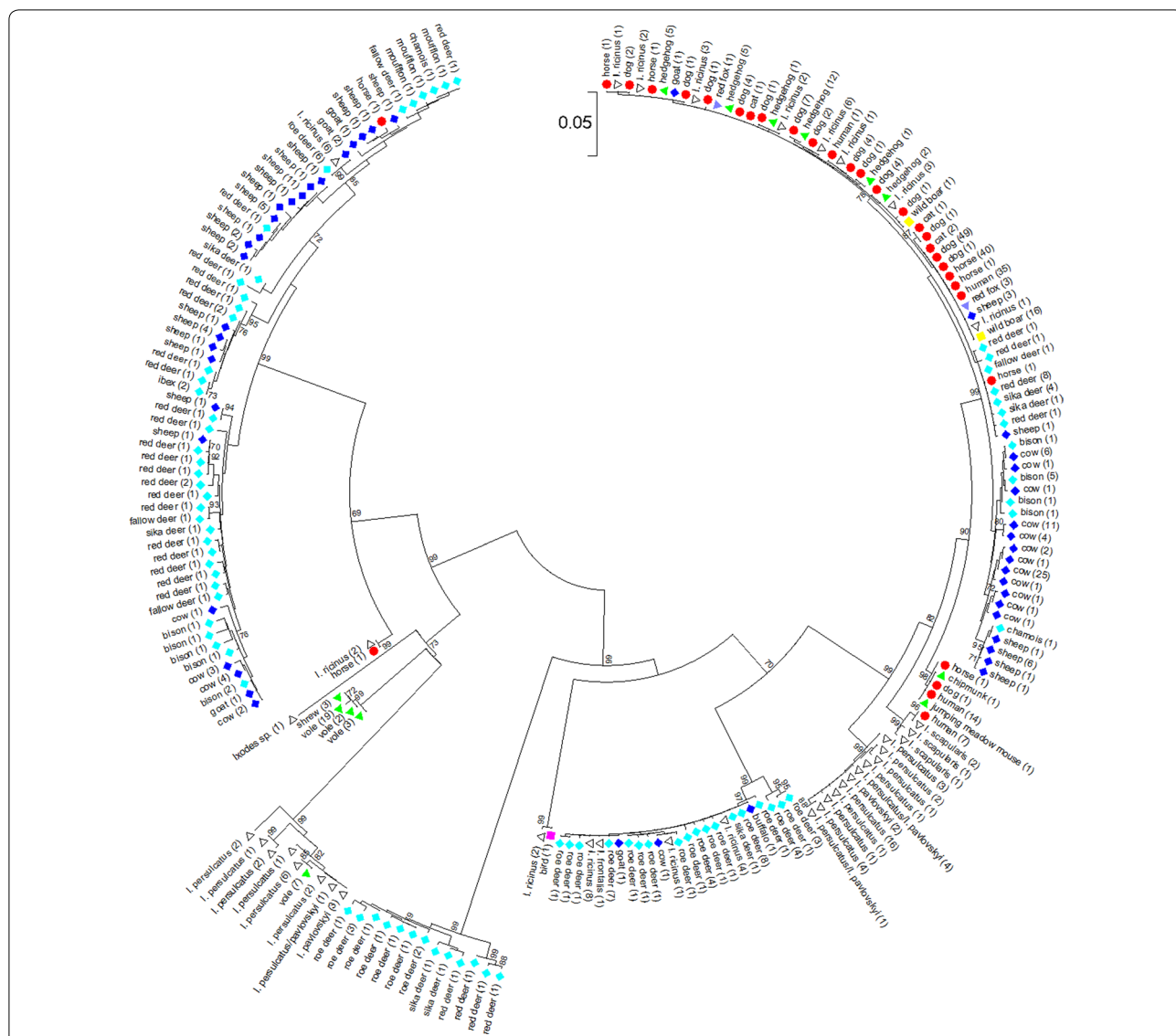
Fig. 2 Phylogenetic tree calculated from the *ankA* sequences of 623 samples without ambiguous nucleotides. Tree construction was achieved by the NJ method using the Jukes-Cantor matrix with the complete deletion option. Bootstrap values ≥ 69% are shown next to the branches. The scale-bar indicates the number of nucleotide substitutions per site. The final data set contained 510 positions. Identical *ankA* sequences are displayed only once per species. The number in parenthesis indicates the frequency with which the respective sequence was found. *Key*: red circles, sequences from humans, dogs, horses and cats; dark blue diamonds, sequences from domestic ruminants (cattle, sheep, goats and water buffalo); light blue diamonds, sequences from wild ruminants (roe deer, red deer, sika deer, fallow deer, European bison, mouflon, chamois and ibex); green triangles, sequences from small mammals (hedgehogs, voles, shrews, chipmunk and jumping meadow mouse); yellow squares, sequences from wild boars; purple triangles, sequences from red foxes; pink square, sequence from a bird, white triangles, sequences from ticks

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Supplementary information

Supplementary information accompanies this paper at https://doi.org/10.1186/s13071-020-04350-5.

Additional file 1: Table S1. Reference, host species, ST, CC, MLST cluster, allele numbers, *ankA* gene cluster, *drhm* status, APH_0919/APH_0922 status, country of origin, year of sampling, disease state of the host and GenBank accession numbers for the 686 *A. phagocytophilum* strains.

Additional file 3: Figure S1. Phylogenetic tree calculated from the concatenated housekeeping gene sequences of 520 samples without ambiguous nucleotides. Tree construction was achieved by the NJ method using the Jukes-Cantor matrix with the complete deletion option. Bootstrap values $\geq$ 64% are shown next to the branches. The scale-bar indicates the number of nucleotide substitutions per site. The final data set contained 2877 positions. Identical ST are displayed only once per species. The number in parenthesis indicates the frequency with which the respective ST was found. *Key*: red circles, sequences from humans, dogs, horses and cats; dark blue diamonds, sequences from domestic ruminants; light blue diamonds, sequences from wild ruminants; green triangles, sequences from small mammals; yellow squares, sequences from wild boars; purple triangles, sequences from red foxes; white triangles, sequences from ticks.

Additional file 4: Figure S2. Phylogenetic tree calculated from the *ankA* sequences of 623 samples without ambiguous nucleotides. Tree construction was achieved by the NJ method using the Jukes-Cantor matrix with the complete deletion option. Bootstrap values $\geq$ 69% are shown next to the branches. The scale-bar indicates the number of nucleotide substitutions per site. The final data set contained 510 positions. Identical *ankA* sequences are displayed only once per species. The number in parenthesis indicates the frequency with which the respective sequence was found. *Key*: red circles, sequences from humans, dogs, horses and cats; dark blue diamonds, sequences from domestic ruminants; light blue diamonds, sequences from wild ruminants; green triangles, sequences from small mammals; yellow squares, sequences from wild boars; purple triangles, sequences from red foxes; pink square, sequence from a bird, white triangles, sequences from ticks.

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Reference

1. Langenwalder DB, Schmidt S, Silaghi C, Skuballa J, Pantchev N, Matei IA, Mihalca AD, Gilli U, Zajkowska J, Ganter M, Hoffman T, Salaneck E, Petrovec M, Loewenich FD. The absence of the *drhm* gene is not a marker for human-pathogenicity in European *Anaplasma phagocytophilum* strains. Parasites Vectors. 2020;13:238. https://doi.org/10.1186/s13071-020-04116-z.

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