Table S1: Genetic distances within the genus estimated using K2P model of substitutions, between 18SrRNA lineages of Adeleorina parasites included in Fig. 3 and Fig. S1. Genetic distance inside and between clades are provided

|  |  |
| --- | --- |
| Clade | Genetic distance (d ± SD) |
| Full lenght sequences(Fig. 3) | 1000 bp (Fig. S1 A) | 585 pb(Fig. S1 B) |
| *Hepatozoon* species from amphibians (Clade A) | 0.024 ± 0.002 | 0.021 ± 0.002 | 0.020 ± 0.004  |
| *vs.* | *Hepatozoon* species from reptiles (Clade B) | 0.052 ± 0.004 | 0.049 ± 0.005 | 0.063 ± 0.008 |
| *Hepatozoon* species from reptiles (Clade C) | 0.053 ± 0.006 | 0.050 ± 0.007 | 0.054 ± 0.008 |
| *Hepatozoon* species from mammals (Clade D) | 0.065 ± 0.005 | 0.053 ± 0.005 | 0.064 ± 0.009 |
| *Hepatozoon* species from reptiles (Clade E) | 0.055 ± 0.004 | 0.051 ± 0.006 | 0.063 ± 0.010 |
| *Hemolivia* (clade F) | 0.055 ± 0.004 | 0.048 ± 0.005 | 0.058 ± 0.009 |
| *Haemogregarina* sp*.* (clade G -Old World) | 0.079 ± 0.007 | 0.066 ± 0.007 | 0.088 ± 0.012 |
| *Haemogregarina* sp*.* (clade H-New world) | 0.082 ± 0.011 | 0.082 ± 0.011 | 0.081 ± 0.011 |
| *Haemogregarina* sp*.* (clade I-New world) | 0.098 ± 0.008 | 0.050 ± 0.007 | 0.063 ± 0.008 |
| Outgroup | 0.074 ± 0.006 | 0.089 ± 0.009 | 0.093 ± 0.013 |
| *Hepatozoon* species from reptiles (Clade B) | 0.022 ± 0.002 | 0.023 ± 0.002 | 0.034 ± 0.004 |
| *vs* | *Hepatozoon* species from reptiles (Clade C) | 0.034 ± 0.005 | 0.032 ± 0.005 | 0.037 ± 0.005 |
| *Hepatozoon* species from mammals (Clade D) | 0.044 ± 0.004 | 0.040 ± 0.004 | 0.055 ± 0.007 |
| *Hepatozoon* species from reptiles (Clade E) | 0.037 ± 0.003 | 0.037 ± 0.004 | 0.051 ± 0.008 |
| *Hemolivia* (clade F) | 0.032 ± 0.003 | 0.051 ± 0.004 | 0.039 ± 0.006 |
| *Haemogregarina* sp*.* (clade G -Old World) | 0.054 ± 0.006 | 0.065 ± 0.006 | 0.076 ± 0.010 |
| *Haemogregarina* sp*.* (clade H-New world) | 0.065 ± 0.010 | 0.065 ± 0.009 | 0.065 ± 0.010 |
| *Haemogregarina* sp*.* (clade I-New world) | 0.083 ± 0.008 | 0.082 ± 0.009 | 0.093 ± 0.010 |
| Outgroup | 0.054 ± 0.005 | 0.051 ± 0.006 | 0.079 ± 0.011 |
| *Hepatozoon* species from reptiles (Clade C) | 0.019 ± 0.006 | 0.019 ± 0.006 | 0.019 ± 0.006 |
| *vs* | *Hepatozoon* species from mammals (Clade D) | 0.040 ± 0.005 | 0.037 ± 0.005 | 0.041 ± 0.006 |
| *Hepatozoon* species from reptiles (Clade E) | 0.039 ± 0.005 | 0.036 ± 0.005 | 0.037 ± 0.005 |
| *Hemolivia* (clade F) | 0.030 ± 0.005 | 0.027 ± 0.005 | 0.030 ± 0.006 |
| *Haemogregarina* sp*.* (clade G -Old World) | 0.058 ± 0.008 | 0.053 ± 0.008 | 0.063 ± 0.010 |
| *Haemogregarina* sp*.* (clade H-New world) | 0.050 ± 0.009 | 0.050 ± 0.008 | 0.050 ± 0.008 |
|  | *Haemogregarina* sp*.* (clade I-New world) | 0.081 ± 0.009 | 0.078 ± 0.010 | 0.081 ± 0.010 |
|  | Outgroup | 0.056 ± 0.008 | 0.053 ± 0.007 | 0.064 ± 0.010 |
| *Hepatozoon* species from mammals (Clade D) | 0.034 ± 0.003 | 0.027 ± 0.003 | 0.033 ± 0.004 |
| *vs* | *Hepatozoon* species from reptiles (Clade E) | 0.035 ± 0.003 | 0.031 ± 0.005 | 0.039 ± 0.006 |
| *Hemolivia* (clade F) | 0.035 ± 0.004 | 0.029 ± 0.004 | 0.036 ± 0.005 |
| *Haemogregarina* sp*.* (clade G -Old World) | 0.060 ± 0.006 | 0.053 ± 0.006 | 0.071 ± 0.010 |
| *Haemogregarina* sp*.* (clade H-New world) | 0.058 ± 0.009 | 0.058 ± 0.008 | 0.058 ± 0.009 |
| *Haemogregarina* sp*.* (clade I-New world) | 0.079 ± 0.008 | 0.075 ± 0.009 | 0.082 ± 0.010 |
| Outgroup | 0.057 ± 0.005 | 0.050 ± 0.006 | 0.072 ± 0.010 |
| *Hepatozoon* species from reptiles (Clade E) | 0.017 ± 0.002 | 0.016 ± 0.002 | 0.005 ± 0.002 |
| *vs* | *Hemolivia* (clade F) | 0.031 ± 0.004 | 0.028 ± 0.004 | 0.035 ± 0.007 |
| *Haemogregarina* sp*.* (clade G -Old World) | 0.048 ± 0.005 | 0.047 ± 0.006 | 0.067 ± 0.010 |
| *Haemogregarina* sp*.* (clade H-New world) | 0.065 ± 0.009 | 0.065 ± 0.009 | 0.060 ± 0.010 |
| *Haemogregarina* sp*.* (clade I-New world) | 0.076 ± 0.007 | 0.075 ± 0.009 | 0.081 ± 0.011 |
|  | Outgroup | 0.049 ± 0.005 | 0.052 ± 0.006 | 0.071 ± 0.013 |
| *Hemolivia* (clade F) | 0.011 ± 0.003 | 0.009 ± 0.002 | 0.013 ± 0.003 |
| *vs* | *Haemogregarina* sp*.* (clade G -Old World) | 0.047 ± 0.005 | 0.042 ± 0.006 | 0.058 ± 0.009 |
| *Haemogregarina* sp*.* (clade H-New world) | 0.047 ± 0.009 | 0.047 ± 0.006 | 0.047 ± 0.008 |
| *Haemogregarina* sp*.* (clade I-New world) | 0.069 ± 0.008 | 0.066 ± 0.008 | 0.074 ± 0.010 |
| Outgroup | 0.045 ± 0.005 | 0.040 ± 0.005 | 0.061 ± 0.010 |
| *Haemogregarina* sp*.* (clade G -Old World) | 0.008 ± 0.002 | 0.005 ± 0.002 | 0.009 ± 0.003 |
| *vs* | *Haemogregarina* sp*.* (clade H-New world) | 0.049 ± 0.009 | 0.049 ± 0.009 | 0.049 ± 0.009 |
| *Haemogregarina* sp*.* (clade I-New world) | 0.076 ± 0.008 | 0.074 ± 0.009 | 0.082 ± 0.010 |
| Outgroup | 0.045 ± 0.005 | 0.041 ± 0.006 | 0.063 ± 0.010 |
| *Haemogregarina* sp*.* (clade H-New world) | 0.014 ± 0.005 | 0.014 ± 0.005 | 0.014 ± 0.005 |
| *vs* | *Haemogregarina* sp*.* (clade I-New world) | 0.075 ± 0.010 | 0.075 ± 0.011 | 0.075 ± 0.009 |
| Outgroup | 0.051 ± 0.010 | 0.051 ± 0.009 | 0.050± 0.009 |
| *Haemogregarina* sp*.* (clade I-New world) | 0.059 ± 0.009 | 0.059 ± 0.010 | 0.059 ± 0.003 |
|  | Outgroup | 0.064 ± 0.008 | 0.059 ± 0.008 | 0.066 ± 0.009 |
| Outgroup | 0.006 ± 0.002 | 0.004 ± 0.002 | 0.007 ± 0.004 |