

Supplementary Information

Title

The geography and timing of genetic divergence in the lizard *Phrynocephalus theobaldi* on the Qinghai-Tibetan plateau

Author list

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Supplementary Information S1

Sample sites, haplotypes and individuals of *Phrynocephalus theobaldi*, for mtDNA (a), *AME* (b) and *RAG-I* (c)
(a)

Sample site	Latitude (°)	Longitude (°)	MtDNA haplotype [specimen number]
1	29.4671	86.1068	40[11N0101]
2	29.4087	85.5703	35[11N0205,11N0204,11N0201,11N0202],36[11N0203],38[11N0207]
3	29.5690	85.8346	35[11N0305,11N0308,11N0302,11N0304,11N0310,11N0303,11N0301,11N0312,11N0309],39[11N0307,11N0311]
4	29.5004	84.5607	32[11N0402,11N0401,11N0406,11N0403,11N0405,11N0404,11N0408,11N0409,11N0407]
5	29.6653	84.1642	32[11N0508,11N0504,11N0505,11N0502,11N0506,11N0507],33[11N0503]
6	30.8682	83.7873	32[11N0602,11A0603]
7	30.7917	81.3781	71[11N0701,11N0702]
8	30.7247	81.3676	71[11N0803,11N0802,11N0801]
9	30.6855	81.3135	71[11N0902],72[11N0901]
10	30.3854	81.1539	73[11N1001]
11	31.4363	80.5239	67[11N1106,11N1105,11N1104,11N1102,11N1103],68[11N1101]
12	31.6625	80.3162	70[11N1204],69[11N1202,11N1203,11N1201]
13	32.1264	80.0801	69[11N1304,11N1308,11N1305,11N1306,11N1310,11N1307,11N1303,11N1302,11N1312,11N1309,11N1301], 67[11N1311]
14	32.3962	80.044	46[11N1401, 11N1402],50[11N1403]
15	32.3666	80.3671	45[11N1501],46[11N1502],59[11N1504,11N1506], 60[11N1503]
16	32.3660	80.7538	58[11N1602],79[11N1601]
17	32.4606	81.9143	61[11N1702]
18	32.5436	80.6392	80[11N1803]
19	32.5365	80.5477	46[11N1907,11N1906],58[11N1902, 11A1904,11N1905,11N1901,11N1909,11N1910,11N1908],63 [11N1903]

20	32.4138	79.7666	58[11N2007],64[11N2006,11N2003,11N2002,11N2004,11N2005]
21	32.4602	80.9279	46[11N2105,11N2104,11N2106,11N2103],53[11N2102],56[11N2107],57[11N2101]
22	33.7488	80.4482	80[11N2201,11N2205,11N2202],81[11N2204],82[11N2203]
23	33.6063	79.3203	76[11N2301],77[11N2302]
24	33.4593	79.8318	76[11N2403,11N2401,11N2402,11N2404]
25	33.5148	80.9059	76[11N2505,11N2502,11N2504,11N2506,11N2503]
26	33.1164	80.247	79[11N2606,11N2602,11N2605,11N2607,11N2604]
27	33.1874	80.8971	78[11N2703,11A2702],83[11N2701]
28	32.5832	80.0459	58[11N2802,11N2801]
29	32.5612	80.1197	46[11N2901,11N2904,11N2902,11N2905],58[11N2903],62[11N2906,11N2907]
30	32.4266	80.0114	46[11N3003,11N3006,11N3007,11N3009,11N3005,11N3014,11N3010,11N3017,11N3020,11N3011,11N3015] 49[11N3002],54[11N3013],55[11N3016]
31	30.0300	83.4902	32[11N3103,11N3102,11N3101]
32	30.8853	83.7183	32[11N3203,11N3202,11N3201,RDQ6]
33	29.5650	85.8526	35[11N3304,11N3308,11N3307,11N3301],39[11N3306,11N3305,11N3303,11N3302],17[RDQ12],18[RDQ11]
34	29.9643	85.4416	37[11N3402],36[11N3401]
35	28.5932	87.0844	43[11N3505,11N3508,11N3511,11N3504,11N3501,11N3510,11N3503,11N3502,11N3507,11N3509, 11N3512],44[11N3514]
36	29.1659	87.6883	41[11N3601,11N3603],42[11N3602]
37	29.1516	88.62	6[11N3701,11N3703,11N3707,11N3705,11N3709],11[11N3706,11N3704],9[11N3708],14[11N3710]
38	29.3631	89.8471	7[11N3805,11N3802,11N3804,11N3803],8[11N3801]
39	29.3333	89.3377	5[11N3907],4[11N3906,11N3903],10[11N3905],12[11N3902,11N3904],13[11N3908,11N3901]
40	29.3795	90.8131	15[11N4001,11N4004,11N4003,11N4005],20[11N4006,11N4002]
41	29.3819	91.8627	15[11N4101]
42	29.2588	91.5336	19[N154],25[N155],28[N221,N220]
43	29.2573	91.596	29[N223],27[N222]
44	29.2825	91.8117	22[N157,N158,N156]

45	29.2388	92.0122	25[N159,N163]
46	29.1129	92.6462	25[N167,N166,N168,N164]
47	29.0839	92.7673	25[N176,N175],27[N172,N171,N173,N174,N178,N177]
48	29.9933	93.2489	25[N181]
49	29.3814	94.4155	25[N191]
50	29.3800	90.86	16[T275],15[T268,T269,T273,T277,T280N,T272,T267, T269B]
51	29.3200	91.82	22[T098, T100,T102,T103,T104,T106, T098B], 23[T099B T099], 24[T101]
52	29.2700	88.91	1[T151,T148,T153,T158,T160],2[T146,T154],3[T149,T145,T155,T156]
53	29.3200	85.23	32[T172,T171,T176,T177,T182,T186],34[T139,T163,T164,T166,T169,T170,T173,T175,T181,T183]
54	29.5700	84.85	35[T191,T192,T190]
55	29.8800	83.73	30[T196,T197,T198],32[T194,T199]
56	30.2800	82.95	31[T202],32[T200,T201,T203,T205,T206]
57	30.7400	81.64	71[T207,T208,T209,T210]
58	31.4900	80.44	65[T215,T233],66[T214,T221,T238],67[T212,T218,T213,T219,T222,T229,T230,T232,T236,T239,T241,T244, T240, T237,T224,T227,T211]
59	33.3900	79.74	74[T247],75[T252],76[T246,T249,T250,T245,T251,T253,T254,T255,T256,T259,T261,T262,T263,T264, T248]
60	32.5400	80.06	46[T291,T299,T300,T297], 47[T294,T295],48[T290,T298],51[T304], 52[T296,T301],58[T292,T293,T302,11N6004]

(b)

<i>AME</i> Haplotype	Individual
<i>AME</i> _Hap_1	T100,T101,T280N,T273,T272,T268,T267,11N4006,11N4004,11N4002,11N4001,11N3801,11N3802,11N3805,11N3901,11N3903,11N3904,11N3905,11N3908,11N3708,11N3703,11N3701,11N3603,11N1502,11N1504,11N1602,11N1904,11N2106,11N2102,11N2801,11N2904,11N2905,11N3009,11N3016,11N2607,11N2606,11N2703,11N2506,11N2204,11N2202,N220,N221
<i>AME</i> _Hap_2	11N3702,11N0901,11N0902
<i>AME</i> _Hap_3	11N3601
<i>AME</i> _Hap_4	11N3501,11N3504,11N3507,11N3509,11N3511,11N3512,11N3514,11N3303,11N0304,11N0305,11N0308,11N0309,11N0310,11N0311,11N0207,11N3401,11N0506,T196,11N3102,11N2503
<i>AME</i> _Hap_5	11N3301
<i>AME</i> _Hap_6	11N1102,11N1101,11N1106,11N1103,11N1104,11N1105,11N1203,11N1202,11N1201,T229,T224,T213,T211,11N1309,11N1303,11N1305,11N1310,11N1302,11N1304,11N1311,11N1301,11N1312,11N1901,11N2003,T238,11N2802,11N6004,11N3011,T292
<i>AME</i> _Hap_7	11N2604,11N2602,T256,T254,T259
<i>AME</i> _Hap_8	11N2401,11N2402

(c)

<i>RAG-I</i> haplotype	Individual
<i>RAG-I</i> _Hap_1	T100,T101,T280N,T273,T268,T267,11N4006,11N4004,11N4002,11N4001,11N3801,11N3802,11N3805,11N3901,11N3903,11N3904,11N3908,11N3703,11N3701,11N3601,11N3603,11N3501,11N3504,11N3507,11N3509,11N3511,11N3512,11N3514,11N0308,11N0309
<i>RAG-I</i> _Hap_2	T272
<i>RAG-I</i> _Hap_3	11N3905
<i>RAG-I</i> _Hap_4	11N3708
<i>RAG-I</i> _Hap_5	11N3702,11N0901,11N0902
<i>RAG-I</i> _Hap_6	11N3301,11N3303,11N0304,11N0310,11N0311,11N0207,11N3401
<i>RAG-I</i> _Hap_7	11N0305
<i>RAG-I</i> _Hap_8	11N0506,T196
<i>RAG-I</i> _Hap_9	11N3102
<i>RAG-I</i> _Hap_10	11N1102,11N1101,11N1106,11N1103,11N1104,11N1105,11N1202,11N1201,T224,T213,T211,11N1312,11N1904,11N2607,11N2604,11N2602,11N2703,11N2401,11N2402,11N2204,11N2202,T256,T254,T259
<i>RAG-I</i> _Hap_11	11N1203,11N1309,11N1303,11N1305,11N1310,11N1302,11N1304,11N1311,11N1301,11N1502,11N1504,11N1901,11N2003,11N2802,11N2904,11N3009,11N6004,T292
<i>RAG-I</i> _Hap_12	T229,T238
<i>RAG-I</i> _Hap_13	11N1602,11N2106,11N2102,11N2801,11N2905,11N3011,11N3016
<i>RAG-I</i> _Hap_14	11N2606,11N2503,11N2506
<i>RAG-I</i> _Hap_15	N220,N221

Supplementary Information S2

DNA sequences for the *P. theobaldi* haplotypes

The 83 mtDNA haplotypes (aligned) detected in *P. theobaldi*

1

GGCTGAACCATTATAATCATAGCCCTCTCCCCAAATCTAGCAATTATAAATATCTTTA
TCTACATTATTATAACCACCCCAATTTTTTTGACAATAACAAACATATCAACAAAAA
CACTACAAAATTTAACCACAACATGAACAACCTCTATAACAATAACCCTTTCCACT
ACCTTCCTAATACTATCAACCAGCGGCCTACCACCGTTTACAGGATTTATACCAAAA
ATACTAATTCTTAATGAACTTATTTACAAAACTTACAGCACTAGCAACCCTAGCA
ATTATAACATCACTAATTAGTTTATTATTTTACTTACGAATCACATACCTAATTATAAT
ACTCACATCACCAACAACAACCACATCATCAACAAAATGACGAGCCCCAAAACCAA
AAATTACAATAATAACAATAAATTCCAACAGCACTATTCATTACTCACCTAACC
CCAGCAATCCCGTTCTAAAGAAGCTTAGGATT-AAACTTATTAAACCGGTGGCCTTC
AACGCCACAAACAAGGGGG-AGCCCTTAGCTTCTGAAAGACCTATAGAAGTTTCTT
CTACATCAT

2

GGCTGAACCATTATAATCATAGCCCTCTCCCCAAATCTAGCAATTATAAATATCTTTA
TCTACATTATTATAACCACCCCAATTTTTTTAACAATAACAAACATATCAACAAAAA
CACTACAAAATTTAACCACAACATGAACAACCTCTATAACAATAACCCTTTCCACT
ACCTTCCTAATACTATCAACCAGCGGCCTACCACCGTTTACAGGATTTATACCAAAA
ATACTAATTCTTAATGAACTTATTTACAAAACTTACAGCACTAGCAACCCTAGCA
ATTATAACATCACTAATTAGTTTATTATTTTACTTACGAATCACATACCTAATTATAAT
ACTCACATCACCAACAACAACCACATCATCAACAAAATGACGAGCCCCAAAACCAA
AAATTACAATAATAACAATAAATTCCAACAGCACTATTCATTACTCACCTAACC
CCAGCAATCCCGTTCTAAAGAAGCTTAGGATT-AAACTTATTAAACCGGTGGCCTTC
AACGCCACAAACAAGGGGGGAGCCCTTAGCTTCTGAAAGACCTATAGAAGTTTCT
TCTACATCAT

3

GGCTGAACCATTATAATCATAGCCCTCTCCCCAAATCTAGCAATTATAAATATCTTTA
TCTACATTATTATAACCACCCCAATTTTTTTAACAATAACAAGCATATCAACAAAAA
CACTACAAAATTTAACCACAACATGAACAACCTCTATAACAATAACCCTTTCCACT
ACCTTCCTAATACTATCAACCAGCGGCCTACCACCGTTTACAGGATTTATACCAAAA
ATACTAATTCTTAATGAACTTATTTACAAAACTTACAGCACTAGCAACCCTAGCA
ATTATAACATCACTAATTAGTTTATTATTTTACTTACGAATCACATACCTAATTATAAT
ACTCACATCACCAACAACAACCACATCATCAACAAAATGACGAGCCCCAAAACCAA
AAATTACAATAATAACAATAATGATTCCAACAGCACTATTCATTACTCACCTAACC
CCAGCAATCCCGTTCTAAAGAAGCTTAGGATT-AAACTTATTAAACCGGTGGCCTTC
AACGCCACAAACAAGGGGGGAGCCCTTAGCTTCTGAAAGACCTATAGAAGTTTCT
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4

GGCTGAACCATTATAATCATAGCCCTCTCCCCAAATCTAGCAATTATAAATATCTTCA
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CACTACAAAATTTAACCACAACATGAACAACCTCTATAACAATAACCCTTTCCACT

ACCTTCCTAATACTATCAACCAGCGGCCTACCACCGTTTACAGGGTTTATACCAAAA
ATACTAATTCTTAATGAACTTATTTACAAAAACTTACAGCACTAGCAACCCTAGCA
ATTATAACATCACTAATTAGTTTATTATTTTACTTACGAATCACATACCTAATTATAAT
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CTACATCAT

5

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CTACATCAT

6

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ACCTTCCTAATACTATCAACCAGCGGCCTACCACCGTTTACAGGATTTATACCAAAA
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ACTTACATCACCAACAACAACCACATCATCAACAAAATGACGAGCCCAAAACCAA
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CCAGCAATCCCGTTCTAAAGAAGCTTAGGATT-AAACTTATTAAACCGGTGGCCTTC
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TCTACATCAT

7

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ATACTAATTCTTAATGAACTTATTTACAAAAACTTACAGCACTAGCAACCCTAGCA
ATTATAACATCACTAATTAGTTTATTATTTTACTTACGAATCACATACCTAATTATAAT
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CCAGCAATCCCGTTCTAAAGAAGCTTAGGATT-AAGCTTATTAAACCGGTGGCCTTC
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TCTACATCAT

8

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ATTATAACATCACTAATTAGTTTATTATTTTACTTACGAATCACATACCTAATTATAAT
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AAATTACAATAATAACAATAATAATTCCAACAGCACTATTCATTACTCACCTAACC
CCAGCAATCCCGTTCTAAAGAAGCTTAGGATT-AAGCTTATTAAACCGGTGGCCTTC
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TCTACATCAT

9

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TCTACATCAT

10

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CTACATCAT

11

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ATTATAACATCACTAATTAGTTTATTATTTTACTTACGAATCACATACCTAATTATAAT
ACTTACATCACCAACAACAACCACATCATCAACAAAATGACGAGCCCAAAACCAA

AAATTACAATAACAATAAATTCCAACAGCACTATTCATTACTCACCTAACC
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AACGCCACAAACAAGGGGG-AACCCTTAGCTTCTGAAAGACCTATAGAAGCTTTCTT
CTACATCAT

12

GGCTGAACCATTACAATCATAGCCCTCTCCCCAAATCTAGCAATTATAAATATCTTCA
TCTACATTATTATAAACCACCCCAATTTTTTTAACAATAACAAATATATCAACAAAAAC
ACTACAAAATTTAACCACAACATGAACAACCTCTATAACAATAACCCTTTCCACTA
CCTTCCTAATACTATCAACCAGCGGCCTACCGCCATTTACAGGATTTATACCAAAAA
TACTAATTCTTAATGAAGCTTATTTACAAAACTTACAGCACTAGCAACCCTAGCAA
TTATAACATCACTAATTAGTTTATTATTTTACTTACGAATCACATACCTAATTATAATA
CTTACATCACCAACAACAACCACATCATCAACAAAATGACGAGCCCCAAAACCAAA
AATTACAATAACAATAAATTCCAACAGCACTATTCATTACTCACCTAACC
CAGCAATCCCGTTCTAAAGAAGCTTAGGATA-AAACTTAATAAACCGGTGGCCTTC
AACGCCACAAACAAGGTGGGAGCCCTTAGCTTCTGAAAGACCTATAGAAGCTTTCT
CCTACATCAT

13

GGCTGAACCATTACAATCATAGCCCTCTCCCCAAATCTAGCAATTATAAATATCTTCA
TCTACATTATTATAAACCACCCCAATTTTTTTAACAATAACAAATATATCAACAAAAAC
ACTACAAAATTTAACCACAACATGAACAACCTCTATAACAATAACCCTTTCCACTA
CCTTCCTAATACTATCAACCAGCGGCCTACCGCCATTTACAGGATTTATACCAAAAA
TACTAATTCTTAATGAAGCTTATTTACAAAACTTACAGCACTAGCAACCCTAGCAA
TTATAACATCACTAATTAGTTTATTATTTTACTTACGAATCACATACCTAATTATAATA
CTTACATCACCAACAACAACCACATCATCAACAAAATGACGAGCCCCAAAACCAAA
AATTACAATAACAATAAATTCCAACAGCACTATTCATTACTCACCTAACC
CAGCAATCCCGTTCTAAAGAAGCTTAGGATA-AAACTTATTAAACCGGTGGTTTTCA
ACGCCACAAACAAGGTGGGAGCCCTTAGCTTCTGAAAGACCTATAGAAGCTTTCTC
CTACATCAT

14

GGCTGAACCATTATAATCATAGCCCTCTCCCCAAATCTAGCAATTATAAATATCTTCA
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ACCTTCCTAATACTATCAACCAGCGGCCTACCACCATTTACAGGATTTATACCAAAAA
ATACTAATTCTTAATGAAGCTTATTTACAAAACTTACAGCACTAGCAACCCTAGCA
ATTATAACATCACTAATTAGTTTATTATTTTACTTACGAATCACGTACCTAATTATAAT
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AAATTACAATAACGATAATAATTCCAACAGCACTATTCATTACTCACCTAACC
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AACGCCACAAACAAGGTGGGAGCCCTTAGCTTCTGAAAGACCTATAGAAGCTTTCT
CCTACATCAT

15

GGCTGAACCACCATAATCATAGCCCTCTCCCCAAATCTAGCAATTATAAATATTTTC
ACTTACATTATTATAACTACCCCAATTTTTTTAATAATAACAAATATATCAACAAAA
CACTACAAAATTTAACCACAACATGAACAACCTCTGCAACAATAACCCTCTCCACT

GCCTTCCTAATATTATCAACCAGCGGCCTACCGCCATTACAGGATTTATACCAAAA
ATACTAATTCTTAATGAACTTATTTACAAAAACTCACAACACTAGCAGCTCTAGCA
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16

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TACATCAT

17

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TACATCAT

18

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19

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20

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CTACATCAT

21

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TACATCAT

22

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TACATCAT

23

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TACATCAT

24

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25 ??????????????ATAGCCCTCTCCCCAAATCTAGCAATTATAAATATTTTC
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CTACATCAT

26 ??????????????ATAGCCCTCTCCCCAAATCTAGCAATTATAAATATTTTC
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27 ????????????????ATAGCCCTCTCCCCAAATCTAGCAATTATAAATATTTTC
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28 ????????????????ATAGCCCTCTCCCCAAATCTAGCAATTATAAATATCTGC
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CTACATCAT

29 ????????????????ATAGCCCTTTCCCCAAATCTAGCAATTATAAATATCTGC
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CTACATCAT

30
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CCTACATCAT

31

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CCTACATCAT

32

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CCTACATCAT

33

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CCTACATCAT

34

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CCTACATCAT

35

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CCTACATCAT

36

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CCTACATCAT

37

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CCTACATCAT

38

GGCTGAACCATTATAACAATAGCCATCTCCCCAAACGTAGCAATCATAAATATCTCC
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CCTACATCAT

39

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CCTACATCAT

40

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CCTACATCAT

41

GGCTGAACCATCATAACCATAGCCATCTCCCCAAACGTAGCAATCATAAATATCTCC
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CTATATCAT

42

GGCTGAACCATCATAACCATAGCCATCTCCCCAAACGTAGCAATCATAAATATCTCC
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CTATATCAT

43

GGCTGAACCATTATAACCATAGCCCTCTCCCCAAACCTAGCAATCATAAATATCTCC
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CTACATCAT

44

GGCTGAACCATTATAACCATAGCCCTCTCCCCAAACCTAGCAATCATAAATATCTCC
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CTACATCAT

45

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46

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47

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48

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49

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51

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52

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56

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57

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58

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61

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62

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63

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64

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66

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67

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68

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69

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70

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71

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72

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73

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74

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AACACCACAAACAAGGGA-AAACCCTTAGCTTCTGAAAGACCCATAGGACTCTCT
CCTACATCAT

75

GGCTGAACCATTATAATTATAGCCCTTTCCCCAAATTTAGCAATTATAAATATCTCCA
CTTACATTATTATAACCACCCCAATTTTTCTAATAATAACAAATACATCAACAAAAAC
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CCTACATCAT

76

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CTCCTACATCAT

77

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CTCCTACATCAT

78

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79

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CTCCTACATCAT

80

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CCTACATCAT

81

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TCTCCTACATCAT

82

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CCTACATCAT

83

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CCCTCCTAATGCTATCAACCAGCGGCCTCCCACCATTACAGGATTTATACCAAAAA
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GCTCACATCGCCAATAACAACCCCATCATCAACAAAATGACGAACCAAAAAACCAA
AAACCACAATAATAACAATAAATACTCCAACAGCACTATTCATCACCCACCTAATC
CCAGCAATCCCCTTCTAAAGAAGCTTAGGATT-AAACTTATTAAACCAGTGGCCTTC
AACACCACAAACAAGGGA-AAACCCTTAGCTTCTGAAAGACCCATAGGACTCTCT
CCTACATCAT

The 8 AME genotype sequences (aligned) detected in *P. theobaldi*

AME_Hap_1

GGGGGAGATGTGAAATCGGTGTGCATGATGCACCAAAGTCCCTTTCAAGCTCTCCATC
CAATGCCACCACCTCTCCACCAGGTACAGCAACAGCCACCTCTGAACCCACACATGCA
GCTACCTGGACATAACACATTTGTGCCAATGACTGGACAGAATACATTAGTGCCACAGT
ATCAACCAGCTCACGCAGGTCCAGTTCACCAGCCAGTTCCACCAGTTGCAGGAGAGC
CACCAATGCACCCTCAGCCACCAGCACATCCAAATCAGCCAATGCACCCTCAGCTACC
AAACCCACCAATGTACCCAGTGCAGCCACTGCCTCCACTGATCCCAGATAGACCTCTT
GAGTCATGGCCAGTACCTGATAA

AME_Hap_2

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CAATGCCACCACCTCTCCACCAGGTACAGCAACAGCCACCTCTGAACCCACACATGCA
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ATCAACCAGCTCACGCAGGTCCAGTTCACCAGCCAGTTCCACCAGTTGCAGGAGAGC
CACCAATGCACCCTCAGCCACCAGCACATCCAAATCAGCCAATCCACCCTCAGCTACC
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GAGTCATGGCCAGTACCTGATAA

AME_Hap_3

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ATCAACCAGCTCACACAGGTCCAGTTCACCAGCCAGTTCCACCAGTTGCAGGAGAGC
CACCAATGCACCCTCAGCCACCAGCACATCCAAATCAGCCAATGCACCCTCAGCTACC
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GAGTCATGGCCAGTACCTGATAA

AME_Hap_4

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ATCAACCAGCTCACGCAGGTCCAGTTCACCAGCCAGTTCCACCAGTTGCAGGAGAGC
CTACAATGCACCCTCAGCCACCAGCACATCCAAATCAGCCAATGCACCCTCAGCTACC
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GAGTCATGGCCAGTACCTGATAA

AME_Hap_5

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CTACCTGGACATAACACATTTGTGCCAATGACTGGACAGAATACATTAGTGCCACAGTA
TCAACCAGCTCACGCAGGTCCAGTTCACCAGCCAGTTCCACCAGTTGCAGGAGAGCCT

ACAATGCACCCTCAGCCACCAGCACATCCAAATCAGCCAATGCACCCTCAGCTACCAA
ACCCACCAATGTACCCAGTGCAGCCACTGCCTCCACTGATCCCAGATAGACCTCTTGA
GTCATGGCCAGTACCTGATAA

AME_Hap_6

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ATCAACCAGCTCACGCAGGTCCAGTTCACCAGCCAGTTCCACCAGTTGCAGGAGAGC
CATCAATGCACCCTCAGCCACCAGCACATCCAAATCAGCCAATGCACCCTCAGCTACC
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AME_Hap_7

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CACCAATGCACCCTCAGCCACCAGCACATCCAAATCAGCCAATGCACCCTCAGCTACC
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AME_Hap_8

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TCAACCAGCTCACGCAGGTCCAGTTCACCAGCCAGTTCCACCAGTTGCAGGAGAGCC
ACCAATGCACCCTCAGCCACCAGCACATCCAAATCAGCCAATGCACCCTCAGCTACCA
AACCCACCAATGTACCCAGTGCAGCCACTGCCTCCACTGATCCCAGATAGACCTCTTG
AGTCATGGCCAGTACCTGATAA

The 15 RAG-1 genotype sequences (aligned) detected in *P. theobaldi*

RAG-1_Hap_1

TGACGATACACAAGCTCTTCTCAGGAAGAAGGAGAAAAGAGCTACGTCTTGGCCTGAT
CTCCTTGCCAAAGTGTTCAAGATTGATGTCAGAGGGGACGTTGACACAATCCACCCCA
CCAATTTTTGCCACAATTGCCGGAATGTGATTCAAAGAAAGTTCAGCAATTCCCCAGGT
GAAGTGTATTTTCCAAGGAAAGATGCCATGGAGTGGCAACCGCATTCGTTGAGCTGCG
ATGTCTGTGGCACTTCCTTCCGTGGGGTAAAGAGAAAGAAGCGGCCCTTAAATCCACC
GTTGAGCAAAAAGCCCAGGGTGTAGCTGGAGGTGCTAGAAAACCAAGCTATGTGAG
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CTCAAAAACACCGTCTAAGAGATCTCAAACCTCAAGTGAAAGCTTTTGCTGAGAAAG
AAGAA

RAG-1_Hap_2

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CTCCTGCCAGGTCTGTGAGCATATTCTGGCTGATCCTGTAGAAACCACATGCAAGCACT
TATTTTGCAGGGCCTGCCTCCTTAAATGCCTCAAAGTCATGGGAAGTTTTTGTCCAGTT
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AAGAA

RAG-1_Hap_3

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AAGAA

RAG-1_Hap_4

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AAGAA

RAG-1_Hap_5

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RAG-1_Hap_6

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RAG-1_Hap_7

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RAG-1_Hap_8

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AAGAA

RAG-1_Hap_9

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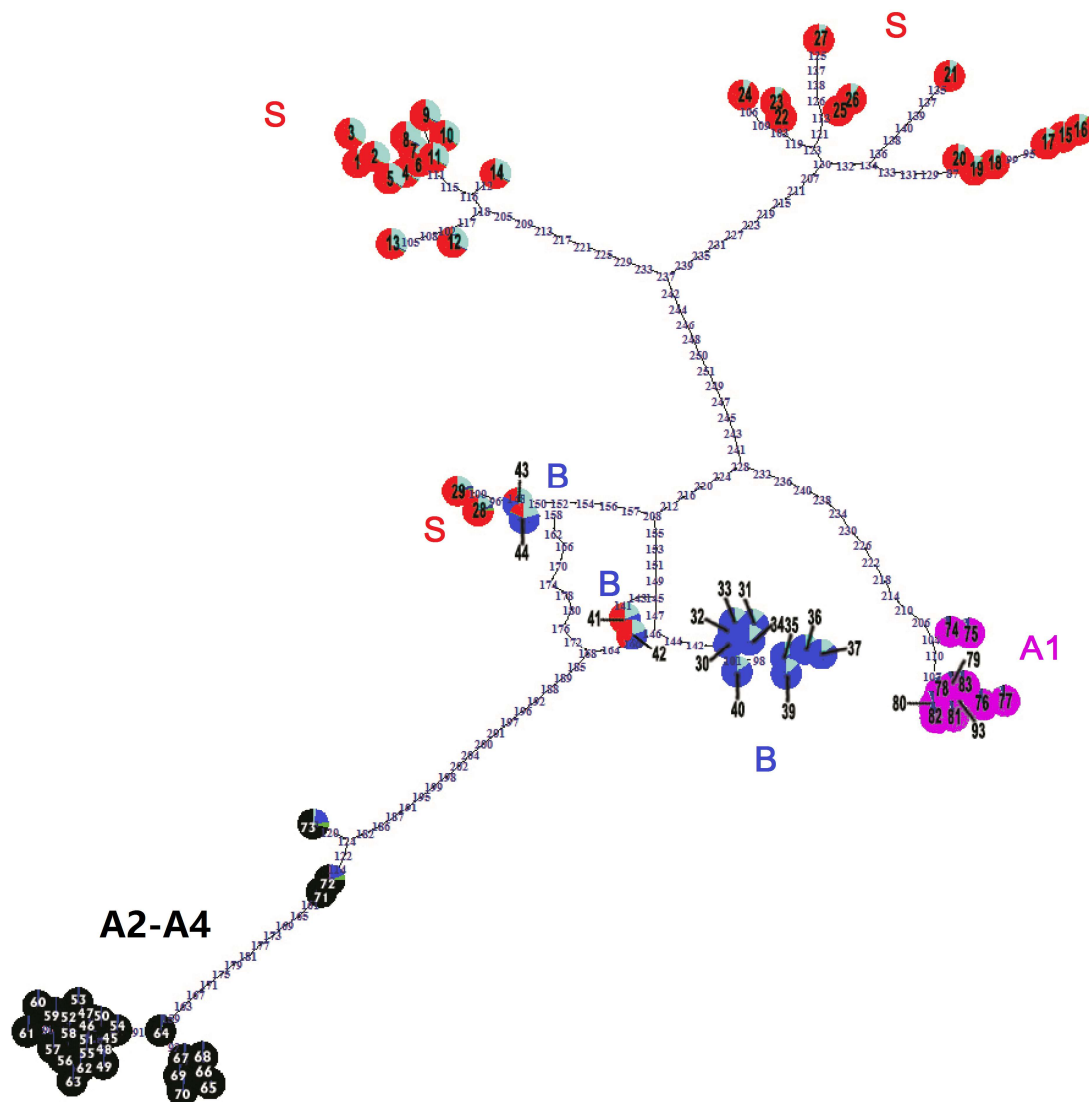
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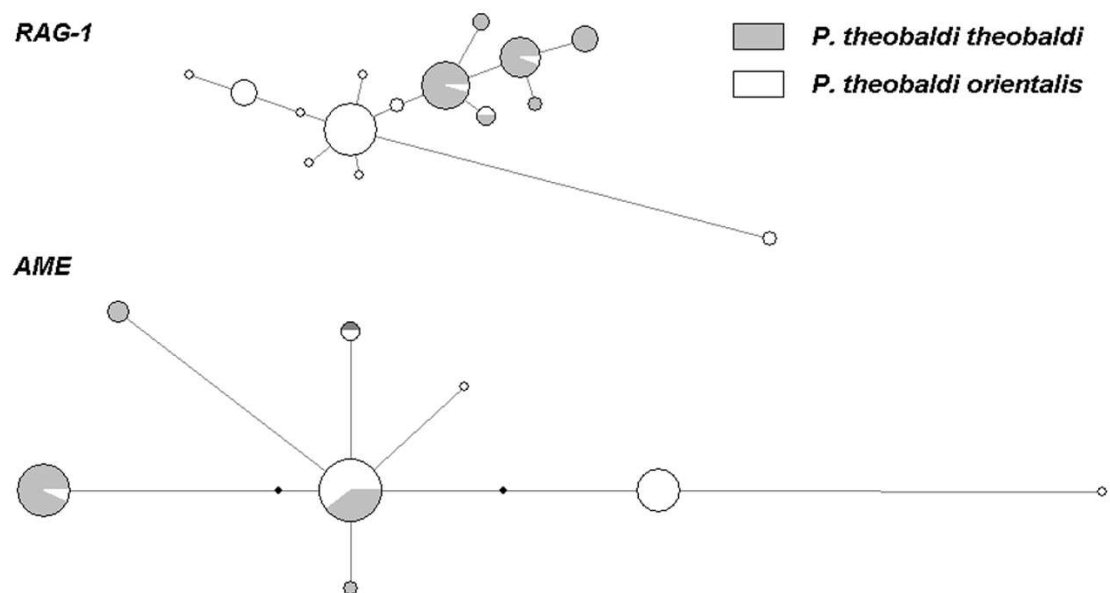
Supplementary Information S3

BPEC parsimony network. The pie charts for each mtDNA haplotype represent posterior probabilities for assignment to each of 6 possible clusters. Haplotypes were only assigned to four clusters with high posterior probabilities. These are indicated on the network as A1, A2-A4, B and S, and correspond to the labels used in Figure 3.



Supplementary Information S4

Median-joining networks for the two nuclear loci (AME and RAG-1).



Supplementary Information S5

Additional detail on fine-scale mtDNA relationships within species other than *P. theobaldi* (see Figure 2a).

