**Table S1. Sample populations and sampling sites of *Parantica sita* collected for this study.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Populations | Site | Region | Latitude (°N) | Longitude (°E) | Collection date | Number |
| BN | Xishuangbanna | Yunnan | 22.13 | 100.87 | 201712 | 14 |
| TBG\_2017 | Tongbiguan, Dehong | Yunnan | 23.89 | 97.63 | 201701-201709 | 19 |
| TBG\_2016 | Tongbiguan, Dehong | Yunnan | 23.89 | 97.63 | 201611 | 21 |
| GLG | Mt. Gaoligong, Baoshan | Yunnan | 24.59 | 98.68 | 201611 | 27 |
| QJ | Mt. Junzi, Qujing | Yunnan | 24.66 | 104.15 | 201706-201709 | 22 |
| KM4\_2016 | Xishan, Kunming | Yunnan | 25.17 | 102.36 | 201604-201607 | 24 |
| KM8\_2016 | Xishan, Kunming | Yunnan | 25.17 | 102.36 | 201608 | 24 |
| KM6\_2016 | Xishan, Kunming | Yunnan | 25.17 | 102.36 | 201706 | 23 |
| KM9\_2016 | Xishan, Kunming | Yunnan | 25.17 | 102.36 | 201709 | 24 |
| LPS | Mt. Luoping, Dali | Yunnan | 26.02 | 99.88 | 201709 | 23 |
| GZ |  | Guizhou | 26.63 | 106.73 | 2015-2018 | 16 |
| JFS | Mt. Jinfo | Chongqing | 29.04 | 107.17 | 201708 | 19 |
| LHG\_2016 | Laohegou Nature Reserve, Pingwu | Sichuan | 32.48 | 104.71 | 201606-201607 | 17 |
| LHG\_2017 | Laohegou Nature Reserve, Pingwu | Sichuan | 32.48 | 104.71 | 201707 | 24 |
| BYL | Bayuelin Nature Reserve, Leshan | Sichuan | 29.18 | 103.07 | 201708 | 24 |
| LS | Shawan, Leshan | Sichuan | 29.20 | 103.57 | 201804 | 24 |
| EMS | Mt. Emei, Leshan | Sichuan | 29.57 | 103.40 | 201704 | 24 |
| XZ | Mote, Linzhi | Tibet | 28.74 | 94.98 | 2016-2019 | 34 |
| TW |  | Taiwan Island and Japan | 23.78 | 120.89 | 201510-201706 | 26 |
| Total |  |  |  |  |  | 429 |

**Table S2 Basic information for the 14 pairs of microsatellite primers used for *Parantica sita***

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Locus** | **Primer sequences（5'-3'）** | | **Motif** | **Number of alleles** | ***Tm* (°C)** | **Range of fragment** | **GenBank accession number** |
| PS2838 | F:AGCAAGACCAACAAATCCGA | | AAC | 5 | 52 | 152–167 | MK838447 |
| R:ACGCCTTTCTGCTTGAGTTG | |
| PS7675 | F:TGTAGTGGAGGATCTTGCGA | | CAC | 7 | 52 | 281–302 | MK838448 |
| R:TTCTGATGGTGGAGGTGCAA | |
| PS3571 | F:TGCTTTGCTTGTAAGTACGCA | | TGA | 8 | 54 | 281–302 | MT009237 |
| R:TGGCTCCACTTCCTGATCAG | |
| PS12794 | F:CCTCAATGAACTGTGGTACGT | | GGAGT | 5 | 55 | 155–175 | MK838449 |
| R:GCTCCCATCACTCCATCTCA | |
| PS598 | F:CCTGTTCCGGATCCTTTCGA | | CATA | 5 | 55 | 188–204 | MK838450 |
| R:ATGATGATGTCGGCACTACC | |
| PS17506 | F:AGATGAACTGAGCCGAGCG | | TGA | 5 | 50 | 152–164 | MK838451 |
| R:TTCACAATTGTCAGCACCGA | |
| PS9770 | F:ACCGAATGAAGTGGACGCTA | | GTGAT | 3 | 55 | 209–219 | MK838452 |
| R:CCTGGACCAAAGACTCTTGC | |
| PS5105 | F:AGCGGTGCATATGAAGGGAG | | TCCTCA | 4 | 55 | 151–169 | MT009235 |
| R:GGGTTGGTTTGGGATGACAC | |
| PS5128 | F:TGCTTTGCTTGTAAGTACGCA | | ACGC | 19 | 52 | 101–193 | MT009236 |
| R:TGGCTCCACTTCCTGATCAG | |
| PS14777 | | F:TGCTTGTCAAATCACCGCAA | TGTC | 11 | 52 | 174–190 | MK838453 |
| R:GGACCATCCGTTTCAGAGTT |
| PS8901 | | F:CGCACTATCACTAACGTCAC | CACGA | 8 | 46 | 255–305 | MK838454 |
| R:AAACGCCACAATATTTAACAA |
| PS11718 | | F:ACGACTAGTACTACAACGACCA | ACA | 6 | 55 | 147–162 | MK838455 |
| R:GGAGTTGTCGTAGGGATGGA |
| PS3003 | | F:CCGTCGCAAAGCCGAATT | CGTGAG | 4 | 55 | 147–165 | MK838457 |
| R:ACGTTCTCTATCTCGCTCCC |
| PS5401 | | F:AGCGCGCTCATTCGTTTAAT | TCAA | 4 | 52 | 128–140 | MK838459 |
| R:ATGCCGGGAGATTGGAAACT |

*Tm*: primer melting temperature.

**Table S3 Polymorphic sites and haplotypes of mtDNA cytochrome oxidase subunit I in 19 populations of *Parantica sita*.**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | site | | | | | | | | | | | | | | | | | | | | | |
|  | 3 | 4 | 28 | 55 | 153 | 156 | 159 | 162 | 168 | 171 | 174 | 180 | 220 | 222 | 225 | 252 | 261 | 282 | 291 | 294 | 300 | 314 |
| HapA1 | T | C | T | G | G | T | T | A | A | G | C | C | T | A | A | A | C | A | T | C | C | T |
| HapA2 | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | A | · | · | · | · | · |
| HapA3 | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | . | · | · | · | · | · |
| HapA4 | · | · | · | · | A | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | C |
| HapA5 | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | T | · |
| HapA6 | · | T | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · |
| HapA7 | · | · | · | · | · | · | · | G | · | . | · | · | · | · | · | · | · | · | · | · | · | · |
| HapA8 | · | · | · | · | · | · | · | · | · | A | · | · | · | · | · | · | · | · | · | · | · | · |
| HapA9 | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · |
| HapA10 | · | · | · | A | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · |
| HapA11 | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | G | · | · | · | · | · | · |
| HapA12 | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | G | · | · | · | · |
| HapA13 | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | T | · |
| HapB1 | C | · | · | · | A | · | A | · | · | A | T | T | · | · | C | · | T | · | C | T | T | · |
| HapB2 | C | · | · | · | A | · | A | · | · | A | T | T | · | · | C | · | T | · | C | T | T | · |
| HapB3 | C | · | · | · | A | · | A | · | · | A | T | T | · | · | C | · | T | · | C | T | T | · |
| HapB4 | C | · | · | · | A | · | A | · | G | A | T | T | · | · | C | · | T | · | C | T | T | · |
| HapB5 | C | · | · | A | A | · | A | · | · | A | T | T | · | · | C | · | T | · | C | T | T | · |
| HapC | C | · | C | · | A | C | A | · | · | · | · | T | C | C | C | · | T | · | C | T | T | · |

Table S3 Polymorphic sites and haplotypes of mtDNA **cytochrome oxidase subunit 1** in 19 populations of *Parantica sita* (continued).

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | site | | | | | | | | | | | | | | | | | | | | | |
|  | 318 | 321 | 327 | 330 | 357 | 360 | 414 | 423 | 456 | 468 | 477 | 480 | 483 | 484 | 486 | 496 | 511 | 543 | 570 | 582 | 588 | 591 |
| HapA1 | T | T | T | A | A | C | T | T | C | A | C | A | C | C | T | T | T | T | T | G | C | G |
| HapA2 | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · |
| HapA3 | · | · | · | · | G | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · |
| HapA4 | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · |
| HapA5 | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · |
| HapA6 | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · |
| HapA7 | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | C | · | · | · |
| HapA8 | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | . | · | · | · |
| HapA9 | · | · | · | · | · | · | · | · | · | · | T | · | · | · | · | · | · | · | · | · | · | · |
| HapA10 | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · |
| HapA11 | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · |
| HapA12 | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · | · |
| HapA13 | · | · | · | · | · | · | · | A | · | · | · | · | · | · | · | · | · | · | · | A | · | A |
| HapB1 | · | C | C | · | T | T | C | · | T | T | T | T | T | · | A | · | · | · | C | · | T | A |
| HapB2 | · | C | C | · | T | T | C | · | T | T | T | T | T | A | A | · | · | · | C | · | T | A |
| HapB3 | · | C | . | · | T | T | C | · | T | T | T | T | T | · | A | · | · | · | C | · | T | A |
| HapB4 | · | C | C | · | T | T | C | · | T | T | T | T | T | · | A | · | · | · | C | · | T | A |
| HapB5 | · | C | C | · | T | T | C | · | T | T | T | T | T | · | A | · | · | · | C | · | T | A |
| HapC | C | C | C | G | T | T | C | · | T | G | T | · | T | · | A | C | C | C | C | A | · | A |

**Table S4 Pairwise *FST* values (below the diagonal) and p-distances (above the diagonal) of mtDNA cytochrome oxidase subunit I from the 19 *Parantica sita* populations in Table S1**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Populations | **LHG\_**  **2017** | **JFS** | **KM6\_**  **2017** | **BN** | **KM9\_**  **2017** | **LPS** | **QJ** | **TBG\_2017** | **KM4\_2016** | **KM8\_2016** | **TBG\_2016** | **GLG** | **LHG\_2016** | **GZ** | **EMS** | **BYL** | **LS** | **XZ** | **TW** |
| **LHG\_2017** |  | 0.003 | 0.002 | 0.002 | 0.002 | 0.002 | 0.002 | 0.009 | 0.004 | 0.002 | 0.004 | 0.004 | 0.011 | 0.002 | 0.041 | 0.038 | 0.041 | 0.037 | 0.051 |
| **JFS** | -0.015 |  | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.008 | 0.003 | 0.001 | 0.003 | 0.003 | 0.011 | 0.001 | 0.042 | 0.039 | 0.042 | 0.039 | 0.052 |
| **KM6\_2017** | -0.008 | 0.018 |  | 0.001 | 0.001 | 0.001 | 0.001 | 0.008 | 0.003 | 0.001 | 0.003 | 0.002 | 0.010 | 0.001 | 0.042 | 0.039 | 0.042 | 0.038 | 0.052 |
| **BN** | -0.022 | -0.005 | -0.039 |  | 0.001 | 0.001 | 0.000 | 0.008 | 0.002 | 0.001 | 0.003 | 0.002 | 0.010 | 0.001 | 0.043 | 0.039 | 0.043 | 0.039 | 0.052 |
| **KM9\_2017** | -0.003 | 0.008 | 0.043 | 0.044 |  | 0.001 | 0.000 | 0.008 | 0.002 | 0.001 | 0.003 | 0.002 | 0.010 | 0.001 | 0.042 | 0.039 | 0.042 | 0.039 | 0.052 |
| **LPS** | -0.021 | -0.041 | 0.000 | -0.018 | -0.009 |  | 0.000 | 0.008 | 0.002 | 0.001 | 0.003 | 0.002 | 0.010 | 0.001 | 0.043 | 0.039 | 0.043 | 0.039 | 0.052 |
| **QJ** | -0.005 | 0.017 | 0.019 | 0.078 | 0.020 | -0.003 |  | 0.008 | 0.002 | 0.000 | 0.003 | 0.002 | 0.010 | 0.000 | 0.043 | 0.039 | 0.043 | 0.039 | 0.052 |
| **TBG\_2017** | 0.040 | 0.039 | 0.131 | 0.093 | 0.129 | 0.062 | 0.138 |  | 0.009 | 0.008 | 0.009 | 0.009 | 0.014 | 0.008 | 0.036 | 0.033 | 0.036 | 0.033 | 0.048 |
| **KM4\_2016** | -0.040 | -0.016 | -0.007 | -0.028 | 0.004 | -0.020 | 0.009 | 0.036 |  | 0.002 | 0.004 | 0.004 | 0.011 | 0.002 | 0.041 | 0.038 | 0.041 | 0.037 | 0.051 |
| **KM8\_2016** | -0.007 | 0.008 | 0.020 | 0.034 | -0.014 | -0.007 | -0.018 | 0.131 | 0.005 |  | 0.003 | 0.002 | 0.010 | 0.001 | 0.042 | 0.039 | 0.042 | 0.038 | 0.052 |
| **TBG\_2016** | -0.039 | -0.020 | 0.005 | -0.018 | 0.002 | -0.021 | 0.018 | 0.019 | -0.044 | 0.010 |  | 0.004 | 0.012 | 0.003 | 0.040 | 0.037 | 0.040 | 0.037 | 0.051 |
| **GLG** | -0.038 | -0.014 | -0.009 | -0.025 | -0.009 | -0.020 | -0.005 | 0.052 | -0.039 | -0.008 | -0.037 |  | 0.011 | 0.002 | 0.041 | 0.038 | 0.041 | 0.037 | 0.051 |
| **LHG\_2016** | 0.111 | 0.099 | 0.206 | 0.157 | 0.213 | 0.131 | 0.217 | -0.044 | 0.102 | 0.214 | 0.082 | 0.127 |  | 0.01 | 0.033 | 0.031 | 0.033 | 0.030 | 0.046 |
| **GZ** | 0.049 | -0.017 | 0.099 | 0.058 | 0.109 | 0.005 | 0.108 | 0.028 | 0.043 | 0.106 | 0.034 | 0.058 | 0.055 |  | 0.043 | 0.039 | 0.043 | 0.039 | 0.052 |
| **EMS** | **0.944** | **0.917** | **0.985** | **0.986** | **0.983** | **0.932** | **0.990** | **0.829** | **0.941** | **0.984** | **0.933** | **0.944** | **0.774** | **0.863** |  | 0.004 | 0.001 | 0.005 | 0.026 |
| **BYL** | **0.853** | **0.822** | **0.897** | **0.881** | **0.898** | **0.844** | **0.903** | **0.706** | **0.848** | **0.899** | **0.835** | **0.859** | **0.636** | **0.754** | 0.032 |  | 0.004 | 0.007 | 0.028 |
| **LS** | **0.946** | **0.919** | **0.989** | **0.992** | **0.987** | **0.934** | **0.995** | **0.827** | **0.943** | **0.988** | **0.935** | **0.947** | **0.771** | **0.861** | -0.016 | 0.030 |  | 0.005 | 0.025 |
| **XZ** | **0.835** | **0.809** | **0.874** | **0.858** | **0.876** | **0.830** | **0.879** | **0.700** | **0.831** | **0.876** | **0.819** | **0.841** | **0.635** | **0.751** | 0.049 | -0.028 | 0.048 |  | 0.028 |
| **TW** | **0.961** | **0.938** | **0.994** | **0.997** | **0.992** | **0.949** | **0.999** | **0.880** | **0.959** | **0.993** | **0.953** | **0.961** | **0.847** | **0.890** | **0.987** | **0.869** | **0.994** | **0.840** |  |

**Table S5 Polymorphism values of the microsatellite loci from the 19 *Parantica sita* populations in Table S1.**

| **Population** | ***N*** | ***Na*** | ***Nea*** | ***Ar*** | ***PIC*** | ***Ho*** | ***He*** | ***PR*** |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| BN | 14 | 3.786 | 2.158 | 4.35 | 0.401 | 0.469 | 0.461 | 0.08 |
| GLG | 27 | 4.929 | 2.109 | 4.07 | 0.418 | 0.406 | 0.469 | 0.11 |
| GZ | 15 | 4.142 | 2.203 | 4.02 | 0.435 | 0.476 | 0.502 | 0.12 |
| JFS | 18 | 4.786 | 2.191 | 4.20 | 0.395 | 0.402 | 0.450 | 0.25 |
| KM4\_2016 | 24 | 4.786 | 2.201 | 4.01 | 0.419 | 0.428 | 0.471 | 0.09 |
| KM8\_2016 | 24 | 4.500 | 2.064 | 3.78 | 0.400 | 0.427 | 0.453 | 0.05 |
| KM6\_2017 | 23 | 4.571 | 2.212 | 3.95 | 0.437 | 0.433 | 0.498 | 0.07 |
| KM9\_2017 | 24 | 4.571 | 2.143 | 3.97 | 0.423 | 0.467 | 0.477 | 0.05 |
| LHG\_2016 | 17 | 4.500 | 2.395 | 4.23 | 0.462 | 0.428 | 0.522 | 0.04 |
| LHG\_2017 | 23 | 5.000 | 2.234 | 4.17 | 0.437 | 0.422 | 0.494 | 0.11 |
| LPS | 23 | 4.500 | 2.079 | 3.87 | 0.418 | 0.421 | 0.474 | 0.08 |
| QJ | 22 | 4.786 | 2.290 | 4.09 | 0.443 | 0.474 | 0.503 | 0.21 |
| TBG\_2016 | 21 | 4.286 | 2.041 | 3.78 | 0.399 | 0.389 | 0.453 | 0.05 |
| TBG\_2017 | 19 | 4.857 | 2.400 | 4.23 | 0.461 | 0.470 | 0.526 | 0.10 |
| BYL | 24 | 5.214 | 2.332 | 4.39 | 0.462 | 0.490 | 0.514 | 0.03 |
| LS | 24 | 4.643 | 2.372 | 4.00 | 0.457 | 0.470 | 0.513 | 0.07 |
| EMS | 24 | 5.214 | 2.331 | 4.35 | 0.476 | 0.497 | 0.534 | 0.07 |
| XZ | 29 | 5.000 | 2.618 | 4.22 | 0.480 | 0.440 | 0.529 | 0.33 |
| TW | 26 | 3.929 | 1.940 | 3.33 | 0.376 | 0.390 | 0.432 | 0.11 |

*N*: number of alleles; *Na*: average number of alleles; *Nea*: Number of effective alleles; *Ar*:allelic richness; *PIC*: polymorphism information content; *Ho*: observed heterozygosity; *He*; expected heterozygosity; *PR*: private allelic richness