**Supplementary Information**

**Genetic diversity of *Procambarus clarkii* populations based on mitochondrial DNA and microsatellite markers in different areas of Guangxi, China**

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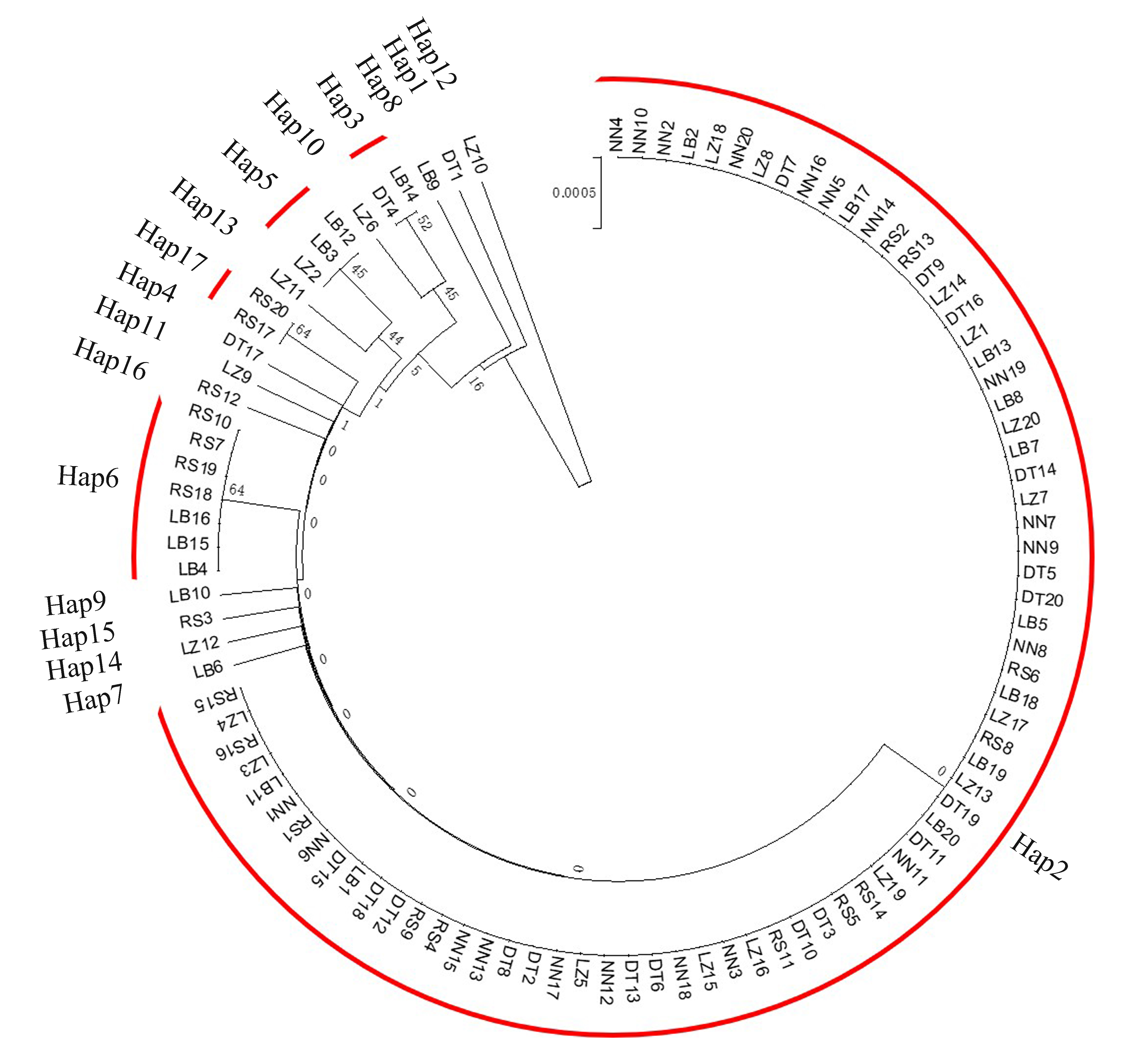
Supplementary Table S1 The primers information of microsatellite detection

|  |  |  |  |
| --- | --- | --- | --- |
| Locus | Primer sequence (5’-3’) | Product size (bp) | Repeat motif |
| PclG-02 | F: CTCCCCATGCACTCTGGCTCTGT | 216-224 | (GATA)3GAGAA(GATA)5 |
| R:TGGCGAATTTTGCCTGTTTCTGTC |
| PclG-04 | F: TATATCAGTCAATCTGTCCAG | 170-290 | (TCTA)3 … (TCTA)2 … (TCTA)29 … (TCTA)2 |
| R: TCAGTAAGTAGATTGATAGAAGG |
| PclG-07 | F: CCTCCCACCAGGGTTATCTATTCA | 100-160 | (TCTA)8 |
| R: GTGGGTGTGGCGCTCTTGTT |
| PclG-08 | F: ACGATAAATGGATAGATGGATGAA | 148-220 | (GATA)16 |
| R: CCGGGTCTGTCTGTCTGTCA |
| PclG-10 | F: TGCTCACGCAAACTTGTATTCAGT | 90-176 | (TAGA)2TA(TAGA)16 |
| R: CAATGGTCCTTGATTTGGTGTTCT |
| PclG-17 | F: GTCGGGAACCTATTTACAGTGTAT | 156-190 | (TCTA)14 |
| R: AAGAGCGAAGAAAGAGATAAAGAT |
| PclG-28 | F: CTCGGCGAGTTTACTGAAAT | 210-270 | (GATA)22(GA)5 |
| R: AGAAGAAAGGGATATAAGGTAAAG |
| PclG-29 | F: GAAAGTCATGGGTGTAGGTGTAAC | 95-165 | (TATC)9 |
| R: TTTTTGGGCTATGTGACGAG |

Supplementary S2 Hardy-Weinberg equilibrium analysis for each locus based on microsatellite

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Populations Locus | NN | DT | RS | LZ | LB |
| PclG02 | 0.3572\* | -0.0340\*\* | -0.1791\*\* | -0.0378\*\* | 0.0191\*\* |
| PclG04 | -0.4234 | -0.7421\*\* | -0.7934\*\* | -0.8898\*\* | -0.9293\*\* |
| PclG07 | -0.0863\*\* | 0.0033\*\* | -0.2836\* | -0.1939\*\* | -0.8010\*\* |
| PclG08 | 0.8385\*\* | 0.5000\*\* | 0.1645 | 0.8998\*\* | 0.7619\*\* |
| PclG10 | -1.0000\*\* | -0.8796\*\* | -1.000\*\* | -0.7074\*\* | -0.9142\*\* |
| PclG17 | 0.3806 | -0.5136\*\* | -0.1357\* | -0.0745\*\* | -0.5067\*\* |
| PclG28 | -0.4467\*\* | -0.4456\* | -0.1208\* | -0.0601 | -0.1469\*\* |
| PclG29 | 0.1273 | -0.0119 | -0.3731\*\* | -0.1383 | -0.5897\*\* |

Note: Statistics by Chi-square test for Hardy-Weinberg equilibrium. \*: significant deviation, *p* < 0.05; \*\*: extremely significant deviation, *p* < 0.01.



Supplementary Figure S1 The UPGMA tree of 100 individuals based on *CytB* sequences.