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Erratum

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CHATMONGKON SUWANNAPOOM, ZHI-YONG YUAN, JIN-MIN CHEN, MIAN HOU, HAI-PENG ZHAO, LI-JUN WANG, TRUONG SON NGUYEN, TRUONG Q. NGUYEN, ROBERT W. MURPHY, JAQUELINE SULLIVAN, DAVID S. MCLEOD & JING CHE (2016) Taxonomic revision of the Chinese *Limnonectes* (Anura, Dicroglossidae) with the description of a new species from China and Myanmar. *Zootaxa*, 4093: 181–200.

Correct versions of Figures 1 and 2:

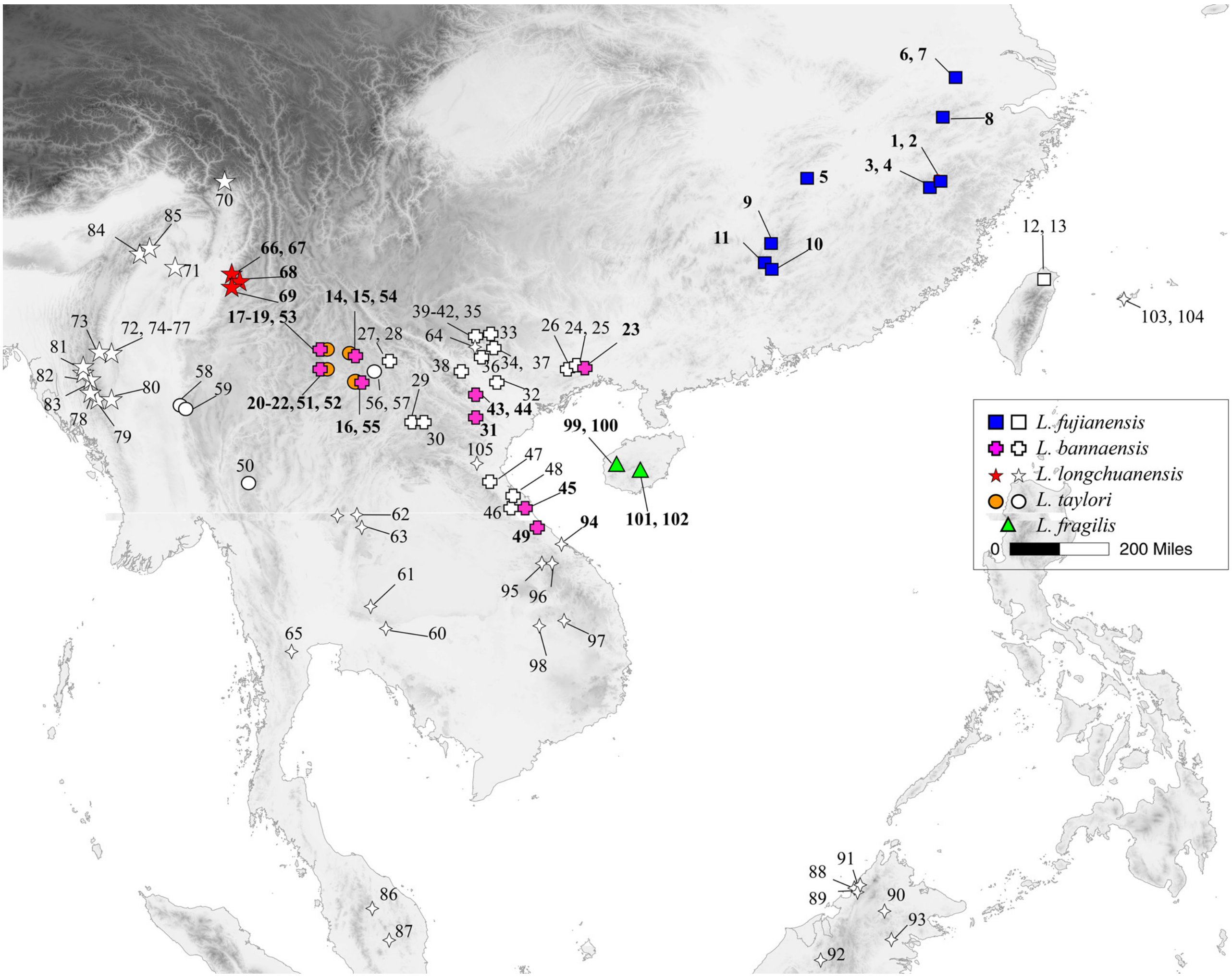

FIGURE 1. Sampling localities of the specimens of *Limnonectes* used in this study. New samples indicated by color: red stars in China = *L. longchuanensis* sp. nov., blue squares = *L. fujianensis*, pink diamonds = *L. bannaensis*, orange circles = *L. taylori*, and green triangles = *L. fragilis*. Samples downloaded from GenBank were indicated by white symbols. Locality numbers refer to Table 1 and Fig. 2.

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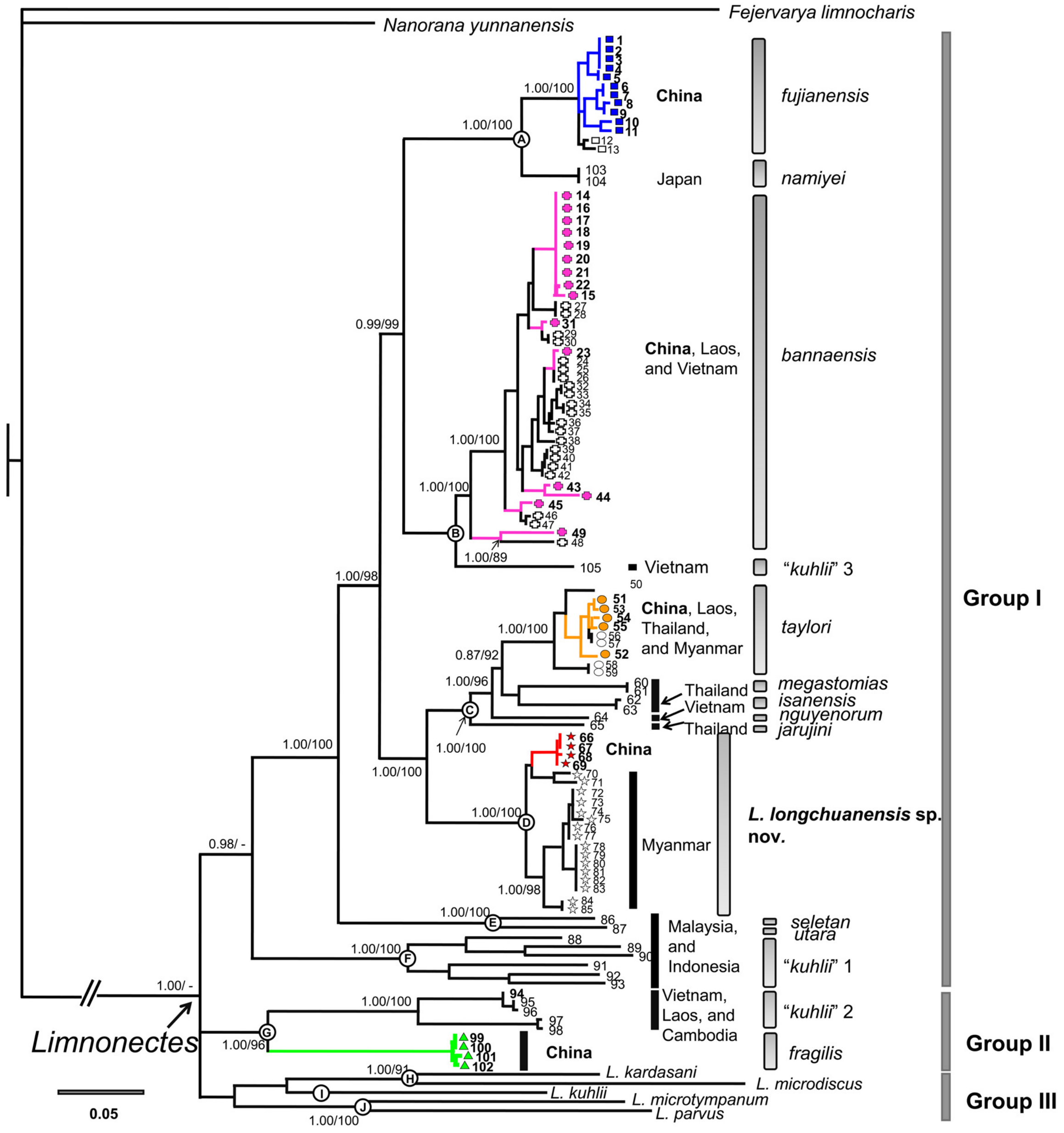

FIGURE 2. Bayesian tree of Chinese *Limnonectes* inferred from mtDNA 12S rRNA, tRNAVal and 16S rRNA genes. Colors of lineages, species names, and symbols correspond to Fig. 1. The numbers above branches represent Bayesian posterior probabilities (BPP), and bootstrap support (BS) for maximum likelihood (ML); "-" denotes low support (BPP < 95% or BS < 70%) in one analysis; no values on branches represent low support in both analyses. The scale bar represents 0.05 nucleotide substitutions per site.