



Fig. 6. Origin, pairwise cytochrome *b* divergences, and proposed new classification of our samples of *P. reguloides* sensu lato. Filled square: *reguloides*, (1) Himachal Pradesh, India ( $n = 2$ ); (2) central Nepal ( $n = 1$ ); (3) West Bengal, India ( $n = 1$ ); half-filled square: *assamensis* (4) west Myanmar ( $n = 2$ ); open square: *ticehursti*, (5) Yunnan, China ( $n = 1$ ); (6) north-western Thailand ( $n = 3$ ); (7) north-western Vietnam ( $n = 1$ ); (8) southern Vietnam ( $n = 2$ ); filled diamond: *goodsoni*, (9) Guangxi, China ( $n = 1$ ), (10) Guangdong, China ( $n = 2$ ), (11) Hong Kong ( $n = 1$ ); open diamond: *fokiensis*, (12) Fujian, China ( $n = 5$ ); star: *claudiae*, (13) Sichuan, China ( $n = 4$ ), (14) Hebei, China ( $n = 1$ ). The values in the upper part of the figure represent pairwise cytochrome *b* divergences in % between different populations: left column: within least-inclusive taxa; middle column: between the taxa in the *P. reguloides* (sensu stricto) and *P. goodsoni* clades; and right column: between the *P. claudiae*, *P. reguloides* (sensu stricto) and *P. goodsoni* clades.<sup>1</sup>The smallest genetic distance between the samples from localities 13 and 14 is 0.2%. <sup>2</sup>The largest distance between individuals at one locality is 0.7% (locality 6).