

Figure 1. Majority-rule consensus tree from Bayesian analysis based on the 3' region of the cytochrome oxidase I gene of the subgenus *Agametrus* and several outgroup taxa (in grey) of the genus *Platynectes*. Posterior probabilities are provided only for splits indicating 0.95 or higher probability. Tip labels include (from left to right) GenBank accession number, taxon name, country of origin, and the DNA voucher label. In the main splits the mean genetic distances are shown (in percent) calculated under the Kimura 2-parameter model.

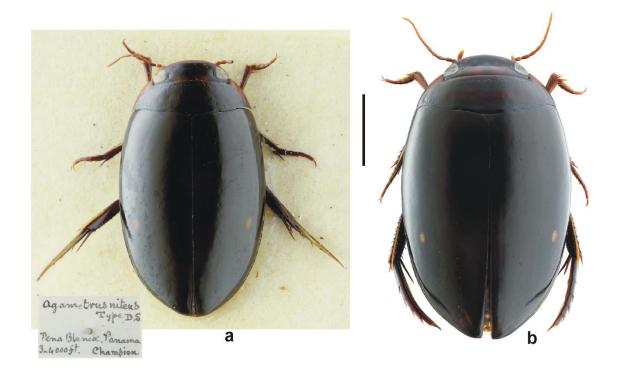


Figure 2. habitus of Central American *Platynectes*. a: holotype of *P. nitens* (Sharp); b: paratype of *P. zoque* sp. nov. Scale bar = 2 mm.

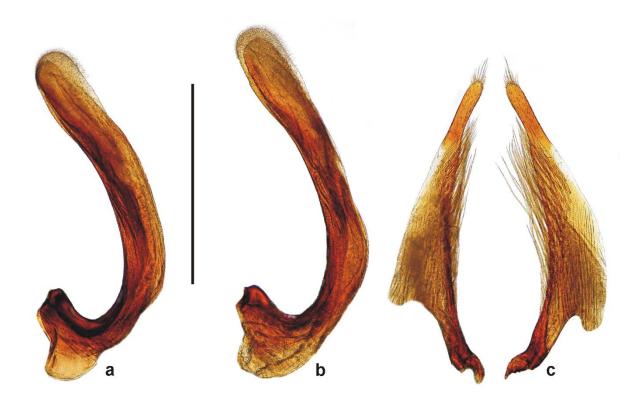


Figure 3. Male genitalia of *Platynectes* spp. a: *P. nitens* (Sharp); b-c: *P. zoque* sp. nov. a, b: median lobe in lateral view; c: parameres. Scale bar = 1.0 mm.



Figure 4. Habitat of *Platynectes nitens* (Sharp) in Boquete, Chiriqui, Panama.