

**Figure S1:** Bayesian phylogenetic tree based on *Aphanomyces* *astaci* mitochondrial rnnS sequences obtained from *A. astaci*-infected *Procambarus* *clarkii* specimens from Reservoir Cachí (Costa Rica). The red line indicates the Costa Rican samples. Values above the branches represent Bayesian posterior probabilities (>0.95) and ML bootstrap support values (> 75), respectively. Scale bar indicates substitutions per site. The original strains (\*), used as references and identified in previous studies by RAPD-PCR (Huang et al.,1994; Diéguez-Uribeondo et al. 1995; Kozubikova et al. 2011), correspond to Group A (L1=a), Group B (Pl=b), Group C (Kv1), Group D (d2=AP03, d1=Málaga-5, d3=JPNP12), and Group E (Li10=e). The other sequences were obtained from Makkonen et al. (2018) and Martín-Torrijos et al. (2018, 2019).