

Abstract

Molecular genetic techniques were used to determine the identity of two catfish individuals that could not be identified as indigenous *Clarias gariepinus* after phenotypic analysis. The unidentified catfish were compared to 126 reference samples, using sequences of the mitochondrial DNA control region. The reference dataset included African catfish from South Africa and Kenya, as well as GenBank records for this species and for three species of Southeast Asian catfish, including the potentially invasive walking catfish, *C. batrachus*. Visual inspection of sequences showed parallel polymorphisms in the unidentified catfish and *C. batrachus* that did not occur in *C. gariepinus*. A bioinformatics approach using the Basic Local Alignment Search Tool (BLAST) of the National Center for Biotechnology Information confirmed that the unidentified catfish show more similarity to catfish of Asian origin compared to *C. gariepinus*. Finally, a phylogenetic approach showed that the catfish analysed group according to continent of origin (Africa and Asia) with strong bootstrap support, and with the unidentified fish contained in the Asian cluster. We conclude that the unidentified catfish are most likely imported *C. batrachus*.