DNA barcode based delineation of freshwater fishes from northern Western Ghats of India, one of the world's biodiversity hotspots

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Abstract

DNA barcodes analyzed by using relevant techniques provide an imperative approach towards validation of prevailing taxa and putative species. Here, molecular methods were used for assessment of 246 barcodes belonging to 81 fish species from northern Western Ghats of India, using, Barcode gap analysis, barcode index number, automatic barcode gap discovery, Poisson tree processes and general mixed Yule-coalescent, these methods had their potential to discriminate 97.53%, 93.90% 95.06%, 93.82% and 92.59% of species respectively. But, some of them tended to estimate the inconsistent number of species leading to discrepancies between the morphological concept and inference from molecular phylogenetic reconstructions. So, we took a standard approach to recognize those methods that produced consistent results, three of five such methods were identified that revealed three hidden cryptic species complexes in *Monopterus indicus*, *Parambassis ranga* and *Systomus sarana*. Further, to validate these three genetically diverged species, we used diagnostic character based approach along with nine unidentified species through BLOG and WEKAs SMO classifier. Those methods were unable to identify these species, which might be due to the limited number of specimens used for the analysis. This is the first effort to generate the DNA barcode reference library of freshwater fishes from northern Western Ghats of India, one of the world's biodiversity hotspots. These barcodes when analyzed through the defined workflow, will provide valuable measures to prove the efficiency of molecular species delimitation methods in taxonomic discrimination which aid conservation of biodiversity.