



## Systematics of the *Etheostoma cinereum* (Teleostei: Percidae) species complex (subgenus *Allohistium*)

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### Abstract

We examined geographic variation within the Ashy Darter, *Etheostoma cinereum*, of the mitochondrially encoded cytochrome *b* gene (*cyt b*) and nuclear recombination activation gene 1 (RAG1) as well as pigmentation, 6 meristic variables, and 20 morphometric variables for patterns indicative of speciation within the complex. Four geographically disjunct entities were identified by at least one of the datasets corresponding to the Cumberland, Duck, Elk, and upper Tennessee river systems. Monophyly of *cyt b* and RAG1 sequences, modal meristic differences, moderate morphometric divergence, and unique pigmentation in specimens from the Cumberland River suggest this entity represents an evolutionary species under many different species concepts and is described herein as *Etheostoma maydeni*. Other populations exhibit varying degrees of divergence in the different datasets and have conflicting relationships in phylogenetic analyses using *cyt b* and RAG1 sequences, leaving the evolutionary history and taxonomic status of the Duck, Elk and upper Tennessee populations unclear.

**Key words:** *Etheostoma maydeni*, Cumberland River, endemic, darter

### Introduction

The Ashy Darter, *Etheostoma cinereum* Storer was described from specimens collected near Florence, Alabama, in the Tennessee River system (Storer 1845). Little formal investigation into the distribution of and variation within this species occurred prior to Shepard & Burr (1984) who found the species extirpated from much of its historic range and morphological variation suggesting the species was composed of “...three somewhat distinct populations: Cumberland drainage, Duck drainage, and upper Tennessee drainage.” Declining populations (Powers & Mayden 2002) in need of active management triggered an investigation of genetic diversity within and among populations for cytochrome *b* (*cyt b*) that revealed genetically divergent management units (MU) restricted to the three major river systems with extant populations of *E. cinereum*: Cumberland, Duck, and Upper Tennessee rivers (Powers *et al.* 2004). The genetic divergence of these MUs coinciding with morphological divergence identified by Shepard & Burr (1984) suggests cryptic biodiversity within *E. cinereum*. The lack of type specimens (Collette & Knapp 1966) and apparent extirpation from the Tennessee River proper and any tributary within 300 rkm of the type locality of Florence, AL, left resolving the systematics of these MUs problematic. Recent rediscovery of *E. cinereum* in the Elk River provided not only an opportunity to examine this population for morphological and genetic variation, but also provided a surrogate to topotypic *E. cinereum* as the Elk confluences with the Tennessee River less than 50 rkm from Florence with no clear biogeographic barriers between them, thus making systematic revision less uncertain. The objectives of this study were to compare meristic, morphometric, pigment, and genetic variation within and among extant populations of the *E. cinereum* complex (Fig. 1) in order to test the hypothesis that *E. cinereum* represents a single evolutionary species.