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Letter to the Editor

## Nomenclatural changes should not be based on equivocally supported phylogenies: Reply to Yang et al. 2015 <sup>☆</sup>

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## ABSTRACT

Phylogenies produced by Yang et al. 2015 provide reasonably well-supported hypotheses of relationships among 11 proposed tribes of cyprinine fishes and present an interesting hypothesis about the origin of a number of polyploid cyprinine lineages. However, support for relationships within some of the tribes is equivocal. Herein we address the treatment of African diploid and tetraploid cyprinine genera within tribe Smiliogastrini. More specifically, we reject the revalidation of *Enteromius* based on the evidence presented and discuss the ramifications of the proposed revalidation.

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### 1. Introduction

The novel phylogenies of subfamily Cyprininae produced by Yang et al. (2015) (hereafter referred to as Yang et al.) clarified the relationships within the subfamily and provide a tribal classification. The most significant result of the study is its contribution to understanding the origin of several tetraploid and hexaploid lineages of cyprinines based on a nuclear RAG1 gene tree. Yang et al.'s production of paralogous RAG1 sequences, which involves a tedious cloning process, allows for the development of copy specific primers that will aid studies of origins of polyploidy and polyploid–diploid interrelationships within Cyprininae. In addition to the phylogenies produced and the classification scheme presented, Yang et al. also proposed a number of nomenclatural changes within the subfamily. Here we address the changes proposed within the tribe Smiliogastrini, the evidence that supports these changes, and the effects of the changes on African members of this group.

### 2. Equivocal support, taxon sampling, and consequences of revalidating the non-monophyletic *Enteromius*

Within each phylogeny published by Yang et al. (Figs. 1–4), the authors retain several branches with less than 50% bootstrap support. While the inclusion of these unsupported branches does not

render the phylogenies invalid, such results support multiple, equally-likely interpretations of relationships (i.e., are equivocal). The analysis with the greatest representation of African cyprinines is the one based on a 791–taxon dataset (Yang et al., Fig. 2), comprising data from five mitochondrial genes (CO1, Cyt *b*, 16S rRNA, ND4 and ND5) for 465 taxa and supplemental data for Cyt *b* only or Cyt *b* plus an unspecified gene for another 326 taxa. Focusing on the African members of Smiliogastrini in Yang et al. (Fig. 2), one clade, comprising *Systemus*, 'Barbus' (*Enteromius*), *Barboides*, *Pseudobarbus*, and *Clypeobarbus*, is well-supported (bootstrap score of 90). Collapsing branches with <50 support results in a polytomy with three *Systemus* clades, numerous 'Barbus' (*Enteromius*) clades (including *Barboides* and *Clypeobarbus*), and a well-supported clade comprising *Pseudobarbus* and '*Pseudobarbus*'. Nothing more can reasonably be inferred about relationships among these taxa from Yang et al.'s phylogeny.

Yang et al. commented that previous molecular studies of Cyprininae were incomplete due to restricted taxon sampling, limited mitochondrial markers, exclusion of nuclear markers, and in ignoring the issue of paralogy in polyploid taxa (Yang et al., p. 98). The current study addressed these problems at the subfamily level but suffers the same limitations at the intra-tribal level. This is evident within the African representatives of Smiliogastrini (Table 1). The limited taxon sampling within this group, most notably the African diploid 'Barbus' (*Enteromius*), likely contributed to equivocal branch support at many of the nodes (Table 1; Yang et al., Fig. 2e). Most striking is the absence of the type species '*Barbus*' (*Enteromius*) *potamogalis*, recently removed from synonymy with '*Barbus*' *ablades* (Roberts, 2010), from Yang et al.'s analysis. In addition to the limited taxon sampling within this group, nuclear markers for these species were largely absent in the

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**Table 1**

Valid taxa of African members of the Smiliogastrini tribe and numbers of taxa included in Yang et al. (2015). Data derived from Catalog of Fishes (Eschmeyer, 2015).

Group	Valid species	Number of taxa in each analysis			
		465-taxon	791-taxon	Mitogenome	RAG1
' <i>Barbus</i> ' ( <i>Enteromius</i> )	254	26	47	1	2
<i>Pseudobarbus</i>	9	0	7	0	0
<i>Clypeobarbus</i>	7	0	2	0	0
<i>Barboides</i>	2	1	2	0	0

analysis (Table 1). The poor resolution of Smiliogastrini in Yang et al. provides no support for revalidation of the generic name *Enteromius* Cope, 1867 (type species: '*Barbus*' *potamogalis*) to accommodate all African diploid '*Barbus*', as Yang et al. proposes.

Revalidating *Enteromius*, for what even Yang et al. acknowledges is a polyphyletic group based on their analyses, has many taxonomic consequences within this group. The genera *Barboides*, *Clypeobarbus*, and *Pseudobarbus*, which are well resolved and monophyletic in Yang et al.'s analysis, and diagnosable based on a mix of independent morphological and molecular characters (Skelton, 1988; Conway and Moritz, 2006; Conway and Stiassny, 2008; Swartz et al., 2009), are nested within *Enteromius* and would be subsumed by its validation.

We also disagree with Yang et al.'s designation of a '*Pseudobarbus*' group for all southern African tetraploid barbs that cannot be placed in *Pseudobarbus*. *Pseudobarbus* is distinguished from the other southern African '*Barbus*' tetraploids in possessing a flexible primary dorsal spine; whereas other tetraploid '*Barbus*' possess an ossified primary dorsal spine (Skelton, 1988; Swartz et al., 2009). A more apt treatment of the unresolved southern African tetraploids recovered by Yang et al. and previous studies (Machordom and Doadrio, 2001; Tsigenopoulos et al., 2002) is to designate a new genus, or genera, to accommodate these species, or to revise *Pseudobarbus* to include these additional species.

There is wide recognition that using '*Barbus*' to denote all African barbs (recommended by Berrebi et al., 1996) is itself a problem needing a solution. The approach others have taken to address this problem has been to recognize and elevate monophyletic groups from within the larger '*Barbus*' (Berrebi et al., 1996, 2014; Berrebi and Tsigenopoulos, 2003; Conway and Moritz, 2006). The large African hexaploid barbs were removed from '*Barbus*' and placed within *Labeobarbus* or *Varicorhinus* (Tsigenopoulos et al., 2010), though many taxonomic issues within these groups remain (Levin et al., 2013). The monophyletic southern African tetraploids were removed from '*Barbus*' and recognized as *Pseudobarbus* (Skelton, 1988), and the morphologically distinct *Clypeobarbus* and *Barboides* were also recently elevated (Conway and Moritz, 2006; Conway and Stiassny, 2008). Yang et al.'s (2015) revalidation of *Enteromius* confounds these efforts toward a practical solution to the '*Barbus*' problem.

Even these practical efforts to resolve the '*Barbus*' problem have been slow to take effect; particularly in developing African countries. In addition to a paucity of local taxonomists (Skelton and Swartz, 2011); many researchers within Africa lack reliable access to literature and often rely on outdated taxonomies. The complexities of disseminating and implementing taxonomic and nomenclatural changes in developing countries necessitate a thorough and cautious approach to proposing changes. Increased taxon sampling and inclusion of nuclear markers will improve resolution of the

African '*Barbus*' phylogeny, and will support recognition of stable, monophyletic groups within this problematic taxon. The name, *Enteromius*, clearly the oldest available generic name for African barbs, can be applied to a well-resolved group of '*Barbus*' species, encompassing the type species, '*Barbus*' (*Enteromius*) *potamogalis*, at that time.

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