



Correction : Characterization of hybridization within a secondary contact region of the inshore fish, *Bostrychus sinensis*, in the East China Sea

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Following the publication of this article, the authors have requested that the Acknowledgements section be amended to thank Weidi Yang for his assistance with their *Bostrychus sinensis* photograph that was chosen for the front cover of the January 2018 issue of the journal.

This error has been corrected in both the PDF and HTML versions of the paper.

Also, the legends for Supplementary Figures 1 and 2 were not posted online.

The authors apologize for any inconvenience caused.

Supplementary Figure 1: *Cytb* (A) and *RyR3* (B) gene trees for 739 individuals [534 from this study and 205 from Qiu et al. (2016)]. For the sake of presentation, the relationships of only the 113 different haplotypes of *Cytb* and

68 distinct alleles of *RyR3* are shown. “ECS” and “SCS” mark the two sister groups of *Cytb* haplotypes and *RyR3* alleles, which are reciprocally monophyletic, congruent, and diagnostic for the ECS and SCS lineages, respectively. ECS and SCS sequences are distinguished by their lower- and upper-case lettering, respectively, whereas haplotype and allele frequencies of >0 for the six geographic samples are shown to the right. Posterior probabilities are presented for those groups with >50% support, whereas branch lengths are drawn proportional to their median estimates of expected substitutions/site.

Supplementary Figure 2: First and second PCoA coordinates for the codominant genotypic distances of the six geographic samples. The percentage of total variation, which is explained by each coordinate, is given in brackets.

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