

Comparison of Environmental DNA Metabarcoding and a Traditional Survey Method for Assessing Fish Diversity and Distribution Along Salinity Gradient in an Urban Brackish Reservoir, China

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Table S1. species detected in the the Xinglinwan Reservoir using eDNA and TSM.

Species	Genus	Family	Order	eDNA meta	Traditional
<i>Oreochromis niloticus</i>	<i>Oreochromis</i>	Cichlidae	Cichliiformes	+	+
<i>Clupanodon thrissa</i>	<i>Clupanodon</i>	Clupeidae	Clupeiformes	+	+
<i>Mugil cephalus</i>	<i>Mugil</i>	Mugilidae	Mugiliformes	+	+
<i>Megalops cyprinoides</i>	<i>Megalops</i>	Megalopidae	Elopiformes	+	+
<i>Monopterus albus</i>	<i>Monopterus</i>	Synbranchidae	Synbranchiiformes	+	+
<i>Lateolabrax japonicus</i>	<i>Lateolabrax</i>	Lateolabracidae	Perciformes	-	+
<i>Hypophthalmichthys molitrix</i>	<i>Hypophthalmichthys</i>	Xenocyprididae	Cypriniformes	+	-
<i>Homatula laxiclathra</i>	<i>Paracobitis</i>	Nemacheilidae	Cypriniformes	+	-
<i>Cyprinus carpio</i>	<i>Cyprinus</i>	Cyprinidae	Cypriniformes	+	-
<i>Tridentiger bifasciatus</i>	<i>Tridentiger</i>	Gobiidae	Gobiiformes	+	-
<i>Hemiculter leucisculus</i>	<i>Hemiculter</i>	Xenocyprididae	Cypriniformes	+	-
<i>Hemiculter bleekeri</i>	<i>Hemiculter</i>	Xenocyprididae	Cypriniformes	+	-

Note: TSM and eDNA represent the traditional survey method and eDNA metabarcoding, respectively. “-” indicates species absent from TSM and eDNA; “+” indicates species present from TSM and eDNA

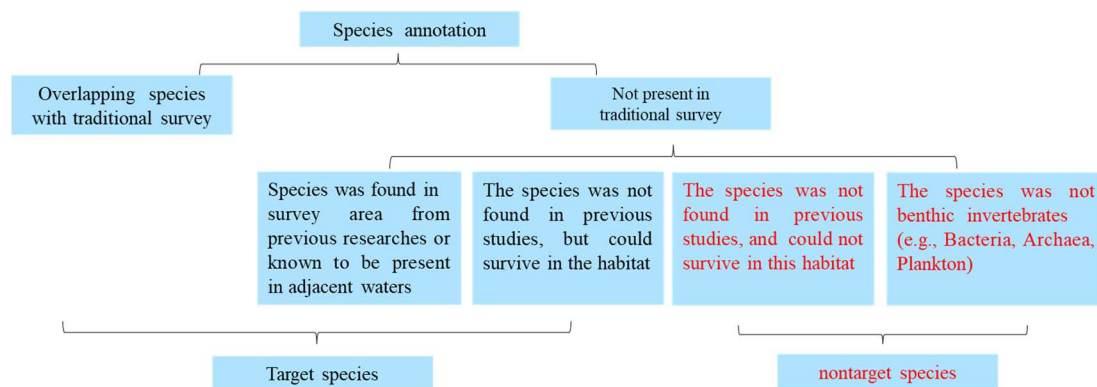


Figure S1. Species-filtering steps identifying target species.

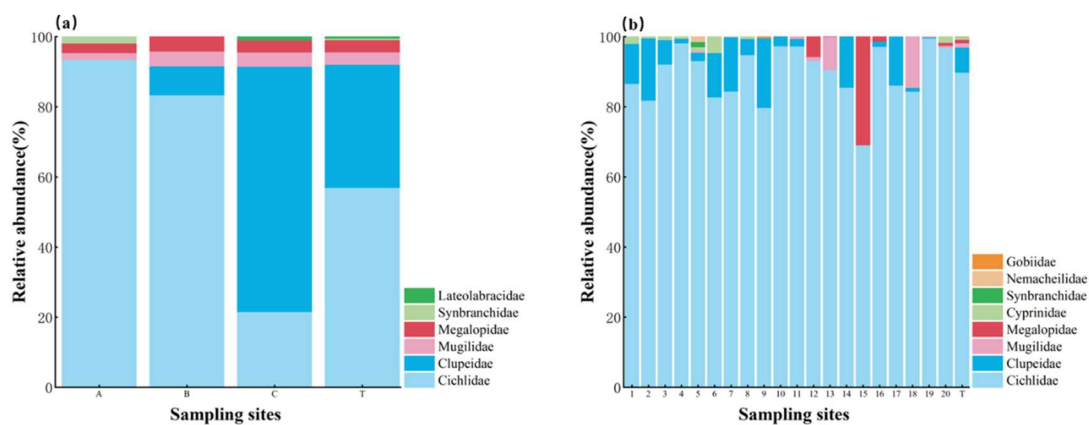


Figure S2. Relative abundance (%) of fish at the family level with TSM (a) or eDNA (b) in per sampling site.

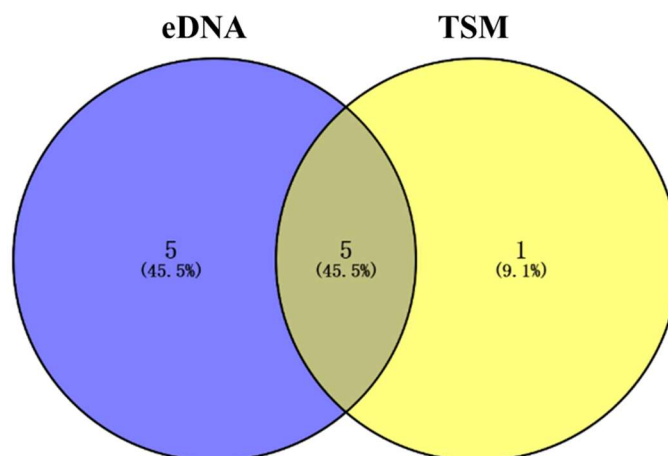


Figure S3. Species richness of fish identified using the TSM and eDNA for the open water sampling sites (sites 5, 7, 11, 13, 14, and 16).

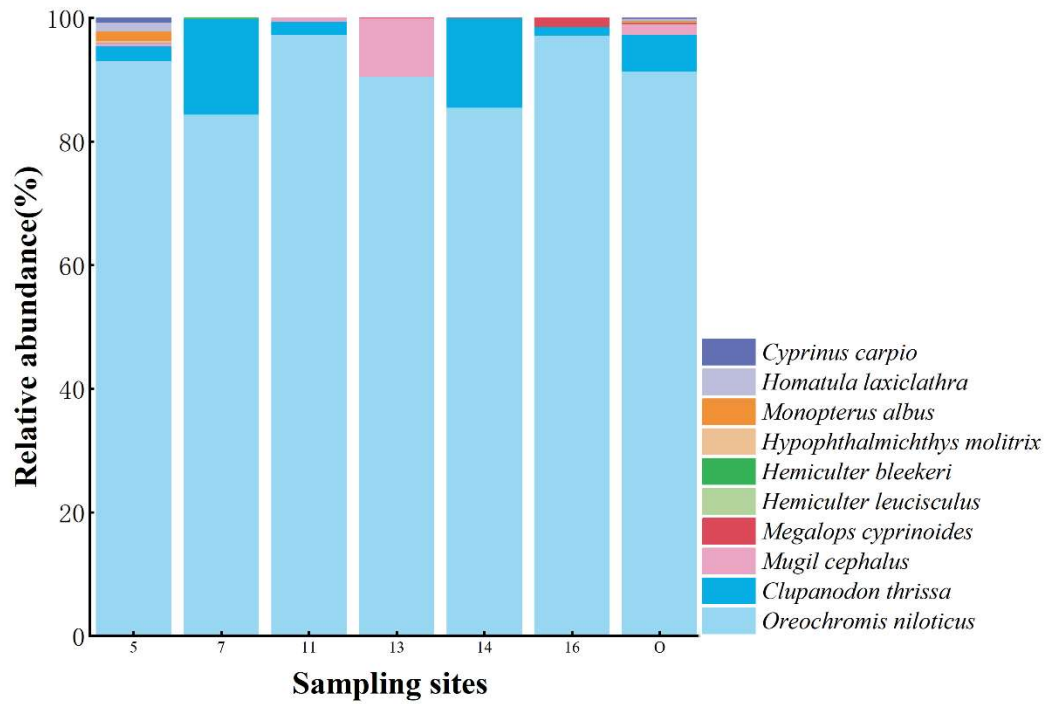


Figure S4. Relative abundance (%) of fish at the species level with eDNA for the open water sampling sites (sites 5, 7, 11, 13, 14, and 16). The relative abundance of fish for overall open water is marked with O.