DNA metabarcoding reveals adaptive seasonal variation of individual trophic traits in a critically endangered fish

Kurt Villsen¹, Emmanuel Corse², Emese Meglécz¹, Gaït Archambaud-Suard⁴, Hélène Vignes⁵, Alexander V. Ereskovsky⁶, Rémi Chappaz⁴, Vincent Dubut¹

¹Aix Marseille Université, CNRS, IRD, Avignon Université, IMBE, Marseille, France
²Centre Universitaire de Mayotte, Dembeni, Mayotte, France
³MARBEC, Univ Montpellier, CNRS, Ifremer, IRD, Montpellier, France
⁴INRAE, Aix Marseille Université, RECOVER, Aix-en-Provence, France.
⁵CIRAD, Univ Montpellier, INRAE, Montpellier SupAgro, AGAP, Montpellier, France
⁶St. Petersburg State University, St. Petersburg, Russia
⁷Koltzov Institute of Developmental Biology of Russian Academy of Sciences, Moscow, Russia

Correspondence: Kurt Villsen, kurt.villsen@imbe.fr; or Vincent Dubut, vincent.dubut@gmail.com

SUPPLEMENTARY FIGURES S1 to S3

Figure S1. The relative abundance of prey in the diet of Zingel asper.
Figure S2. Summary of hierarchical clustering analysis
Figure S3. Correlation between traditional and Hill number-derived estimates of INW and BIC
Figure S4. Correlation between prey genus haplotype richness and prey minimum number of individuals (MNI)
Figure S1. The relative abundance of prey in the diet of *Zingel asper*. Barplots summarize the main prey groups identified in *Zingel asper*’s feces. Pie-charts indicate the proportion of variants corresponding to both prey and non-prey groups. The proportion of prey items are based on the cumulative Minimal Number of Individuals (MNIs).
Figure S2. Summary of hierarchical clustering analysis. A) Dendogram, B) Gap statistic results to determine the number of clusters (k) C) Cluster proportions by season (excluding YOY) D) Cluster proportions by size class. Cluster colors correspond to: Cluster 1 (Baetis fuscatus) = Green, Cluster 2 (Ecdyonurus) = blue and Cluster 3 (Orthocladiinae and rare prey) = purple.
Figure S3. Correlation between traditional and Hill number-derived estimates of INW and BIC.
Figure S4. Correlation between prey genus haplotype richness and prey minimum number of individuals (MNI)

$R^2 = 0.03, p < 0.001$