## Quantification of mixed contributions of primary producers from amino acid $\delta^{15}N$ of marine consumers: a Bayesian approach

García-Seoane, R., Viana, I.G., Bode, A.

Instituto Español de Oceanografía (IEO-CSIC), Centro Oceanográfico de A Coruña, 15001 A Coruña, Spain. E-mail address: <u>rita.garcia@csic.es</u> / <u>rita.garcia@ieo.es</u>

Estimations of the trophic position (TP) and the food web nitrogen baseline from compoundspecific isotope analysis of individual amino acids (CSIA-AA) are challenged when the diet of consumer organisms relies on different proportions of vascular and non-vascular primary producers. Here we provide a new method to infer such proportions using the  $\delta^{15}N$  patterns from individual AAs ( $\delta^{15}N_{AA}$ ) in the consumer. Combining published and new data, we first characterized the  $\delta^{15}N_{AA}$  signatures in primary producers and determined the isotopic enrichment ( $\beta$ ) for the major taxa of primary producers. Then, we applied MixSIAR Bayesian isotope mixing models to investigate the transfer of these signatures to marine primary consumers (molluscs, green turtles, zooplankton and fish), and their utility to quantify autotrophic sources. Reliable source proportions were quantified, using appropriate combinations of trophic discrimination factors (TDFs), and were used to estimate  $\beta$  values for each consumer. We demonstrated that phytoplankton, macroalgae and vascular plants have singular  $\delta^{15}N_{AA}$  fingerprints that can be tracked from the  $\delta^{15}N_{AA}$  values in their primary consumers, and can be used to estimate mixed baseline sources. This method is useful to accurately estimate  $\beta_{mix}$  values from consumer  $\delta^{15}N_{AA}$  signatures with no requirement to sample or characterize the primary producers supporting the food web, thus providing reliable TP estimates in complex environments dominated by vascular and non-vascular autotrophs. This study evidences a suitable integration of  $\delta^{15}N_{AA}$  fingerprinting and MixSIAR for quantitative estimations of autotrophic sources, complementing other methods to quantify resource utilization in natural systems. This method represents a major advance to unravel trophic dynamics at the aquatic/terrestrial interface using CSIA-AA.