

Metabarcoding reveals waterbird diet in a French Ramsar wetland: implications for ecosystem management



Environmental and/or climate changes, occurring at a global or local scale, can significantly impact the diets, health, and population dynamics of waterbirds. This study aimed to develop an effective tool, using DNA metabarcoding of fecal samples, for monitoring waterbird diets during the breeding season in a Ramsar freshwater wetland in Northern France. We collected bird feces across eight marshes with varying anthropic usage. The majority of samples (69%) were from five waterbird species: Eurasian coot (*Fulica atra*), Eurasian moorhen (*Gallinula chloropus*), mallard (*Anas platyrhynchos*), mute swan (*Cygnus olor*), and grey heron (*Ardea cinerea*). DNA was extracted from 116 samples, with plant and invertebrate primers used to undertake multi-marker metabarcoding. Despite a negative impact of uric acid on DNA amplification, we observed significant dietary variations among bird species and sampling sites. Wetland bird diets primarily consisted of four arthropod families, dominated by Chironomidae and Asellidae. The number of plant families detected was higher, consisting of 33 families, with Poaceae highly prevalent within wetland bird diets. This study shows that using DNA metabarcoding to explore interactions between waterbirds and trophic resources is a promising approach to assist wetland management and assess the effect of environmental changes.

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