

# The predator problem and PCR primers in molecular dietary analysis: swamped or silenced; depth or breadth?

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## Abstract

Dietary metabarcoding has vastly improved our ability to analyse the diets of animals, but it is hampered by a plethora of technical limitations including potentially reduced data output due to the disproportionate amplification of the DNA of the focal predator, here termed ‘the predator problem’. We review the various methods commonly used to overcome this problem, from deeper sequencing to exclusion of predator DNA during PCR, and how they may interfere with increasingly common multi-predator-taxon studies. We suggest that multi-primer approaches with an emphasis on achieving both depth and breadth of prey detections may overcome the issue to some extent, although multi-taxon studies require further consideration, as highlighted by an empirical example. We also review several alternative methods for reducing the prevalence of predator DNA that are conceptually promising but require additional empirical examination. The predator problem is a key constraint on molecular dietary analyses but, through this synthesis, we hope to guide researchers in overcoming this in an effective and pragmatic way.

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