

Using next-generation sequencing for food web analyses; a detective story involving endemic landsnails and earthworms

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The study of food webs is of major importance in ecology; however, feeding is sometimes difficult to observe or quantify for species that are rare, very small, aquatic or nocturnal. The assessment of such species' diet often relies on the study of prey remains (e.g., arthropod cuticle) in predator gut contents or faeces. However, this method often lacks precision at the species level, and is not applicable for soft-bodied prey such as snails, slugs, earthworms, etc. The development of molecular techniques targeting prey DNA remaining in the guts and faeces predators appears to be a good alternative. As it is based on DNA barcoding, this approach is both very precise in terms of species identification and applicable to soft-bodied prey. We used next-generation sequencing (454-pyrosequencing) to analyse the diet of *Powelliphanta augusta*, an endangered carnivorous landsnail endemic to New Zealand that was suspected to feed mainly on earthworms. This technique is capable of sequencing many thousands of DNA fragments simultaneously from mixed samples, which allows molecular identification of all prey species in a single faecal sample. Although earthworm tissue was not detectable in snail faeces, earthworm DNA was still present in sufficient quantity for molecular tools to detect and analyse it. Based on faecal samples collected from 40 landsnails, our results provide a complete map of the earthworm-based diet of *P. augusta*. These results are helping to ensure that snails translocated to new areas have access to an appropriate range of prey species, enhancing their likelihood of survival.

