

Comparison of metabarcoding techniques for dietary assessment in herbivores and omnivores

ABSTRACT

Dietary assessment plays a crucial role in comprehending the ecological dynamics and nutritional needs of herbivores and omnivores. The metabarcoding technique has emerged as a potent tool for exploring the dietary composition of these animals. However, various metabarcoding techniques have been developed, each with its own advantages and limitations. This study aims to compare the performance of different metabarcoding techniques in herbivores and omnivores diet. We systematically reviewed 159 published manuscripts in Scopus and Google Scholar, and thematic analysis was conducted across several categories, including the marker, platform, and database utilized. Preliminary findings reveal significant variations among metabarcoding techniques across these two animal groups. The trnL gene exhibited higher taxonomic resolution for herbivorous species, whereas the combination of the 'trnL + 16s rRNA' gene exhibited superior performance for omnivorous species. The Illumina platform emerged as the most commonly used method for analyzing the diets of both herbivores and omnivores, with the primary reference database being the National Centre for Biotechnology Information (NCBI). This study offers valuable insights into the strengths and limitations of different metabarcoding techniques for dietary assessment in herbivores and omnivores and optimizing metabarcoding protocols, facilitating more precise and reliable diet analyses within these ecological groups.