ARPHA Conference Abstracts 4: e64895
doi: 10.3897/aca.4.e64895

Conference Abstract

Are multiplexed metabarcoding panels comparable to individual marker gene library preparations?

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Received: 23 Feb 2021 | Published: 04 Mar 2021

Citation: Eastwood N, Orsini L (2021) Are multiplexed metabarcoding panels comparable to individual marker gene library preparations? ARPHA Conference Abstracts 4: e64895. https://doi.org/10.3897/aca.4.e64895

Abstract

Analysis of multiple marker genes using metabarcoding of environmental DNA (eDNA) can offer information greater than that from sequencing single marker genes, such as responses from across the phylogenetic tree to environmental gradients (Cordier et al. 2019). Furthermore, multiple regions of the same gene can be sequenced to improve phylogenetic resolution (Fuks et al. 2018). However, separate amplification reactions and library preparation steps for each marker can be costly and time consuming.

Here, we have designed and optimised a multiplex panel of four marker genes (two regions of 18S rRNA gene, one region of the 16S rRNA gene and one region of the rbcL gene). By combining steps into a single reaction, the labwork required is decreased, reducing cost and time. This multiplex is compared with a widely available commercial microbial (bacterial and fungal) screening panel and individual library preparations of each marker gene.

Keywords

Multiplex; Metabarcoding; eDNA;

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Presented at

1st DNAQUA International Conference (March 9-11, 2021)

Hosting institution

University of Birmingham, UK

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