**Assessing the potential of metabarcoding for measuring beta diversity using three plots of Costa Rican dry forest**

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Can environmental metabarcoding find a place in the ecologist's toolkit for measuring beta diversity? Using Illumina MiSeq sequencing technology and the trap contents from a total of nine Malaise traps distributed across three plots of Costa Rican dry forest of varying successional age, we set out to answer this question. Through the use of multiple marker regions (COI and 16S) and multiple primer sets for each, we generated distribution patterns both within and between sites for terrestrial arthropods and their associated prokaryotes and concluded that metabarcoding on its own was both able to differentiate between sites and that observed beta diversity varied between the markers, and by extension the taxonomic groups they target. The addition of further marker regions (18S, rbcl) in future is anticipated to further support these conclusions.