



Conference Abstract

# Comparison of eDNA and traditional troglofauna sampling methods

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## Abstract

Environmental DNA (eDNA) and metabarcoding have recently been combined with the aim of detecting species through the small amounts of DNA animals shed into the environment. The technique has successfully been applied in the biomonitoring of vertebrates and decapods and, in a collaborative project with the Trace and Environmental DNA laboratory, Curtin University, we tested its utility in troglofauna sampling. Traditional troglofauna surveys have low yields and consequently, provide limited information about species' ranges. The ability to detect more occurrences of a species and better define the species' range by combining traditional troglofauna sampling and eDNA is very exciting. The study area we used is in the central Pilbara and prior survey of the area had documented a moderate troglofauna community. We collected 147 samples from 74 drill holes that comprised 58 scrapes samples, 75 litter trap samples and 14 water samples. Pairs of scrape and water samples were collected from each drill hole, with one set sent for morphological identification and the second set frozen for metabarcoding. A pair of water samples comprised lowering a bailer down the drill hole, retrieving 1 L of water from the top of the water column (for eDNA) after which stygofauna net haul sampling was undertaken. Trap samples collected 124 troglofauna specimens, scrapes 37 troglofauna and net hauls two species of stygofauna and no troglofauna; troglofaunal groups collected include cockroaches, diptera, bugs, schizomids, millipedes, pseudoscorpions, palpigraids, isopods,

beetles, silverfish, pauropods and symphylans. Surface species were abundant in the traps (7,760 specimens) and present in most scrapes (81 specimens); they mostly comprised mites and collembola, with lower numbers of flies and ants. The high diversity of animals collected and inevitable human contamination could be expected to pose significant hurdles to use of eDNA. The preliminary eDNA results are compared with the results of traditional sampling.

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