

Using DNA barcodes as an indicator of insect dispersal among source and restored stream habitats

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The restoration of aquatic invertebrate communities following disturbance is dependent on connectivity to a source population. Dispersal of aquatic insects is a key process allowing colonization of new habitat and linking existing populations among habitats. Here, we used mitochondrial DNA (COI) sequences to assess the genetic similarity (as a measure of connectivity) for individuals of aquatic insects among 10 sites from four streams representing both source and disturbed streams in the Taranaki Region, New Zealand. Three common aquatic insect species were targeted based on differences in their dispersal capabilities: *Archichauliodes diversus* (Megaloptera; active larvae, poor flight), and *Hydropsyche colonica* and *Pycnocentroides aeris* (Trichoptera; sessile larvae, strong flight). *A. diversus* showed the greatest sequence diversity (19 haplotypes) followed by *P. aeris* (14 haplotypes) and *H. colonica* (4 haplotypes). Despite relatively high levels of sequence diversity, *A. diversus* was genetically similar throughout the study area, suggesting adequate dispersal among source and disturbed habitats. Individuals of *H. colonica*, with much lower levels of haplotype diversity, were also genetically similar between source and disturbed habitats. In contrast, *P. aeris* had one haplotype that was more common in source versus disturbed habitats. We conclude that taxa were relatively well connected between source and disturbed habitats and that COI sequences can provide a useful indicator for tracking restoration efforts.