

## STREAM ECOLOGY

# Measuring stream network connectivity: how close is close enough?

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*The success of stream restoration projects may depend on understanding the links between landscape patchiness and aquatic insect dispersal.*

Teachers: this article can be used for NCEA Achievement Standards in Biology (2.3, 3.5, 3.6). See other curriculum connections at [www.niwa.co.nz/pubs/wa/resources](http://www.niwa.co.nz/pubs/wa/resources)

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New Zealand's landscape has become highly fragmented over the last century with the clearance of large tracts of forest and the conversion of land to pasture. The remaining patches of forest are often isolated from each other, and populations of some sensitive terrestrial animals have suffered as a result. For example, native forest birds must now cross an inhospitable matrix of developed land to move between remaining forest patches. In other words, the connectivity of their habitat has been lost.

Although not widely recognised, loss of connectivity also affects streams and rivers. Sensitive adult aquatic insects may not be able to fly overland between catchments. Within streams, barriers such as culverts or degraded water may limit dispersal by invertebrate larvae and fish.

Understanding the implications of this loss of connectivity between different parts of a stream network and adjacent catchments is important in planning stream restoration in which the aim is to re-establish sensitive aquatic species. This is because the success of natural recolonisation depends partly on whether patches of suitable habitat are large enough and spaced close enough together between the area being restored and the colonist populations, which are often holding out in headwater streams surrounded by remnant native forest.

### GIS study

Novel methods have been developed to analyse spatial patterns of landscapes fragmented by landuse change. The same approach could be useful for measuring connectivity of stream riparian habitats. We are conducting a study to analyse the spatial structure of forested patches near stream boundaries. We are using vegetation data from the New Zealand Land Cover Database, and stream networks from the NZ TOPO datasets available from Land

Information New Zealand. This analysis was carried out using a Geographic Information System (GIS) linked to a software package for landscape patch analysis. We wanted to see whether measures of connectivity, when applied to riparian areas, were related to the genetic differences found in a stream caddisfly from a previous study (see *Water & Atmosphere* 8(3): 17-18).

We measure genetic differences as **genetic distance**, which is estimated from gene frequencies using DNA or allozymes. These distances indicate how related different populations are, and provide some clues to how often populations mix between sites, at least over long timescales.

In the earlier study, we collected caddisflies for genetic analysis from a range of stream sites. Using GIS, we mapped all areas of forest and scrub within 200 m of a stream edge at these sites. Using the resulting network of forest/scrub riparian strips (see example below) we calculated several measures – or metrics – of connectivity among sites. We made comparisons within regions because our



Example of riparian strips mapped around two of the study sites. The superimposed polygons were used in determining a "representative scale" for measuring the data set.

### Measuring dispersal

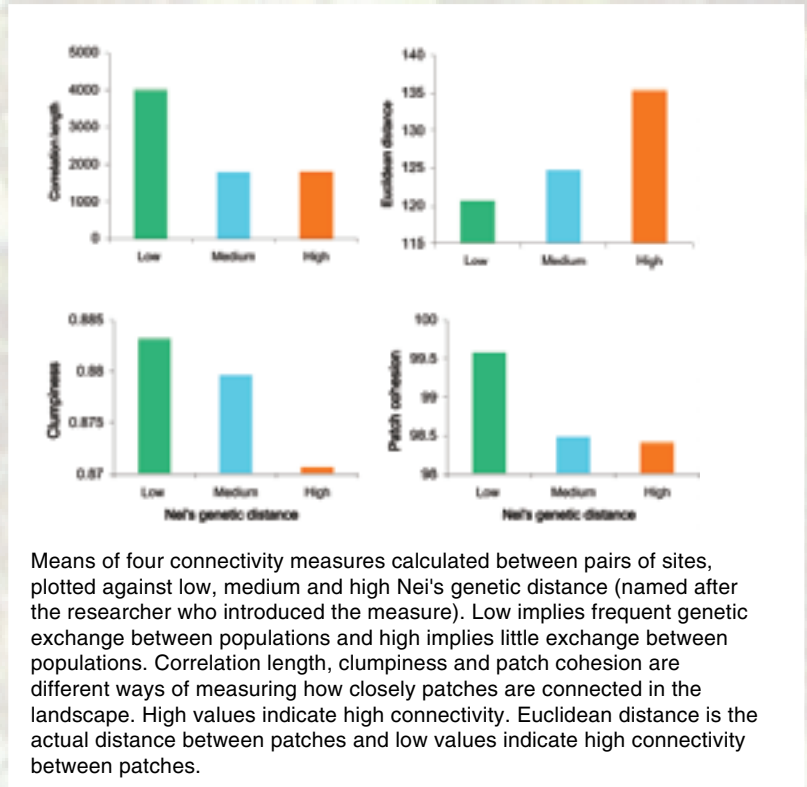
It's not easy to measure directly the distances travelled by the adult stages of aquatic insects. Imagine how difficult it would be to track a tiny caddisfly as it moves through vegetation at a stream edge! Even though only a few adults may need to reach a site to start a population there, the chances of finding and tracking these individuals are very slim. However, other methods have been used to indirectly measure dispersal distances.

Studies carried out overseas have tracked the movement of individuals labelled with radioactive isotopes, either unintentionally through the uptake of radioactive waste discharged into waterways, or as part of planned mark-recapture experiments. These studies have suggested that some mayflies disperse around 1 km and some caddisflies can fly up to 16 km. Dispersal distances can also be inferred through the level of genetic similarity among populations sampled at different spatial scales. Genetic analyses provide a picture of the level of population mixing over longer evolutionary timescales. It may take hundreds or even thousands of generations for genetic differentiation to occur, although differentiation may be enhanced when small populations become established in new areas.

Work in New Zealand has indicated large genetic differences among populations of a common caddisfly separated by more than 100 km, but similar genetic make-up between sites around 10 km apart (Smith & Collier 2001). Populations in neighbouring streams in separate catchments were genetically different, while populations at similar spatial scales within the same catchment were genetically similar. This suggested that the caddisflies were moving along stream and river networks rather than across the land. This result agrees with studies of adult caddisfly movement alongside streams which have shown that most adults stay within 20–30 m of the stream edge, and few travel more than 200 m away from water (Collier & Smith 1998).

previous genetic work demonstrated that historical landmass changes still influence current genetic patterns for the same species occurring in different regions.

Several landscape metrics showed interesting relationships with genetic distance. The figure above shows how low genetic distance is associated with higher levels of connectedness. In other words, genetically similar populations tend to occur at pairs of sites that have higher connectivity. These initial results support the hypothesis that the degree of riparian connectivity may influence the permeability of



Means of four connectivity measures calculated between pairs of sites, plotted against low, medium and high Nei's genetic distance (named after the researcher who introduced the measure). Low implies frequent genetic exchange between populations and high implies little exchange between populations. Correlation length, clumpiness and patch cohesion are different ways of measuring how closely patches are connected in the landscape. High values indicate high connectivity. Euclidean distance is the actual distance between patches and low values indicate high connectivity between patches.

the landscape to adult aquatic insects, and therefore the interchange between populations along and between stream networks.

### Integrated approach needed

This work is in its preliminary stage. In the future we plan to develop and apply measures suitable for analysing connectivity within streams. We will also look in more detail at the quality of riparian vegetation connecting stream segments. In addition, the spatial resolution of the data will be improved by using better aerial photographs.

Spatial studies such as these are useful for providing a basis for planning the arrangement of stream restoration works at the landscape scale. However, simply getting to a site is only half the recolonisation battle. Freshwater organisms must be able to complete their life-cycles at a site in order to establish self-sustaining populations. This means that habitat at restored sites must be suitable for colonists.

So, understanding the likelihood of restoration sites being recolonised by sensitive species depends on:

- developing ecologically appropriate measures of habitat connectivity;
- integrating these measures with knowledge of species' habitat requirements for successful life-cycle completion. ■

**Further reading**  
 Collier, K.J.; Smith, B.J. (1998). Dispersal of adult caddisflies (Trichoptera) in forests alongside three New Zealand streams. *Hydrobiologia* 361: 53–65.  
 Smith, P.J.; Collier K.J. (2001). Allozyme diversity and population genetic structure of the caddisfly *Orthopsyche fimbriata* and the mayfly *Acanthophlebia cruentata* in New Zealand streams. *Freshwater Biology* 46: 795–805.

This work is being undertaken in the FRST programme "Biodiversity of NZ Aquatic Environments" (C01X0219).