

Figure 2. Geometric means of periphyton biomass and invertebrate abundance in 83 rivers classified according to the flood frequency  $FRE_3$ , where a flood is defined as flows higher than three times the median flow.

chlorophyll *a* decreases. This means that there is a high chance of finding more periphyton in rivers with fewer floods. However, for invertebrates, numbers tend to increase with  $FRE_3$  up to 15–20 floods per year, but decrease for higher values.

Our study showed that not only did periphyton biomass decrease with increasing  $FRE_3$ , but also the taxonomic richness and diversity of periphyton decreased significantly. For invertebrates it was less clear how taxonomic richness and diversity varied with changing  $FRE_3$ .

factors such as whether the substrate is cobbly or silty, and levels of nutrient concentrations. However,  $FRE_3$  does indicate some trends.

Figure 2 shows the geometric means of periphyton biomass and invertebrate abundance found in the 83 study rivers with  $FRE_3$  in six classes (0–5, 5–10, 10–15, 15–20, 20–25, >25 floods per year). The figure shows that as the number of floods per year increases, periphyton

These were more related to the average flow conditions, for example the median flow.

The conclusion was that  $FRE_3$  is the most useful of the 35 flow variables for classifying rivers according to habitat for benthic biota. It explained 20% of the variance of periphyton biomass, richness and diversity, and invertebrate abundance.

We suggest that  $FRE_3$  can be used as a basis for interrogating flow records by using the following procedure:

- Obtain daily flow data from the site and period of interest.
- Calculate the median value and multiply it by three.
- Count how many times the flow exceeds this value and divide by the number of years in the period. This value is the  $FRE_3$ .
- Place the river in one of the six categories of flood frequency then read off from Figure 2 whether it is likely to have high or low biomass/abundance of benthic biota. ■

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## Chewing up the woody debris: enzymes for all seasons

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*Studies of enzyme activity are helping us to understand how organic matter is processed in streams.*

YOU MAY HAVE SEEN THEM on television advertisements ... colourful little spheres with huge mouths munching out those “impossible” stains. Chances are your laundry contains one of the numerous enzyme-containing detergents. The reason those enzymes are so good is that they work on such a wide range of organic muck and they do it at room temperature.

Have you ever stopped to think of what happens to all the organic debris produced by plants (e.g., grass, leaves, wood) going into the environment? Well, the enzymes produced by microorganisms, primarily bacteria and fungi, are responsible for the breakdown and natural recycling of most of that organic matter. In turn, the microorganisms that grow on the simple organic compounds produced by enzymatic breakdown form the basis of the food chain to support invertebrates and higher consumers.

We have been using enzyme “fingerprints” to trace the basis of organic matter processing in streams.

The principle of this technique is to deduce what types of compounds are important to stream microbes by comparing the activities of a suite of enzymes associated with microbial communities exposed to differing environmental conditions.

The microbial communities studied are those living in “biofilms” – the often slimy layer of living material attached to the rocky streambed or attached to decaying vegetation. These sessile organisms adapt their individual metabolism and community structure to their food sources from either the overlying flowing water or the adjacent vegetation. While they are responsible for the production of thousands of enzymes, only a few specific enzymes digest food compounds such as carbohydrates and proteins. Specific reagents are commercially available to measure the metabolic activity of a wide range of enzymes. Many have been used for studying environmental processes, largely litter decay in soil. Some of these reagents were chosen for this preliminary study (see panel). The measurement process involves either incubation of whole rocks, or homogenisation of leaf material, with enzyme substrates.

We have investigated biofilms from streams draining catchments having different vegetation cover – pasture, pine and native bush. The results have been encouraging. Measurable activity has been present for each of the enzyme groups and



# Enzymes used to characterise environmental decay processes

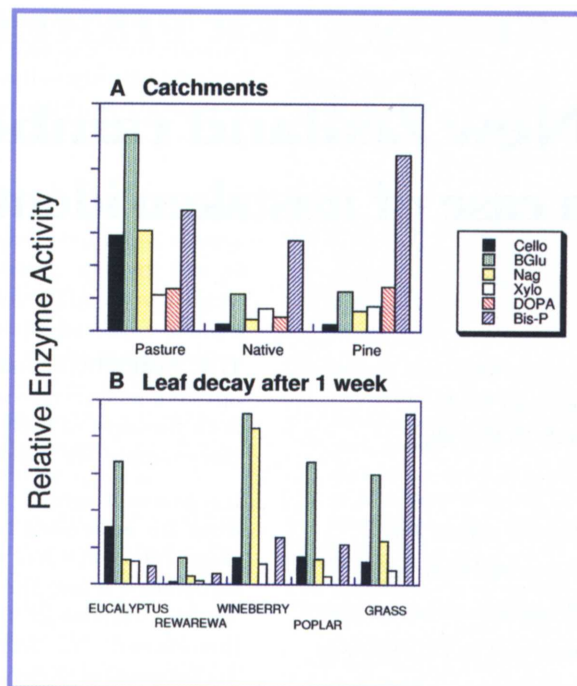
Process	Enzyme	Substrate	Code
Cellulose degradation	$\beta$ -glucosidase	Cellobiose	CELLO
			BGLU
Hemicellulose degradation	$\beta$ -xylosidase	Xylobiose	XYLO
	$\beta$ -N-acetylglucosaminidase	N-acetylglucosamine	NAG
Lignin	Phenol oxidase	Lignin, phenols	DOPA
Phosphorus mineralisation	Phosphodiesterase	Nucleic acids	BIS-P

far right: Relative enzyme activities of streambed biofilms and leaf litter. See panel (above) for enzyme abbreviations.

some differences are distinguishable between catchments. The pasture stream showed relatively elevated activities of enzymes decaying carbohydrates (CELLO and BGLU) while the pine catchment showed high BIS-P activity, indicating turnover of nucleic acid material.

Other experimental designs are being used to investigate stream carbon processing. We have used enzyme activities to compare carbon sources for microbes from leaves of various riparian trees. The leaves were attached to clay tiles and incubated in streams and our experimental channels located at Whatawhata. We followed their rate of decay and enzyme activity over several months. The leaf litter showed markedly different enzyme signatures for the various leaf types. Generally the less woody leaves showed a rapid onset of cellulose degrading enzymes while the woody material (e.g., rewarewa) showed minimal activity. Analysis of the leaf litter decay over time and our ongoing monitoring programme of seasonal changes in enzyme activity of organic matter in different catchment types will provide a better picture of

Whatawhata channels with leaf-packs deployed at the beginning of the litter decay experiment.  
(Photo: John Quinn)



the rates and pathways of carbon processing that, together with instream primary production, supports microbial communities in streams.

Together these preliminary experiments have demonstrated that the microbial enzyme signatures are useful tools for identifying the key classes of organic material that drive stream food webs. This information will enhance our understanding of the processes by which land use alters stream ecosystems and aid in the selection of trees for riparian planting to help restore community structure for sustainable river management. ■

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## Further reading

Cooper, A.B., Quinn, J.M. and Davies-Colley, R.J. (1994). The Whatawhata project: plans for riparian research. *Water & Atmosphere* 2(2): 15-18.