Mining metagenomes for novel enzymes

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Recent advances in high throughput sequencing have led to the accumulation of metagenomic sequences from a wide range of ecosystems. These metagenomic sequences can now be accessed and exploited by non specialists using different available bioinformatics tools. Recent research into the possible genomic resources from a soil metagenome reinforces the optimism of searching for and finding potential enzymes of interest. The first step includes *in silico* screening of gene families in order to identify possible targets of interest. The second step includes screening clone libraries for these same (or similar) genes. Screening can be achieved by both genetic and phenotypic approaches although the later is dependent in part on the expression system of the host. The identified clones of interest can subsequently be exploited to produce targeted enzymes. Some initial work has demonstrated the extensive diversity of different ecosystems, with soil being the most diverse. In addition to biodiversity, different ecosystems might be more appropriate for different families of genes. A superficial comparison of different ecosystem metagenomes can help define the ecosystem with the most interest for a given activity. Future work on the functional differences associated with the vast biodiversity of many gene families will also help in future enzyme activity choices.