

OEZY – Optimising *EnZY*me selection for best performing restriction fragment length polymorphism (TRFLP) analysis using ARB

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Restriction fragment length polymorphism (TRFLP) analysis remains a useful technique to obtain insights into the genetic diversity of microbial populations. A crucial parameter of this technique is the selection of appropriate restriction endonucleases (REs) to achieve high resolution of the PCR amplified fragments of the marker gene (usually a ribosomal RNA gene).

However, despite the development of several computer supported programmes to improve the selection of REs for TRFLP analysis, there is still a lack of software that offers both of two aspects: firstly, availability of a sequence database from which sequences can easily and without further formatting and ranking be selected for analysis; secondly, selection of sets of REs for highest genetic resolution while providing the possibility to assess and quantify the correlation of the TRFs to the phylogeny of the target group of marker gene sequences (e.g. 16S rRNA gene sequences).

We therefore designed a new software – OEZY – that overcomes both of those shortcomings and incorporates all of the individual tools that are offered by currently available programmes. OEZY is user friendly and uses ARB as database for easy access to a huge range of aligned ribosomal RNA sequences while still offering to use alternative marker genes submitted to ARB by the user.

OEZY (source code and binary distribution for automated and manual installation) together with a detailed manual and debian installation package is available free of charge from this website.

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