Introduction

The automated ribosomal intergenic spacer analysis (called ARISA) is an analytical fingerprinting technique for characterizing microbial community composition. ARISA analyzes the length of the intergenic spacer region between 16S and 23S rRNA genes (called ITS region) present in almost all Bacteria and Archaea. ARISA has been used to analyze several bacterial communities, including samples from freshwater, marine, and terrestrial environments. It is used for clinical studies to detect and identify microbes species. The main advantages of ARISA are that it is cheaper and quicker than other community profiling techniques.

ADAPTdb

ADAPTdb is a collection of annotated ITS regions using a MySQL database as a data storage backend.

Used data resources:
- RISSC (collection of spacer regions)
- Entrez Sequences and Entrez Genomes database
- Pathogenic information manually extracted from literature and from the Lproks file (for completely sequenced bacterial genomes)

ADAPT

ADAPT is a web-based analyzing program for ARISA data sets using a fingerprint database (ADAPTdb) in order to:
- Predict the taxonomic composition of the underlying microbial communities
- Perform trophic and pathogenic comparisons of the samples from which the ARISA data was obtained

Analyzing steps include:
- ARISA profile filtering (remove noise and uninformative peaks)
- Database search (mapping ITS regions to ADAPTdb to find similar regions using a “binning” strategy)
- Calculate autotrophic/heterotrophic and pathogenic/non-pathogenic values using two different methods
- Performing multiple samples analysis (if more than one sample is provided in the ARISA data set)

Application example

Water samples were collected in 2005 at the coral reefs near the two Line Islands (Kiritimati and Tabuaeran). The islands lie within the same biogeographic region, but show a gradient of human disturbance. The population gradient was used to investigate the influence of human activities on the microbes living in the coral reefs. Bacteria were isolated by filtering about 1l of seawater through a filter. The DNA was then isolated from the bacterial cells, processed using ARISA, and analyzed using the ADAPT program.

The results identified that a range of pathogenic bacterial species were present on the two islands:

- Bacteroides vulgatus
- Clostridium carinii
- Enterococcus munditii
- Haemophilus somnus
- Legionella pneumophila
- Mycobacterium spp.
- Streptococcus spp.

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Further Information

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