Microarrays for molecular detection and typing of microorganisms

AUSTRIAN INSTITUTE OF TECHNOLOGY

Kostić, T.; Konrad-Köszler, M.; Pan, Y.; Sanoussi, S.C.; Weilharter, A.; *Bodrossy, L.; #Stralis-Pavese, N.; Sessitsch, A.

AIT Austrian Institute of Technology GmbH, Health and Environment Department, Seibersdorf, Austria.
current address: *CSIRO Marine & Atmospheric Research, Hobart, Tasmania. #BOKU University Vienna, Vienna, Austria.
tanja.kostic@ait.ac.at

MICROBIAL DIAGNOSTIC MICROARRAYS (MDMs)

MDMs are molecular tools used for simultaneous detection and identification of microorganisms in clinical and environmental samples.

Main advantages of MDMs are high throughput, parallelism and miniaturisation of the detection system.

Furthermore, MDMs allow for high specificity and high sensitivity of the detection.

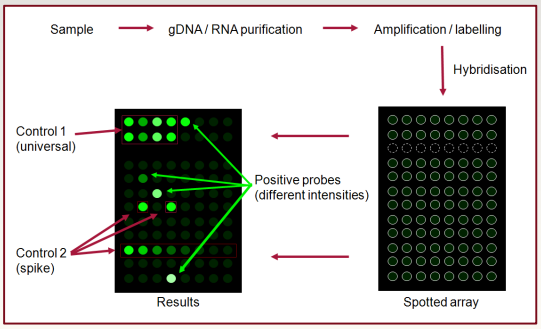

Figure 1: MDM – experimental workflow

TECHNOLOGICAL KNOW-HOW @ AIT

Our expertise include:

- identification of suitable markers for microarray development
- sequence analysis and database establishment
- probe design and *in-silico* probe validation
- set-up and optimisation of microarray platforms based on different experimental approaches
  ("standard method", SSELO, long oligonucleotide arrays)
- sample analysis using already established MDM platforms
  (i.e. methanotroph community analysis, *Salmonella* serotyping, pathogen detection)

PATHOGEN MICROARRAY

Enables parallel detection of 24 most common food and waterborne pathogens and indicator organisms.

Pathogen microarray utilizes the phylogenetic resolution potential of *gyrB* gene in combination with a unique labelling method (SSELO) and a novel concept of competitive oligonucleotides. This assay format allows for both high specificity (identification at species or genus level) and sensitivity (0.1% relative and 10^4 cfus absolute detection limit).

In combination with biological pre-enrichment pathogen microarray is able to fulfil legal requirements for the detection of pathogens in food in terms of both sensitivity (1-10 cfu / 25 g food) and specificity with results obtained more rapidly than with the microbiological reference ISO methods.

Salmonella SEROTYPING MICROARRAY

Salmonella serotyping microarray is based on two phylogenetic markers (*atpD* and *gyrB*) and two flagellar genes (*fliC* and *fljB*). It covers the 43 most prevalent serovars in Austria, UK and Switzerland.

Features of the *Salmonella* serotyping microarray:

- reliable serotyping within 24 hours
- detection limit: 1 cfu / 25 g food matrix
- below-serovar subtyping potential
- parallel serotyping potential

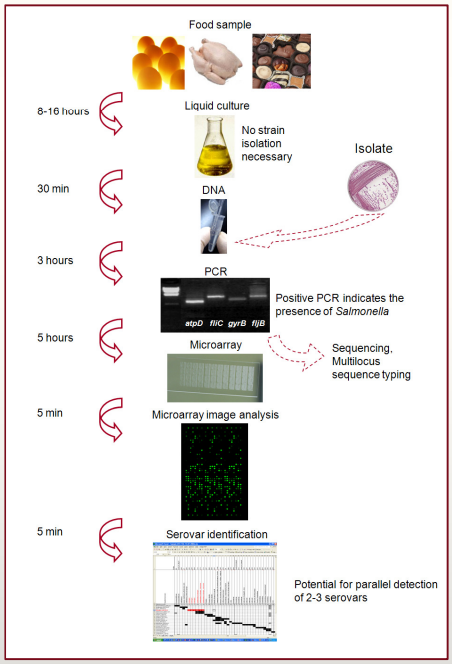

Figure 2: Microarray-based *Salmonella* serotyping

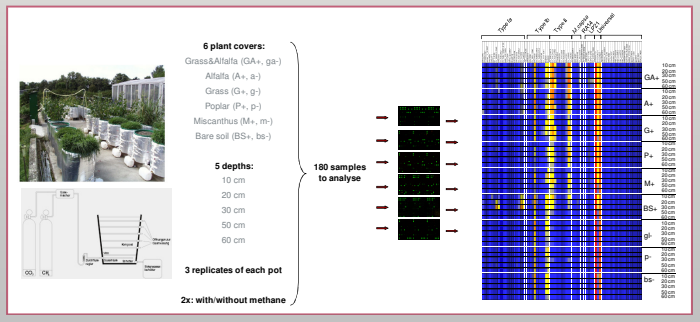

Figure 3: Methanotroph microarray – landfill study

METHANOTROPH MICROARRAY

Methanotrophs are a unique group of bacteria which use methane as sole source for carbon and energy. This taxonomically well defined group of bacteria plays a very important role in mitigating the greenhouse effect.

A microarray targeting the particulate methane monooxygenase (*pmoA*) and ammonia monooxygenase (*amoA*) genes was developed for the detection and quantification of methanotrophs, aerobic ammonia oxidizing bacteria and functionally related bacteria. This microarray was applied for high-throughput analysis of the methanotroph diversity in lysimeters simulating landfill sites with different plant covers.