OMICS Group Conferences
Accelerating Scientific Discovery

2nd International Conference and Exhibition on
Metabolomics & Systems Biology
April 08-10, 2013 Hilton Chicago/Northbrook, USA

Microarray xeroxing "*copying next generation sequencing chips into next generation microarrays*"

Gunter Roth
University of Freiburg, Germany

DNA microarrays have proven as versatile tools for highly parallel analysis of up to 106 molecular interactions in parallel. Even if the chemical synthesis yield is around 99% per base, this is limiting the maximum probe length. M. Baker (Nature Methods, 2011, vol 8, pp. 457) stated clearly, there is a need for longer DNA with better purity.

"*researchers usually want more oligonucleotides, longer oligonucleotides and lower error rates*."

"*If [the achievable length] was 300 base pairs or even a kilobase, there are a lot of things one could do that one can't do now*."

Protein microarrays are an upcoming technology, with broader applications and higher information values (compared to DNA arrays). Also some assays, like kinase assays, are only possible with proteins. But, due to the chemical complexity of the amino acids, the probe length for proteins is even stronger restricted in synthesis, than for DNA. Prices from several hundred up to e.g. 1,360 € per protein array (ProtoArray 5.0, Invitrogen) are a real showstopper for many applications.

Therefore, there is an urgent need and a large market for microarrays with

A reasonable price

Longer probe lengths

Higher purity

Both, for DNA as well as for proteins

A new way of microarray manufacturing: "*Xeroxing*"

Next Generation Sequencing became a complete new market with a billion dollar volume. Interestingly, all Next Generation Sequencing chips contain genomic DNA and the sequencer vendors proclaim to cover quite soon whole human genomes. Our approach to use well established enzymatic reactions is to generate DNA microarray copies from genomic DNA deposited in a Next Generation Sequencing chip. By changing the enzymatic amplification mix also protein microarray copies can be obtained. Therefore, if a sequencing chip contains a whole genome, each copy will contain a genome, a transcriptome or a proteome, if copied correctly. First proof-of-concepts are shown.

guenter.roth@imtek.de