

Dr. Heike Goehler

Team Leader Protein Biochips

Protagen AG

www.protagen.de

Abstract

“From Chip to Bead”

Heike Goehler, Jessica Schwermann, Patricia Pews, Verena Trappe, Klaus Marquardt, Axel Kowald, Daniel Chamrad, Angelika Lueking and Peter Schulz-Knappe

To develop biomarkers with diagnostic and prognostic value for cancer and autoimmune diseases the UNlarray platform was employed. This technology platform combines the expression of complex, tissue-specific human cDNA libraries and the systematic arrangement of the heterologous proteins on planar arrays. Serum samples of patients suffering from Multiple Sclerosis and Prostate Cancer as well as appropriate age- and gender-matched control samples were analysed using these protein arrays. The individual autoimmune profiles were established and candidate markers were selected by their capacity to discriminate diseased and healthy individuals. However, for each investigated disease we have identified several hundred of putative markers indicating a huge biological variance within human autoimmune profiles. To overcome this system-intrinsic difficulty the number of serum samples has to be increased to allow a more in depth statistical analysis and a method with an enlarged dynamic detection range has to be applied to allow the reliable detection of small but significant variations in the autoimmune profile of single serum samples.

Recently we established bead-based arrays to detect autoantibodies in serum samples. As classical microarrays bead-based arrays allow multiplex analyses since up to 500 color-coded microspheres incubated with a selected serum sample can be simultaneously analysed using the Luminex FlexMap3D device. Thereby, each antigen is covalently linked to distinct color-coded microspheres and a pooled bead set is used for serum sample analysis.

To compare the performance of bead-based arrays and microarrays we set up a panel of experiments using the same proteins and serum samples on both platforms. Thereby, 80 % of the antigen/autoantibody interactions were found with both methods indicating that microarray and bead-array based analysis led to valid but not fully identical results. Microarrays were superior in terms of the number of applied antigens per analysis. While more than 3.000 antigens can be placed on a microarray slide bead-based arrays allow the usage of only 500 analytes per run. In contrast, the dynamic detection range of bead-based arrays was found to be two decades increased compared to microarrays.

To select the most promising markers from our already available collection we will use bead-based arrays due to the higher dynamic range of the method. Thus, both tested array technologies have different strengths and the combination of both will improve the discovery of biomarkers with diagnostic and prognostic value.

Biography

Dr. Heike Göhler studied Biology and Microbiology at the Friedrich-Alexander Universitaet, Erlangen-Nuernberg and obtained a PhD in biochemistry from the Freie Universitaet Berlin working both on the identification of human protein interaction networks and on the aggregation of yeast prions. These research projects were located at the Max-Planck-Institute for Molecular Genetics and the Max-Delbrueck-Center for Molecular Medicine, where Dr. Göhler continued her work as a postdoctoral fellow. Thereafter she worked as a group leader at the Medical Proteom Center, University Bochum on alterations of the autoimmune profile during neurological diseases. Since 2009 she has been team leader at the Protagon AG, Dortmund, being responsible for the discovery of biomarkers for Multiple Sclerosis.