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Real High-Throughput glycoanalysis: Utilizing a High-Performance Analysis-System based on xCGE-LIF

Tycomics is a rapidly emerging field that can be viewed as a complement to other "omics" approaches including proteomics and genomics. Hence, there is a dramatic dynamic increase in the demand for sophisticated databases and analytical tools in glycobiology respectively, glycobiotechnology.

Here, the development of a innovative glycoanalysis system (method, software and database) and its application to different fields with respect to sample preparation, separation and data analysis is presented. First, an optimized modular sample preparation method and a workflow are presented with respect to performance and feasibility regarding high-throughput. Second, with up to 96 capillaries in parallel, the fully automated separation with an impressive sensitivity is shown to result in massive reduction of the effective separation time per sample. Third, automated data analysis with a newly developed modular software-tool for data-processing and-analysis, interfacing a corresponding oligosaccharide-database is demonstrated. Using this high-performance glycoanalysis system, the generated "normalized" electropherograms of glycomoieties ("fingerprints") can be evaluated on three stages: (1) simple" qualitative and quantitative pattern comparison ("fingerprint"-analysis), (2) identification of compounds in complex mixtures via database matching ("glycoprofiling") and (3) extended structural analysis using exoglycosidase sequencing in combination with xCGE-LIF based glycoprofiling. Applicability of the system is demonstrated for different types of glycosamples such as the "glycome" of single (recombinant) glycoproteins with respect to biopharmaceuticals and vaccines or of human milk, respectively of whole human blood serum.

In summary: this novel modular high-performance glycoanalysis system allows fully automated, highly sensitive, instrument-, lab- and operator-independent "real" high-throughput glycoanalysis.

Biography

U. Reichl has studied biology and completed his Ph.D. in chemical engineering at the University of Stuttgart (Germany) in 1991. He is heading the Bioprocess Engineering Department as a director of the Max Planck Institute for Dynamics of Complex Technical Systems in Magdeburg and he is a Scientific Member of the Max Planck Society. He has published more than 100 peer-reviewed papers on animal cell culture, vaccine production, downstream processing of biologicals, and mathematical modeling in bioprocess engineering.

E. Rapp has studied chemistry and completed his Ph.D. in analytical chemistry at the University of Tübingen (Germany) in 2001. He is senior scientist, heading the Bio/Process Analytics at the Max Planck Institute for Dynamics of Complex Technical Systems in Magdeburg. He has published more than 40 peer-reviewed papers on fundamentals and development of miniaturized separation techniques, their hyphenation with NMR spectroscopy and mass spectrometry and their application to animal cell culture based production of vaccines, recombinant (glyco)proteins and other biologicals.

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