Analytical Nanotechnologies in Proteomics

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10 years ago the combination of two technologies – genomic that allows to sequence genes of biosystems and mass-spectrometry analysis - converted the protein biochemistry into the Proteomics. This combination made possible to analyze hundreds and thousands of proteins at the same time by one scientist as opposed to the possibility to analyze such amount of proteins by tens or hundreds of scientists.

Since that time Proteomics has developed rapidly, but its current achievements are worse then those of Genomics. Why? It happens because there is no technology in Proteomics that could be analogous to the genomics' polymerase chain reaction (PCR) that allows to multiply single molecules of nucleic acid. Due to PCR there is no detection limit in genomics.

An opposite situation dominates in Proteomics. The detection limit of existing high through output technologies does not exceed 10^{-12} M, while the most part of protein molecules in tissue and biological fluid is lower of this limit. If blood plasma is concerned we detect not more than 10-20% of all types of proteins existing here. There is the other difficulty. It is the necessity to detect low abundant proteins in biological material at the presence of high abundant proteins. The difference in the concentrations for some proteins equals 10^{10} which is dynamic concentration barrier (DCB). To overcome both barriers it is supposed to use analytical nanodetectors that do not measure concentration of proteins but count single protein molecules and their complexes (atomic-force, electron scanning microscopes, nanowire and nanopore detectors and others). Molecular counting technology in combination with the technology that allows to fish up and concentrate protein molecules on the surface consisting of high specific immobilized antybodies, aptamers and other ligates are used. At the same time reversible interaction reaction of antibody/aptamer with antigen must be converted into the irreversible.

Theoretical calculations show that the combination of this two technologies allows to create new technologies having detection limit being close to reverse Avogadro number (10^{-20} – 10^{-21} M)