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Identifying and quantifying 10,000 proteins in 10 hours – feasible, possible, done?

Roman Zubarev
Karolinska Institutet, Sweden

It took proteomics more than 15 years from its inception to reach the bottom of the proteome – that is, to observe whole or almost whole expressed proteome (≥10,000 proteins). The very few reports on this achievement published so far have exercised almost no limitation on the amount of used material, labor or instrumental cost. Despite the recent advances in mass spectrometric instrumentation, it is clear that routine application of the whole-proteome analysis will require development of instruments and methods going far beyond the current state of the art. In particular, the very large dynamic range of cellular proteome – some seven orders of magnitude – exceeds by >100 times the dynamic range of the most advanced proteomics instruments. Traditionally, dealing with this problem requires extensive separation of proteins and peptides before the LC/MS analysis, which is one of the limitations of the whole proteomics as it is currently practiced. The task is therefore to reduce the pre-LC/MS separation to a bare minimum. In principle, a well-designed LC/MS experiment can analyze over 1000 unique proteins per hour of LC gradient. Therefore, aiming at detecting and quantifying 10,000 proteins in 10 h is a realistic (although at this moment not yet reached) goal.

In our laboratory, we pursue three parallel approaches, each of which should in principle be capable of reaching the above goal. These approaches will be described; their relative advantages will be discussed, and the most recent results presented.

Biography

Roman Zubarev has 25 years of experience in biological mass spectrometry. He has obtained his Ph.D from the Uppsala University (Sweden), and pursued postdoctoral studies in Cornell, where he has co-discovered electron capture dissociation. He has published close to 200 papers in peer-reviewed journals and monographies and is an Executive Committee member (Treasurer) of the Human Proteome Organization (HUPO).

Roman.Zubarev@ki.se