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EDITORIAL

Clinical Proteomics in Mexico: where do we stand?

Proteómica clínica en México: ¿dónde nos encontramos?

Proteomics is a burgeoning and interesting field. In the last few years, there have been increasing application developments. Of special interest is the potential for the discovery of new disease biomarkers. From 2001 to date, more than 800 publications for clinical proteomics can be found in PubMed, and nearly half of them have been issued in the last four years. A disheartening fact is that none of those publications comes from Mexico, where a vibrant proteomics community is present. Most of the groups are working on plant biology, nitrogen fixation, biotechnology, and even method development. That is the case of Herrera et al., who are working on phosphopeptide enrichment.¹ The variety of topics currently developed in Mexico are analyzed in the review of Encarnación-Guevara,² where it becomes evident that several groups have started to explore the clinical applications of proteomics in Mexico recently. Interestingly, some of those efforts are beginning to generate very exciting results. Regarding biotechnology, for example, Camacho-Millán et al. have studied local toxin isolates to find ways to control local pests; during their toxin characterization, they found a Cry toxin with the potential application as a vaccine adjuvant.³ Defects in metabolic pathways are other examples where proteomics has great potential. Salvador-Severo et al. have evaluated how some changes in mitochondrial proteins, particularly in the oxidative phosphorylation pathway, contribute to metabolic diseases.⁴

One of the most exciting developments in the last few years is the MALDI imaging. With this approach, results available for most of the pathology departments with top-notch proteomic studies can be correlated. For example, serial sections can be analyzed by a pathologist and another section can be analyzed by MALDI to identify the main peptides, metabolites or even drug or drug derivatives in the tissue. In this sense, Manzanares-Meza et al. contribution is a comprehensive review of several of the most interesting results using these technologies.⁵

An ultimate goal of the clinical proteomics studies is the identification of new biomarkers. Nevertheless, this is a long and convoluted process. Quezada et al. have evaluated some of the difficulties that have given examples of few biomarkers that have found their way to the clinic.⁶ One of the many complications in biomarker development starts with the availability of biological samples, the starting material for any study. Therefore, systematized ways need to be developed to obtain, handle and store the samples if we are to succeed in the field. Aguirre-Guillén et al. discuss some of the problems as well as the opportunities to improve this topic, and how the combination of omics technologies with good sample availability could improve diagnosis in different diseases like leukemia in a developing country such as Mexico.⁷ Reyes-Vivas et al. used serum from patients with Cow-Milk Allergies to identify some of the more immunogenic proteins in milk by MALDI-TOF fingerprinting. Carrying out a similar approach, they are also studying child cataract to describe changes in protein content or post-translational modifications during the pathological development.⁸

Several signaling pathways are altered in cancer, and those changes contribute to the survival of cancer cells. Therefore, many studies are developed to understand the molecular mechanisms that accompany some of those changes. Guzmán-Ortiz et al. evaluate how the proteome is modified during cell adaptation to chemotherapy in a cell line model, with the idea to understand basic concepts of the chemoresistance development and to identify new ways to attack the problem and resensitize the cancerous cells.⁹

In summary, this special issue of the *Boletín Médico del Hospital Infantil de México* reveals the initial but exciting results about clinical proteomics in Mexico. Clearly, a vibrant future is ahead with the formidable task of understanding the complexity of the proteome and the strong implications in the health/disease balance.

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