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Perspective

Proteomics in Exercise and Sports Science: Still a Useful Tool

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Perspective

Exercise is a non-pharmacological agent well known to prevent and treat several diseases, especially those associated with physical inactivity. Proteome modulation in response to exercise is a cornerstone of this process since the modulation of metabolic enzymes and structural proteins are key events in phenotype modification, observed during cardiovascular improvement and skeletal muscle hypertrophy in response to exercise training [1]. In this sense, the analysis of protein expression profile upon diverse conditions in health and disease led to countless progress in the field of health research. Despite being widely performed for a long time, this type of analysis was coined as "proteomics" in the early 90´s.

The advance of proteomic tools coupled with mass spectrometry technology and the popularization of bioinformatic tools used in data analysis were responsible to complement the significant amount of genomic and transcriptomic data generated in the past years, giving us a wider view of the molecular mechanisms involved in complex pathologies such as metabolic disorders and cardiovascular diseases [2]. It's fair to say that proteomics and, more recently, metabolomics have integrated the OMICs tools leading us to a more profound understanding of these diseases. In this context, several molecular players and cell pathways were included in the pathogenesis of obesity, diabetes and hypertension [3].

The field of exercise and sports science have also benefited with the OMICs scope, especially with proteomics. Due to technical limitations, a reduced number of these studies were conducted in human samples, being limited to skeletal muscle and body fluids. In most cases, rodents are used, however, equines, swine's, fish, and other animal samples may be used as well [4-6]. Moreover, the proteomic analysis may also be conducted in cell cultures using an in vitro exercise model to better understand the molecular process involved in muscle contraction. One particular advance of this method is the analysis of skeletal muscle secretome, to date, one of the hot topics in exercising research [7].

Retrospectively, classic in gel (e.g. 2-DE) proteomic analysis was mainly used to investigate the effect of exercise stimuli in skeletal and cardiac muscle from animal models [8,9]. Furthermore, the development of fluorescent gel staining (e.g. DIGE) enhanced significantly the accuracy and sensitivity of proteomic data, being also used in many studies in this filed, such as the effect of high intensive exercise training (HIT) over the skeletal muscle proteome [10]. Moreover, exercise dose-response in proteome modulation was, and, still is, one of the focus of exercise and sports science in proteomics [11].

More recently, trough gel-free techniques, such as the wide variations of liquid chromatography and MS analysis, thousands of proteins were screened, showing several proteins to be altered by different training intensities and exercise regimen. As a fact, the progression of in-gel techniques to gel-free methods has significantly enhanced the number of identified proteins in these studies [12]. In addition, system biology tools are being successfully used to complement the proteomic data and assess the complex protein-to-protein interactions and their association network within an exercise stimuli context [13].

Biomarkers identification is still a promising issue to be continuously explored in exercise and health research, especially in non-invasive samples, such as urine and saliva [14]. However, despite its clinical significance [15], alterations in salivary proteome in response to exercise is still poorly explored, Thus, if well explored, targeting urinary and saliva biomarkers may further contribute to the field of exercise physiology to assess exercise dose-responses, training intensity, and overtraining status. The parameters may contribute significantly to the entire process of training planning and its execution [16].

At least, as mentioned before, muscle secretome is one of the actual exciting topics in exercise and sports proteomics. The release of extracellular micro vesicles, growth factors, and myokines trough muscle contraction in response to exercise highlights the skeletal muscle as an endocrine organ, mediating several biologic events such as inflammation regulation, muscle hypertrophy, and cell metabolism [17]. Furthermore, secretome profiling is fundamental to

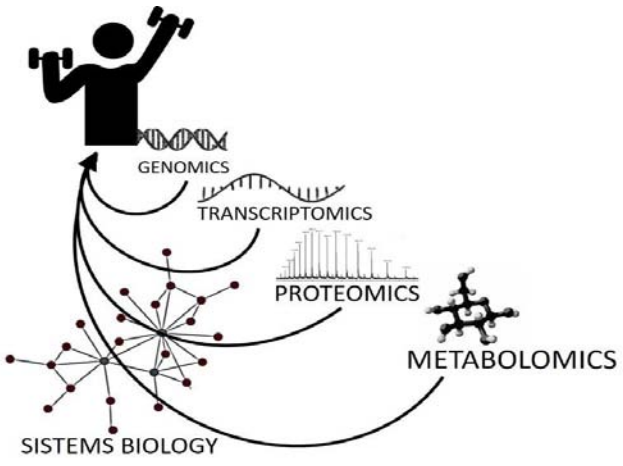

Figure 1: OMICs dynamics in exercise and sports science.

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identify novel biomarkers associated with tissue injury, and muscle remodeling in response to training. Considering its biologic potential, this is still an open gap to be widely explored by proteomic tools.

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