



EDITORIAL

Sportomics: Futbol Club Barcelona's approach to personalized injury prevention

Sportomics combines “omics” sciences with classic clinical laboratory analyses to mimic the real challenges and conditions faced during sports training and competition.¹ It relies on analytical methods with high processing power to analyze large volumes of data and is a promising field of investigation in translational sports medicine. Sportomics comprehensively relies on the “athlete’s biological passport” for the systematic study of sport-induced responses and adaptations at any level (genome, transcriptome, proteome, metabolome, etc.).² The use of omics data provides a comprehensive understanding of the biological processes and systems underlying athletic performance and injury risk, to finally identify novel intervention targets.

Fútbol Club Barcelona (FC Barcelona) has used Sportomics to understand exercise-induced metabolic alterations and the relationship with acute and chronic fatigue of its players. This helped to study the association between internal and external load indicators during training or game sessions and estimate injury risk.

We have over five years of experience studying our players' genome, epigenome, transcriptome, proteome, and metabolome through different scenarios and sports. For instance, we contributed to various studies about **genomics**, uncovering previously undescribed genetic predictors of tendinopathy in elite team sports athletes. Our research identified specific single nucleotide polymorphisms (SNPs) as genetic markers, including rs11154027, rs4362400, and rs10263021.³ Also, we found a trend for the association of higher risk of muscle injury with the XX genotype in professional footballers presenting the R577X polymorphism (rs1815739) in the gene encoding α -actinin-3 (ACTN3). Moreover, in the same players, there was a significant effect of this genetic variant for the time needed to return to play.⁴ Recently, these results have been replicated in 315 top-level professional football players from the Spanish football first division (i.e., LaLiga).⁵ Finally, we found a significant association between the rs13946 C/C polymorphism in the COL5A1 gene and anterior cruciate ligament (ACL) injury in women footballers and not in male footballers.⁶

Regarding **transcriptomics**, we studied the effects of external load on elite athletes during a handball match and throughout the season 2021–22, and we identified deregulation in the immune system, mitochondrial functions, and various metabolic pathways during the match. Additionally, it establishes correlations between GPS external load variables and pathways associated with amino acids, inflammation, and oxidative environment. These findings offer insights into athletes' immediate and chronic responses to physical effort.⁷

We also performed **proteomics** studies in blood and saliva and are currently evaluating how the plasma proteome responds to sports stress. This way, we aim to identify proteins that can be used as biomarkers for the non-invasive detection of overreaching fatigue and the risk of suffering an injury during the season. We are now using saliva samples to detect proteomic profiles in our elite female football players to have a non-invasive method. Moreover, identifying different molecular profiles through salivary exosome biomarkers can provide valuable insights into elite female football players phenotypes.

Regarding **metabolomics**, we studied the relationship between internal and external load indicators during a football season. Results showed that the adaptation to external load in footballers drives changes in the steroid hormone biosynthesis and metabolism, as well as in the tyrosine and tryptophan metabolic pathways.⁸ Furthermore, overrepresentation analysis and multivariate analysis of metabolic data showed significant differences in the effect of training on the metabolic profiles of men's and women's teams. Our results demonstrate that the development of metabolic adaptation models in professional football players can benefit from the separate analysis of men's and women's teams, providing a more accurate insight into how adaptation to external load is related to changes in metabolic phenotypes.⁹

Our original goal was to identify biomarkers across the various omics domains individually. However, there was a pivotal shift in our approach when we began integrating

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diverse omics datasets to enhance our ability to predict injury risk. We developed an injury prediction model that leverages data sourced from global positioning systems (GPS) alongside multi-omics data encompassing genomics and metabolomics from elite female footballers.¹⁰ Incorporating nonlinear cumulative load assessments alongside multi-omic data has been instrumental in delineating distinct injury risk profiles. This innovative approach enhances our understanding of the intricate interplay between physiological markers and performance metrics and offers valuable insights for personalized injury prevention strategies.

In our goal to personalize physical activities, workload management, injury risk prediction, and performance enhancement for athletes incorporating multimodal data, we recognize the importance of broadening the scope of data integration beyond omics domains. Specifically, when analyzing data from female athletes, it becomes imperative to incorporate additional factors such as menstrual cycle dynamics and hormonal fluctuations.¹¹ The menstrual cycle profoundly influences various physiological processes, including metabolism, immune function, and musculoskeletal health, that are linked to injury susceptibility. Therefore, incorporating menstrual cycle data into our predictive models can provide invaluable insights into the dynamic interplay between hormonal fluctuations and injury risk profiles. Also, considering the impact of hormones, such as estrogen and progesterone, on ligament laxity, muscle strength, and neuromuscular control is paramount for a comprehensive understanding of injury predisposition in female athletes. By integrating these datasets with omics datasets, we can elucidate the intricate interactions shaping various aspects of an athlete's profile with heightened precision, encompassing diverse dimensions of sports outcomes.

We firmly believe that omics data hold immense potential in identifying internal load biomarkers. By considering hormonal status, biomechanics, cognitive mood status, etc., together with genomic, transcriptomic, proteomic, and metabolomic profiles of the players, the medical teams, coaches, and athletes can derive predictive models capable of stratifying players according to varying risks. Adopting such a comprehensive approach promises highly accurate and personalized interventions in training, competition, recovery, and rehabilitation programs.

Future research endeavors must delve deeper into unravelling the roles of identified genes, proteins, metabolites, and other biological variables (e.g., stress and diet), considering the inherent differences in sex biology that must lead to distinct modeling and studies for male and female athletes.

In summary, our experience underscores the critical need for a nuanced understanding of athletes' physiological makeup and its implications for injury management and performance optimization in professional sports settings. Through continued exploration and integration of diverse biological variables, we can strive towards more refined interventions tailored to the biological specificities of each

athlete, ultimately fostering their success and well-being in sports.

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