SUMMARY

MSc Eng. Paulina Małkowska

Expression of selected inflammatory response-related genes and proteins in response to a progressive exercise test to exhaustion in professional athletes and non-exercisers

Physical activity constitutes a key factor modulating the body's metabolic and immunological balance, primarily by generating controlled physiological stress that triggers a cascade of signals responsible for metabolic remodeling, tissue adaptation, and regulation of the inflammatory response. It is the acute exercise-induced stress that affects the levels of circulating cytokines and the expression of genes involved in stress-response mechanisms, inflammatory processes, and energy homeostasis. Regular training consolidates these adaptive pathways, enabling the body to respond to physical load more efficiently and with greater regulatory precision. Among the markers particularly important for assessing the dynamics of exercise-induced stress are pro- and anti-inflammatory cytokines (TNF-α, IL-4), metabolic proteins functioning as cellular stress sensors (FGF21, GDF15), as well as their receptors. In addition, the evaluation of the leukocyte response – including total leukocyte, lymphocyte, and neutrophil counts – is a crucial component of analyzing the immunological reaction to intense physical effort and the resulting physiological stress.

The aim of this study was to provide a comprehensive characterization of the molecular and immunological response to a progressive exercise test to exhaustion in trained athletes and physically inactive individuals. The analysis included the determination of plasma concentrations of FGF21, GDF15, TNF-α, and IL-4 using ELISA, as well as the assessment of gene expression of these proteins and their receptors (FGFR1, FGFR3, FGFR4, KLB, GFRAL, TNFR1, TNFR2, IL-4R) using quantitative real-time PCR (RT-qPCR). Selected hematological parameters – leukocyte, lymphocyte, and neutrophil counts – were also analyzed as indicators of immune response dynamics. The study involved 15 trained athletes and 15 physically inactive participants, from whom blood samples were collected at six time points: before exercise, immediately after completion, and after 30 minutes, 6 hours, 24 hours, and 48 hours. The exercise protocol consisted of a progressive test to exhaustion, allowing for precise evaluation of aerobic capacity.

The results showed that a single bout of intense exercise does not affect *FGF21* and *GDF15* expression; however, in non-trained individuals, a stronger and faster activation of FGF21 pathway receptors (FGFR3, FGFR4, KLB) was observed, indicating greater stress

sensitivity compared with athletes. The expression profile of *TNF-α* and *TNFR1* in inactive participants confirms a predominance of pro-inflammatory responses, whereas in athletes the absence of changes in inflammatory gene expression reflects the adaptive effects of regular training. At the same time, higher plasma levels of FGF21 and GDF15 in non-trained individuals confirm greater metabolic and mitochondrial strain induced by exercise, while a decrease in TNF-α after 48 hours in athletes indicates more efficient resolution of inflammation. The reduction in IL-4 concentration in non-exercisers suggests a weak anti-inflammatory response in the group without training adaptation.

The findings demonstrate a complex, dynamic response of the body to physical exercise, involving both changes in gene expression and protein levels, which differ between athletes and non-trained individuals. The collected data enhances understanding of the metabolic, inflammatory, and stress-related regulatory mechanisms accompanying physical exertion and identify molecular pathways particularly activated depending on training status. The results may be used to design personalized training programs, monitor physiological adaptation to exercise, and identify biomarkers useful for assessing performance and recovery.