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Microbiome features associated with performance in an athletic cohort and nonathletic controls

Abstract:
We investigated whether gut microbiome characteristics predict performance capacity and influence acute biomarker responses across different exercise modalities. One male collegiate cohort, consisting of endurance and strength athletes, as well as physically active controls, completed maximal anaerobic Wingate and aerobic Bruce treadmill tests. Metagenomic (shotgun) sequencing was used to profile stool at baseline and after exercise, and serum panels were used to capture inflammatory and metabolic markers. At baseline, alpha and beta diversity did not differ between groups, however approximately one-third of the detected species were unique to a group. Longitudinal analyses revealed an increase in Alistipes communis specific to strength after the Wingate test and identified 88 species that differentiated groups during the Bruce test. Correlation networks linked performance to taxa. Bifidobacterium longum and B. adolescentis were strongly associated with $VO_{2\mathrm{max}}$ and power outputs. While most circulating markers showed similar time courses in all groups, SPARC and adiponectin varied by modality and training background. After the Wingate test, strength-trained athletes showed distinct associations between their microbiome and biomarkers. This group also exhibited baseline enrichment of Clostridium phoceensis and Catenibacterium, which was associated with a reduced Bruce response. These findings suggest associations between specific gut taxa and aerobic capacity or power. Training background may shape microbiome to host coupling during recovery in a modality-dependent manner.

Keywords: gut microbiome, VO2max, Wingate test, Bruce test, biomarkers, recovery

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Biography: Dr Kinga Humińska-Lisowska is Head of the Genetics in Sports Laboratory and Laboratory Centre Coordinator at the Gdańsk University of Physical Education and Sport. Her work spans human and sport genetics, with current projects on exercise-induced muscle damage, inflammation, and the impact of physical activity on the gut microbiome. She investigates molecular bases of training adaptation using whole-metagenome and multi-omics approaches, and translates advanced genetic analyses into diagnostics for personalized medicine. She leads cross-sector collaborations and has published widely with recognized awards for young scientists.

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