

Identification of microbial signatures and functional attributes of athlete's gut microbiome

To determine the microbial signature and functional composition of the athletes, we will perform the gut microbiome comparison of athletes and sedentary control using shotgun metagenomic analysis. The fecal samples will be suspended in 150 µl TE buffer which will be directly processed for DNA isolation using E.Z.N.A.® Stool DNA Kit. The quality of DNA will be assessed using Nanodrop/Qubit and sequencing, followed by library preparation and sequencing by shot-gun method using Illumina platforms. The analysis will involve quality control using fastqc and multiqc, followed by trimming using trimmomatic. The next step would be the host read removal using Bowtie2 followed by removing all unaligned reads. The aligned reads will be subsequently used for assembly using Metaspades and orf prediction using Metagenemark. Simultaneously, the taxonomy will be assigned to the aligned reads against the nr database of Kaiju program. This will be followed by generating the PCA plots and different diversity indices such as Shannon, Chao1 for Alpha and Unweighted and weighted UniFrac for beta diversity. Binning will be performed using metaBAT2 and maxBin in the package metaWRAP using assembled contigs. CheckM will be used for checking the contaminations in the assembled bins. Bins with completeness more than 70% and contamination less than 5% will be included in comparative analysis. Further, the microbiome dataset of athletes and sedentary control will be compared to determine the microbial and related functional signatures.