The Osteoarthritic Hip Joint Seems to Have a Distinct Microbiome When Compared to Nonarthritic Controls

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Emerging research suggests that the joint microbiome may influence the pathogenesis of hip osteoarthritis. We aimed to explore and compare the microbiome profiles in osteoarthritic hip joints versus non-arthritic controls to uncover potential microbial contributions to the disease.

METHODS:

A prospective-cohort study included 40 patients undergoing hip arthroplasty—20 with osteoarthritis and 20 with hip fractures (i.e., non-arthritic hips) as controls. A total of 120 samples from synovial fluid (SF), femoral head cartilage (C), and acetabular fossa (AF) were collected. Quantitative analysis, including DNA quantification and quality control, were performed using fluorometry (FLUOStar-Optima-Picogreen). This was followed by polymerase-chain-reaction (using Q5-enzyme) to confirm presence of bacterial DNA in the samples, prior to constructing 16S-libraries for sequencing. Seventy-nine samples with adequate DNA amplification underwent Next-Generation Sequencing of the 16sDNA-V3-V4 region amplicons on an Illumina platform. Statistical analyses assessed sequencing data to identify and compare microbial communities between groups, focusing on the detection and quantification of various taxa using non-parametric tests and chi-square tests.

RESULTS:

No significant differences were found in the median relative abundance of taxa at the genus level between groups (0 [IQR:0-64] for osteoarthritis vs. 11 [IQR:0-258] for fractures; p=0.3). Predominant genera included Sphingomonas (23.4%), Corynebacterium (16.6%), Micrococcus (15.3%), Chloroplast (8.1%), and Massilia (6.7%). However, the 'osteoarthritis-group' exhibited more variety of taxa (n=26) as compared to the 'fracture-group' (n=16). In osteoarthritic samples, genera such as Bradyrhizobium (10.6%), Akkermansia (8%), and Faecalibacterium (5.3%) were identified, while hip fracture samples revealed Cutibacterium (13.2%), Kocuria (5.6%), and Clostridium (5.4%). Notably, the location of the sample significantly affected microbial abundance, with the highest median relative abundance being found in AF samples (442 [IQR:6,2984]), as compared to C (0 [IQR:0,16]) and SF (19 [IQR:0,359]; p<0.01) samples.

DISCUSSION AND CONCLUSION:

Distinct microbial profiles in osteoarthritic hips compared to non-arthritic controls may suggest a potential microbial influence on arthritis development and prosthetic joint infections. The significant diversity of bacterial taxa in osteoarthritic joints, despite a similar abundance level to controls, indicates a need for further investigation into their role in the pathogenesis of and management of arthritis.

