Genetic study explores the microbiome of hip and knee osteoarthritis

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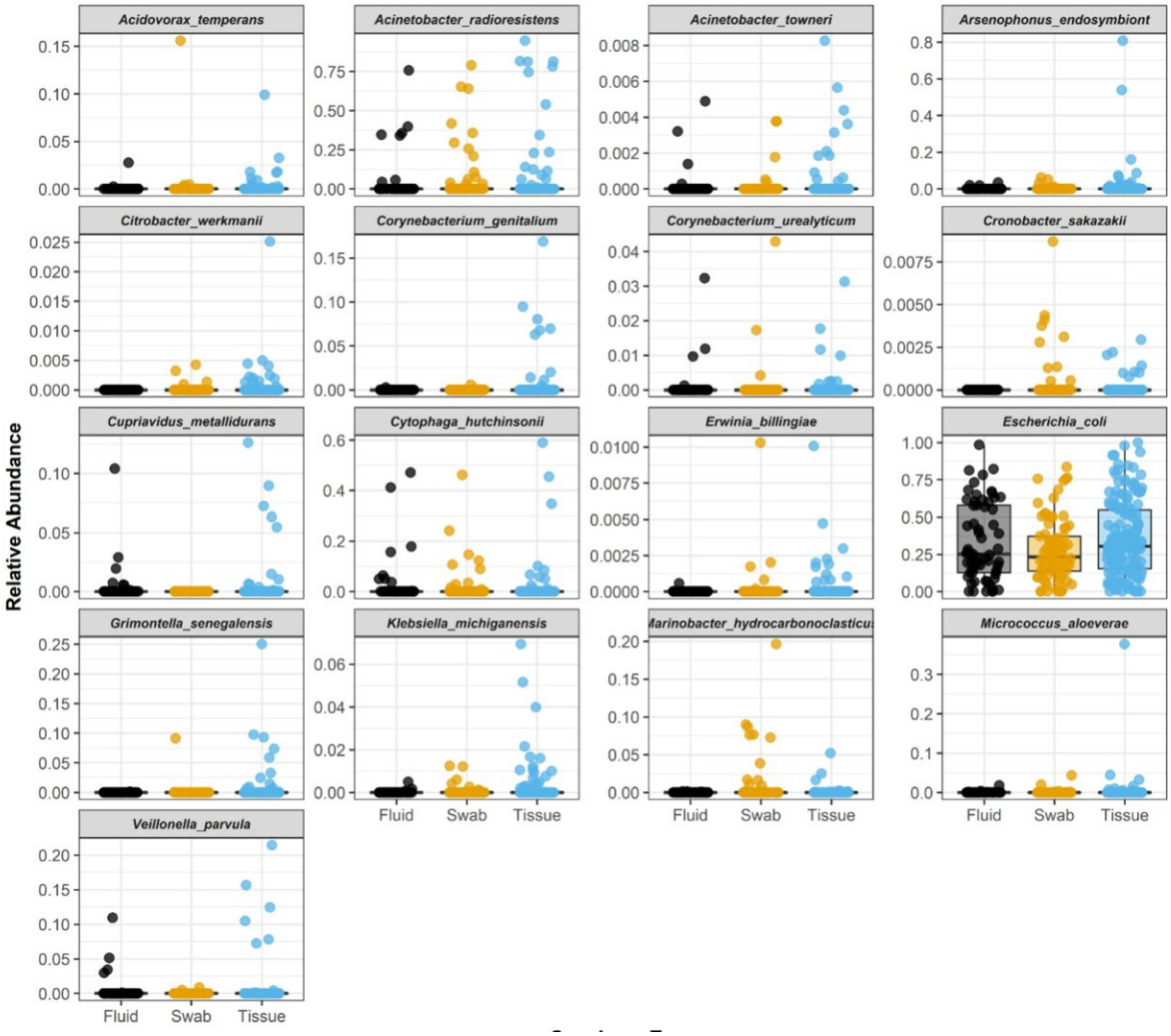

Boxplots show relative abundance distribution of species indicated by ANCOM procedure to be non-randomly distributed across specimen types. Credit: *Journal of Bone and Joint Surgery* (2023). DOI: 10.2106/JBJS.23.00107

Next-generation DNA sequencing (NGS) techniques show the presence of bacterial DNA in surgical specimens of hip and knee arthritis, from patients undergoing first-time total joint arthroplasty, reports a study in the *Journal of Bone and Joint Surgery*.

The findings "add to an increasing body of evidence indicating that native joints harbor microbes, as part of a microbiome, although the clinical relevance of these findings and the mechanism of microbial colonization are still unknown," according to the new research by Javad Parvizi, MD, FRCS, of Rothman Orthopaedic Institute at Thomas Jefferson University and colleagues.

Three arthroplasty specimen types show similar bacterial composition

In recent years, there has been extensive research examining the effect of microbiomes (i.e., the types and diversity of bacteria present in different body sites) on human health and disease. Powerful NGS techniques enable researchers to find evidence of bacterial DNA that would otherwise go undetected. Infection is a major cause of joint failure in patients undergoing total joint arthroplasty, even though no specific bacterial cause is identified in many cases.

In the past, it was thought that the native hip and knee joints, as well as other body areas unaffected by surgery or other potential causes of contamination, were sterile. However, recent microbiome studies have found bacterial DNA in many "body sites previously assumed to be sterile," for example, in a developing fetus, the breast, and the shoulder joint.

In the new study, Dr. Parvizi and colleagues obtained intraoperative samples of synovial fluid, deep-tissue specimens, and intramedullary swabs from the operative hip or knee from 117 patients undergoing first-time hip or knee arthroplasty. Samples were collected with strict attention to sterile technique in order to minimize the risk of bacterial contamination.

The researchers then utilized a commercial NGS platform to analyze the types and diversity of the microbial DNA in each specimen. Analysis of more than 800,000 DNA "reads" led to the identification of 361 different species of bacteria. Overall, bacterial DNA was found in specimens from 113 of 117 patients with hip or knee osteoarthritis.

Microbiome varies by hospital and recent steroid injection

The five most frequent types of bacteria were Escherichia, Cutibacterium, Staphylococcus, Acinetobacter, and Pseudomonas—all common infection-causing microbes. The findings were generally similar for the three sample types, although the intramedullary swabs showed slightly higher bacterial diversity than synovial fluid or deep-tissue specimens.

Microbiome findings were found to be unrelated to a wide range of patient-related factors, including age, sex, race, and comorbidity. However, the hospital at which the arthroplasty was performed was shown to be a significant factor, explaining 18.5% of the variation in one measure of bacterial diversity. This finding might reflect differences in the types of bacteria found in hospital environments or possible intraoperative contamination.

The only other significant factor was history of corticosteroid injections,

a common treatment for hip and knee osteoarthritis. The results showed "differential abundances" of bacteria in patients with corticosteroid injections in the past six months, again raising the possibility of contamination. However, the researchers note, "the most common species observed in this study were not among the most common in previous skin microbiome studies, suggesting that the microbial profiles detected are not likely explained solely by skin contamination."

The study adds to a growing body of evidence that native joints, traditionally assumed to be sterile and bacteria-free, are somehow exposed to microbes. The researchers emphasize the need for further studies to assess the relationship between the hospital where patients are treated and the bacteria detected in "closed microbiome environments," such as the knee and hip joints.

Dr. Parvizi and co-authors conclude, "These findings contribute to establishing the baseline microbial signal and identifying contributing variables in the osteoarthritic joint, which will be valuable as a comparator in the contexts of infection and long-term arthroplasty success."

More information: Karan Goswami et al, The Microbiome of Osteoarthritic Hip and Knee Joints, *Journal of Bone and Joint Surgery* (2023). DOI: 10.2106/JBJS.22.00594

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