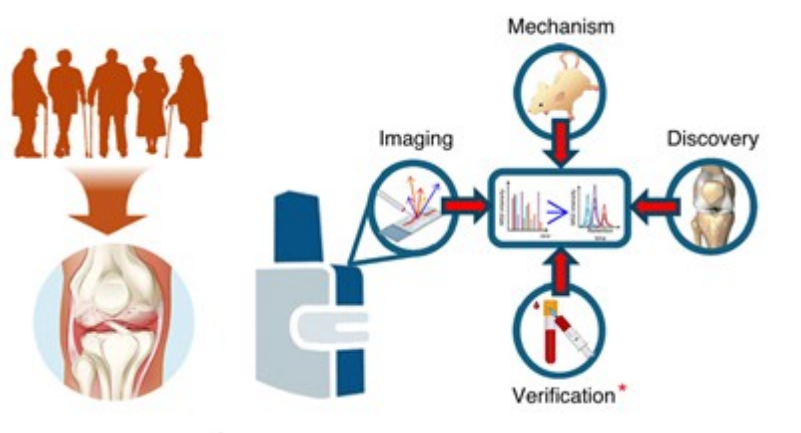
New Molecular Maps of Bone Could Transform Early Osteoarthritis Detection

Researchers used advanced imaging to uncover early molecular changes in bone that may enable earlier diagnosis of osteoarthritis



Spatial MALDI-MSI of osteoarthritic knee joints reveals bone-derived protein signatures linked to disease progression. These candidates will be validated in larger patient cohorts and OA mouse models for biomarker discovery.

CHENGDU, SICHUAN, CHINA, February 10, 2026 /EINPresswire.com/ -- Osteoarthritis often goes undetected until cartilage damage is advanced, limiting treatment options. A new study shows that molecular changes in subchondral bone occur earlier and can signal disease progression before cartilage loss. Using spatial mass spectrometry imaging and synovial fluid proteomics, researchers identified bone-derived protein signatures beneath intact cartilage that were also detectable in joint fluid. These findings point to promising, less invasive biomarkers for earlier diagnosis and improved monitoring of osteoarthritis progression.

Osteoarthritis (OA) affects more than 500 million people worldwide and is a leading cause of pain, disability, and reduced quality of life. Yet by the time OA is diagnosed clinically, often through pain symptoms and radiographic cartilage loss, the disease has already progressed significantly. This delay limits opportunities for early intervention, as cartilage damage is largely irreversible. Scientists have long suspected that changes beneath the cartilage, particularly in the underlying subchondral bone, may occur earlier in disease development, but the molecular nature of these changes has remained poorly understood.

In this new study, researchers set out to determine whether molecular remodeling in bone could provide earlier and more reliable signals of OA progression. Using a combination of spatial matrix-assisted laser desorption/ionization mass spectrometry imaging (MALDI MSI) and synovial fluid proteomics, the team examined human knee joint tissues from patients with end-stage OA and compared them with non-OA controls. This approach allowed the researchers to visualize

the precise location of hundreds of proteins directly within bone and cartilage, rather than averaging signals across whole tissues. Their findings were made available online on January 26, 2026, in Volume 14 of the journal Bone Research.

The research was led by Professor Birgit Schilling, Managing Director of the Proteomics and Metabolomics Core at the Buck Institute for Research on Aging, with contributions from Dr. Charles A. Schurman, postdoctoral research scientist, and Dr. Joanna Bons, staff scientist at the institute.

By enzymatically targeting extracellular matrix proteins and mapping them at high spatial resolution, the researchers were able to clearly distinguish cartilage from bone based on their molecular fingerprints. Importantly, they observed that subchondral bone beneath damaged cartilage showed strong upregulation of specific collagen fragments and post-translational modifications associated with tissue stiffening and remodeling. Surprisingly, similar molecular signatures were also detected in areas of bone underlying cartilage that still appeared structurally intact, suggesting that disease-related bone changes begin earlier than previously recognized.

“Our goal was to move beyond what we can see on X-ray or MRI scans and ask what the tissue is telling us at the molecular level,” said Prof. Birgit Schilling. “What stood out was that the bone carried a very clear disease signal, even in regions where cartilage loss was not yet obvious. This suggests that subchondral bone could serve as an early indicator of osteoarthritis progression.”

The study also revealed that many of the bone-derived protein fragments identified by imaging were detectable in synovial fluid, the lubricating fluid of the joint. This finding is particularly significant because synovial fluid can be accessed with minimally invasive procedures. In contrast, several traditional cartilage-associated markers were reduced in OA joint fluid, highlighting bone remodeling—not cartilage breakdown—as a more promising source of early diagnostic biomarkers.

“These results open the door to developing fluid-based tests that reflect what is happening deep within the joint,” explained Dr. Schurman. “If we can track bone-specific molecular changes over time, it may become possible to identify patients at risk earlier and monitor how they respond to therapy.”

Beyond diagnostics, the findings have broader implications for understanding OA as a whole-joint disease rather than a condition driven solely by cartilage wear. The molecular signatures identified in subchondral bone point to altered cellular activity, including changes in osteoblasts, osteoclasts, and osteocytes, which may influence cartilage health through mechanical and biochemical signaling. By integrating spatial imaging with proteomics and future animal model studies, the researchers aim to clarify how these processes interact during disease initiation and progression.

The motivation for the work stemmed from a long-standing gap between clinical symptoms and molecular understanding of OA. Current treatments largely focus on symptom management, and joint replacement remains the only definitive solution for advanced disease. By identifying early molecular events in bone, this research provides a foundation for developing targeted interventions that could slow or prevent OA progression before irreversible damage occurs.

Overall, the study demonstrates that advanced spatial proteomics can reveal hidden disease biology within human joints. By shifting attention to the molecular landscape of subchondral bone, the researchers offer a new perspective on osteoarthritis—one that may ultimately lead to earlier diagnosis, better monitoring, and more effective, personalized therapies.

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Reference
Titles of original paper: Tissue and extracellular matrix remodeling of the subchondral bone during osteoarthritis of knee joints as revealed by spatial mass spectrometry imaging
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About Buck Institute for Research on Aging, Novato, USA
The Buck Institute for Research on Aging is the world's first independent biomedical research institute devoted exclusively to understanding the biology of aging and age-related disease. Founded in 1999, its mission is to end the threat of age-related diseases and help people live healthier, longer lives by advancing fundamental insights into aging processes and chronic conditions, including neurodegeneration, cardiovascular disease, and diabetes. Researchers at the institute use cutting-edge science and technologies to explore how aging contributes to disease and to train the next generation of aging scientists.

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About Professor Birgit Schilling
Prof. Birgit Schilling is a Professor and Managing Director at the Buck Institute for Research on Aging in Novato, California, USA, and serves as Director of its Mass Spectrometry Center. Her research focuses on complex biological systems, using advanced mass spectrometry to investigate aging, disease mechanisms, and proteomics. She earned her PhD in Organic Synthetic Chemistry from the University of Clausthal, Germany. Prof. Schilling has authored more than 250 peer-reviewed publications and co-developed multiple bioinformatics workflows, with research interests including biomarker discovery, extracellular matrix biology, muscle atrophy, protein turnover, and translational proteomics across basic, clinical, and applied research.

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