

From Biopsy Slide to Tailored Treatment: AI Analysis of Bone Marrow Images Could Improve Myeloma Care

Artificial intelligence can reveal immune patterns in routine biopsy slides, helping physicians better match newly diagnosed multiple myeloma patients to the most effective therapies.

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Doctors treating [multiple myeloma](#) have more treatment options than ever before, including powerful immunotherapies and expanded access to stem cell transplants. Yet deciding which patients need the most intensive therapies, and which may safely avoid them, remains a major challenge.

New research from [Sylvester Comprehensive Cancer Center](#), part of the University of Miami Miller School of Medicine, shows that artificial intelligence can uncover clinically meaningful immune signals hidden in standard bone marrow biopsy slides. Those insights could help physicians tailor treatment strategies for patients newly diagnosed with multiple myeloma.

Arjun Raj Rajanna, a research scientist at Sylvester, will present the findings at the 2026 American Society of Clinical Oncology (ASCO) Annual Meeting.

“We are using AI to move toward a more precision-based treatment approach for patients with multiple myeloma,” Rajanna said. “Instead of asking which drug combination is best overall, we are using AI to ask which treatment strategy best fits the biology of each individual patient.”

The Challenge of Multiple Myeloma Treatment

Multiple myeloma is a blood cancer that develops in the bone marrow. Treatment options have expanded rapidly in recent years. One such therapy is daratumumab [Darzalex], a monoclonal antibody that helps the immune system’s natural killer cells recognize and attack myeloma cells.

Another common treatment is autologous stem cell transplantation. While this approach can extend the time before the cancer returns, it also carries significant side effects and can temporarily weaken the immune system, increasing the risk of infection.

Patients with multiple myeloma often respond very differently to the same therapies. Researchers

believe the bone marrow microenvironment, the complex mix of immune cells and signaling molecules surrounding cancer cells, may help explain why.

At last year's American Society of Hematology Annual Meeting, the research team [presented an AI model](#) capable of reconstructing molecular features of the bone marrow from routine biopsy slides. Building on that work, the researchers asked whether the same images could also reveal meaningful information about a patient's immune system. It's an especially important factor for immunotherapies such as daratumumab, which rely directly on immune cells to be effective.

"Even patients with the same clinical stage or genetic risk can have very different immune microenvironments, treatment sensitivities and long-term outcomes," said senior author of the study, [C. Ola Landgren, MD, PhD](#), director of the Sylvester Myeloma Institute, co-Leader of the Translational and Clinical Oncology Program and the Paul J. DiMare Endowed Chair in Immunotherapy.

Understanding immune biology at diagnosis may be just as important as understanding the tumor's genetic makeup, he said. To explore this, the researchers investigated whether AI-based analysis of bone marrow images could help predict how patients respond to specific therapies.

AI-Guided Treatment Matching

In the current study, researchers used a foundational AI model called GigaTIME to profile immune features from bone marrow biopsy slides. They examined whether those signals could help identify which patients benefit most from daratumumab and which might safely defer a stem cell transplant.

Using GigaTIME, the team estimated levels of CD16, a biomarker associated with natural killer cells, from biopsy slides of 212 newly diagnosed multiple myeloma patients enrolled in the HealthTree Foundation registry. Researchers then analyzed how these patients responded to standard therapy with bortezomib [Velcade], lenalidomide [Revlimid] and dexamethasone (VRd) or D-VRd, which adds daratumumab to the regimen.

The study's primary endpoint was time to next treatment, defined as how long patients remained on their initial therapy before needing to switch. Researchers also measured event-free survival, which reflects how long patients avoided disease progression or a new treatment.

"For patients, longer time to next treatment often translates directly into longer periods of disease control, improved quality of life, fewer treatment-related toxicities and less disruption to daily life," said Dr. Landgren, also professor and chief of the Miller School's [Myeloma Division](#).

The analysis revealed that patients with low AI-predicted CD16 levels who received VRd without transplant experienced a significantly shorter time to next treatment. In contrast, patients in the low-CD16 group had markedly better outcomes when treated with D-VRd. At 18 months, 86.8% of those patients remained event-free, compared with just 28.6% of patients treated with VRd alone.

The researchers also found that, among patients with high AI-predicted CD16 levels, outcomes at 18 months were comparable whether they received D-VRd with or without a stem cell transplant.

“This study does not suggest that transplant is no longer important in multiple myeloma,” Dr. Landgren said. “Rather, the findings support the emerging concept that transplant decisions may become increasingly personalized and biology-driven.”

AI's Role in Personalized Myeloma Care

The findings represent an important early step toward AI-guided precision medicine in multiple myeloma.

“Sylvester has been incredibly supportive of bringing AI into cancer research to directly help patients and clinicians make difficult treatment decisions,” Rajanna said.

While promising, the approach is still in the research phase.

“This is still a research tool at this point, but the signals are strong,” he said. “We still need to further validate these findings prospectively before the AI model can fully move into the clinic.”

Next, the team plans to compare AI-predicted CD16 levels with directly measured immune biomarkers. They are also expanding the model to include larger and more diverse patient datasets, as well as additional immune markers.

“I hope this study highlights that AI can move beyond simply automating workflows and instead become a powerful tool for biologic discovery and clinical decision support,” Dr. Landgren said. “This may represent the beginning of a new era of AI-enabled digital pathology in myeloma.”

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