A Better Eye on Genitourinary Cancers Imaging

A prior knowledge of tumors’ molecular features makes for smarter radiology assessments and more accurate predictions

Understanding the genetic mutations underlying cancer subtypes is a powerful tool in helping interpret MRIs, CT scans and other imaging studies. This is known, and sequencing is routinely performed in some cancers to identify best drug targets and clarify the cancer’s biological behavior. Francesco Alessandrino, M.D., a radiologist and researcher at Sylvester Comprehensive Cancer Center and assistant professor of clinical radiology at the Miller School of Medicine, is working to extend the universe of cancers for which this is routine practice.
Francesco Alessandrino, M.D.

“The eye sees only what the mind is prepared to comprehend,” he says, quoting Robertson Davies, a Canadian novelist. “When we know what patterns are likely, we know where to focus our lens. We look more closely or more expansively to see what we might not have otherwise seen.”

In a 2020 article published in Radiology, Dr. Alessandrino, then at Harvard Medical School, and his colleagues laid out correlations between genomic profiles and imaging patterns in urothelial cancer patients. They demonstrated how knowing specific mutations can help highlight “hotspots” on the CT scan.
“We now know that certain mutations correlate with nodal or osseous metastases, while others correlate with perineal metastases,” they wrote. “This work makes a case for early molecular analysis of mutations and helps connect the dots for radiologists.”

Now at UM, Dr. Alessandrino is expanding his work to other cancers. In partnership with Dr. Marilyn Huang, associate professor of gynecologic oncology and director of translational gynecologic oncology research, he is working on elucidating these correlations in endometrial and other genitourinary cancers.

“We are hoping that genomic radiology will shed light on the biological behavior of these cancers and will help us identify metastases earlier,” he said.

A Reverse Interrogation of Tumor Spread

In radiogenomics, imaging features are noted and may later be linked to genomic factors through genetic sequencing. The reverse approach would be what has been coined “genomic radiology,” with genomic factors known first and imaging features then isolated and followed, based on that knowledge.

Peter Choyke, M.D., director of the Molecular Imaging Branch of the National Institutes of Health, commented on Dr. Alessandrino’s study in an editorial.

“Together with artificial intelligence, the arrival of genomic radiology will further increase the value of oncologic imaging,” he wrote. “By building on these archives (e.g. Cancer Imaging Archive and The Cancer Genome Atlas), it should be possible to provide genome-based predictions of radiologic
findings for the broad spectrum of human cancers.”

**Alessandrino’s Study Findings**

In Dr. Alessandrino’s retrospective study, the team analyzed 103 patients with urothelial cancer, who underwent genomic analysis and were also staged with cross-sectional imaging, including CT, MRI and PET/CTs. They examined the genomic mutations by likely types of metastases, finding that a TP53 mutation was associated with 1.7 times the chance of osseous or nodal metastases, while patients with RB1 mutations were 5.9 times more likely to have peritoneal metastases.

The researchers also subdivided the cases into a high-risk group, (including TP53 and/or RB1 and/or KDM6A mutations), and a low-risk group (having ARID1A, FGFR3, PIK3CA, STAG2 or TSC1 mutations). They found that the high-risk mutational group had a metastasis-free survival (time from diagnosis to the development of metastases) of 3.5 months, versus 17.3 months for the low-risk group. The overall survival was 19 months versus 24.4 months.

**Brighter Prospects for Patients with Metastases**

While the cost of whole-genome cancer genome is dropping to below $1,000, Dr. Choyke notes that much of this information is not currently used, least of all by radiologists. Further, its accumulation is expensive.

“The potential improvements suggested by Alessandrino et al. will require substantial investment in matched genomic and radiologic data sets for a wide spectrum of cancers,” he wrote.
“There are increasingly better prospects for patients with metastatic cancers. More systemic therapies are available, and there is greater knowledge of the clinical impact of certain mutations,” Dr. Alessandrino said. “There is a lot yet to understand about why the cancer metastasizes that way, why patients develop metastases. I think our study and current work moves us in that direction.”