UNC Lineberger sequences 10,000 tumors as part of national cancer genomics effort

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The UNC Lineberger Comprehensive Cancer Center is leading a national, multi-year, collaborative effort to characterize the genetic changes in nearly 30 cancer types. Earlier this year, UNC Lineberger hit a milestone in this effort – sequencing 10,000 samples of cancer tumor tissue.

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The work helped lay the foundation for groundbreaking research completed as part of TCGA. And with approximately 10,000 of the samples sequenced by UNC uploaded to a public database accessible to researchers around the world, the work is expected to continue to fuel new discoveries.

"We expect that the data that UNC gathered for this large-scale sequencing project will be an active discovery resource that scientists use to discover new things for at least another decade, and potentially for more," said **D. Neil Hayes**, MD, MPH, a UNC Lineberger member and an associate professor of clinical research in hematology and oncology at the UNC School of Medicine.

UNC was able to hit the milestone because of key investments in next-generation sequencing technology, Hayes said, as well as because it had the staff to operate that technology and the leadership of key scientific investigators.

"No. 1, it was scientific leadership that made this project possible, and No. 2, it was production capacity," Hayes said. "We had to have the resources to be able to handle roughly 200 samples a month on the sequencing side and on the analytics side, as well as storage space, sequencers, computers, project management expertise – and many of these things were supported by cancer center resources and the state of North Carolina."

Investments in next-generation sequencing technology from the state-funded University Cancer Research Fund were "crucial," said **Piotr Mieczkowski**, director of UNC's High Throughput Sequencing Facility and a research assistant professor of genetics. The University Cancer Research Fund helped UNC to buy faster, more efficient sequencers.

"You have to remember that when everything was happening, next-generation sequencing technology was really very, very new," Mieczkowski said. "In just a few years, we have built real knowledge of how to create various types of libraries and how to perform sequencing on a large scale."