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Building a Cancer Arsenal

With tumor samples collected, local cancer genome project is now cataloging & processing DNA into a giant database

START's Alyssa Moriarty, preclinical administrative coordinator, pulls out a rack of cell boxes from a liquid nitrogen cryogenic tank. The boxes contain samples of tissue from cancer tumors of South Texas patients.

Story by Travis E. Poling
Photography by Lyndsey Johnson / SABJ

Problem: Limited genetic information in the cancer research area slows down the pace of finding causes and treatments.

Solution: Collect thousands of tumor samples from the 10 most common cancers in San Antonio and conduct whole genome sequencing on them.

Cancer Genome Project is in big data phase

BY TRAVIS E. POLING

An ambitious project to create a genomic database available to cancer researchers around the world is entering its next stage of development one year after its launch in San Antonio.

The San Antonio 1,000 Cancer Genome Project has collected far more than 1,000 cancerous tumor samples in collaboration with local oncologists and surgeons and is now setting about building a massive database of cancer genome information for all kinds of tumors, along with clinical data.

The project has raised $1.15 million of the $3 million needed to bring the effort to completion, says Dr. Anthony Tolcher, director of clinical research, president and co-founder of START — and the mastermind behind the cancer genome project.

He is beginning another major financial push with San Antonio philanthropists, foundations and stakeholders to reach $2 million this year.

"The beauty of this is that you're creating information that can be used in many ways," Tolcher says. "This is the unitas of genomic intellectual property to help build companies, new therapies."

South Texas Accelerated Research Therapeutics, or START, was already collecting tumor samples to create a bank of cancer cells used to aid in Phase I clinical trials for numerous cancer treatment developers.

Now, with the cooperation of local doctors who harvest tumor tissue samples to send to the lab, START receives hundreds more

Continued on NEXT PAGE

Above: Dr. Anthony Tolcher, director of clinical research at START, is one of the leaders driving the cancer genome project. The project brings together physicians, academics and tech leaders from across the region locally around collection of data for cancer research.

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samples in San Antonio each year through daily pickups by a "tissue concierge."

Except for the kit used to store and transport the samples from the operating room to the lab, there is no additional cost in sample collection.

"The tissue collection is on the backs of everything else we were doing," Tolcher says. "We make it work for doctors alongside what they're already doing."

Computing horsepower

The money raised for the project is all sunk into actually processing the data.

START's Marcos Rodriguez, tissue concierge, and Teresa Vaught, assistant director of preclinical research, examine cancer tumor tissue samples as part of the San Antonio 1,000 Cancer Genome Project.

Tolcher says the electronic data capture of the genome takes up about three terabytes of storage space because of the 3 billion base pairs in each DNA sample. The next step is to boil down the data to about 200 megabytes on the nexus of the patient's DNA from blood and the genetically corrupted cancer DNA.

San Antonio server and cloud hosting company Rackspace has donated storage space for the data collected.

Sequencing so many samples required a contract with BGI, a firm in China that boasts the largest gene sequencing facility in the world.

START has 1,700 samples available for sequencing and collected 360 new samples in 2013 alone.

An agreement with a company that will turn the genetic and clinical data into a usable database available to all researchers is expected to be announced this summer, Tolcher says.

START also has developed software, with patents pending, which can sufficiently remove identifying information from the clinical reports so it can be used more openly for research. Tolcher says all the patients whose samples are represented in the tissue bank are aware of the project and its goals and have given permission for its use in research.

Until recently, it was believed that there were only five or six errors that caused genetic mutations leading to the formation of cancer. But since 2010, more than 50 possible cancer-causing genetic mutations have been identified.

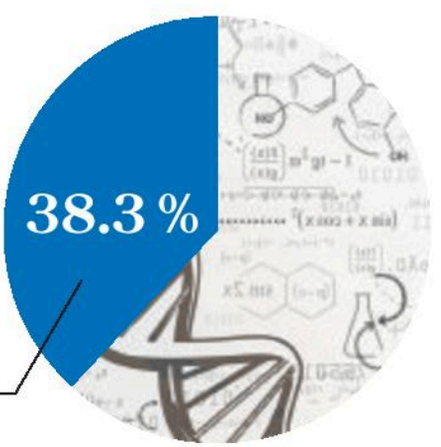
Researchers once paid attention primarily to the 4 percent of the DNA that was coded for proteins when searching for cancer causes. But it turns out that some of the that remaining 96 percent of the genome, once called "junk DNA," contained gene-regulating instructions that could be connected to mutations for cancer and pseudo genes that turned the regulating genetic material off and on, Tolcher says.

The gene sequencing data and clinical data collected as part of the San Antonio project can be used to track which genes and gene abnormalities lead to a patient having a good or bad prognosis and how they might respond to treatment, Tolcher says.

TRAVIS E. POLING is a freelance writer based in New Braunfels.

Total cost of project:
$3 million

Money raised so far:
$1.15 million



Percentage raised so far

Gathering the Evidence on Cancer

For the San Antonio 1,000 Cancer Genome project, the genomic journey into data begins with the delivery of the samples to Oncopath Laboratories, which is headquartered next to START's South Texas Medical Center location, where it is processed. That includes taking thin samples of the tissue that can be stained for viewing on a slide.

Oncopath, a pathological reference lab, also does DNA extraction through a series of washes and spins. If the DNA extraction is successful, pathologists can examine it for the nature of the tumor, says Oncopath Director Xavier Reveles.

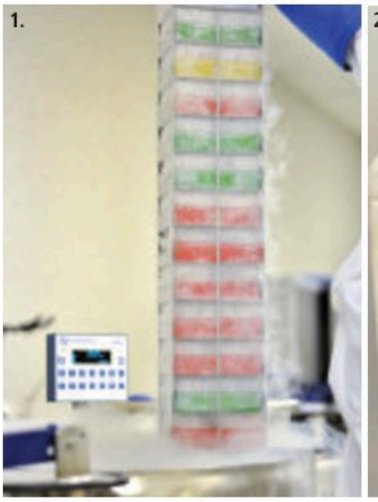
A portion of that DNA is then sent to START for gene sequencing.

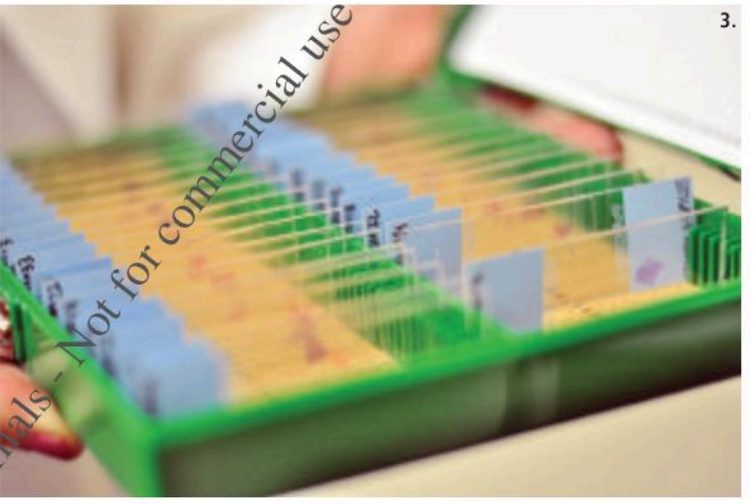
START tries to get a sample of the tissue to grow and then test various chemotherapy drugs on it to determine how effective a treatment might be in battling cancer in the patient, says Teresa Vaught, assistant director of preclinical research at START.

Slices of the sample also are frozen in a cryogenic "bank" for future reference.

Each cryogenic tank, which is about three feet in diameter and four feet high, can hold 42,000 samples, says Madeline Nehls, preclinical research assistant.

Alongside that clinical data is genomic sequencing of the tumor and healthy blood from the same patient.





Size and Space

360
Samples collected in 2013

3 terabytes
Storage space required for the electronic data capture of the genomic sequencing for one genome

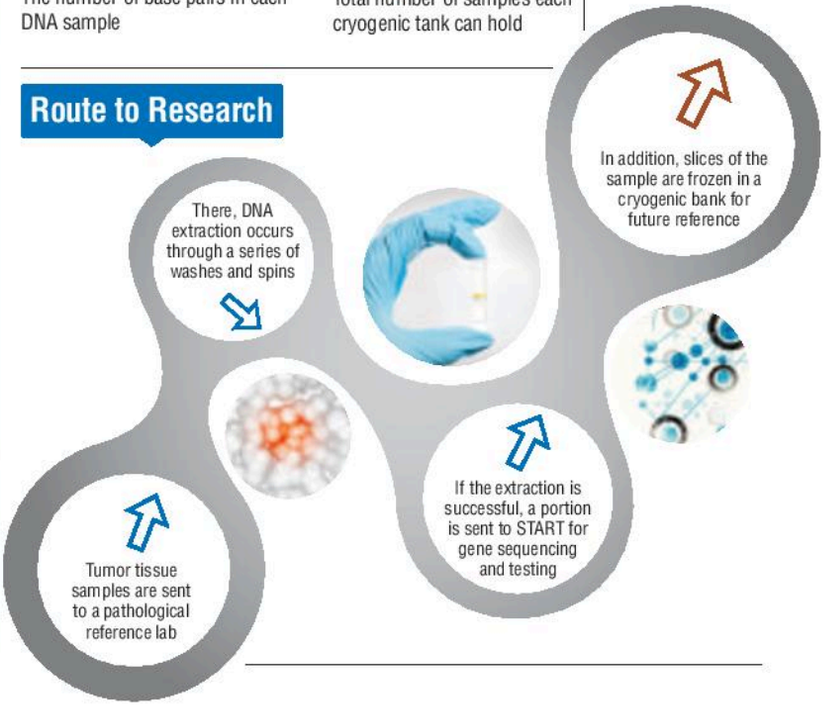
1,700
Number of tumor samples available for sequencing

3 billion
The number of base pairs in each DNA sample

42,000
Total number of samples each cryogenic tank can hold

Above:
1. Cell box racks hold the cancer tumor tissue samples.
2. START 's Tissue Concierge Marcos Rodriguez shows off the boxes that store the samples while they are being transported.
3. Slides that contain tissue samples from the cancerous tumors.

Route to Research



Faces Behind the Places

Teresa Vaught

Assistant Director, Preclinical Research
South Texas Accelerated Research Therapeutics (START)

Time on the job: 2.5 years
College degrees: Bachelor of Science in Agriculture; Doctor of Veterinary Medicine

Your job responsibilities? I facilitate communication between our physicians, nurses, patients, pathologists, hospitals, researchers, and biomedical colleagues to assist in creating a catalogue of human genetic profiles that will advance in the treatment of cancer.

What core subject skills are essential for this job? Genetics, biochemistry, pharmacology, and medicine

Special equipment/safety clothing required? Mortar/pestle, sonicator, cryostat, laminar/biosafety hoods, special chemicals/stains, centrifuge, microscopes, mixers/shakers, autoclave, laboratory glassware, and personal protective equipment (PPE)

Biggest challenges of the job: To advance my knowledge every day in the fight of treating cancer that may help in our community

Part of the job that piques your interest: I am always amazed at how cancer can adapt and change over time. It is like a puzzle in that each piece must be linked together. Then we must figure out how to stop the cancer at different links.

How does it feel to be part of the Cancer Genome Project? I feel incredibly privileged to be working alongside some of the most dedicated oncologists and researchers. As the genome project grows by leaps and bounds, new advances in cancer treatment will be available that did not exist previously.

SPOTLIGHT ON HEALTHCARE