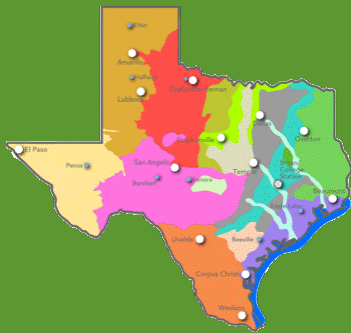


Genomics and Bioinformatics Service (TxGen)



Soil Variation in Texas

AgriLife Genomics &
Bioinformatics Services

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Overview

Established through a directive from Dr. Craig Nessler, Director of Texas A&M AgriLife Research to radically improve genomic research across AgriLife, College of Agriculture and Life Sciences (COALS), and the Texas A&M University System, addressing a central and pressing need for access to the latest genomic technologies, and world-class laboratory and bioinformatics expertise. To meet this ambitious goal, AgriLife Research brought together a team of leading genomics, bioinformatics, molecular, and computational scientists to meet the next generation sequencing (NGS) and bioinformatics needs of the TAMU system and broader scientific community.

The AgriLife Genomic unit received start-up funds from the Texas Emerging Technology Fund as part of a larger AgriLife ETF program under the leadership of Executive Associate Director of Texas A&M AgriLife Research, Dr. Bill McCutchen in 2010. In 2013, the Center for Bioinformatics and Genomics System Engineering was created and approved by the Texas A&M Board of Regents.

The center is led by Executive Director Dr. Charles D. Johnson, who was recruited from the biotech industry to develop a next generation sequencing and bioinformatics facility at Texas A&M. With over 25 years of scientific research and operational leadership experience, Dr. Johnson has an established track record in genomics and bioinformatics research and development (R&D). He recruited an extraordinary team of AgriLife scientists with vast and diverse backgrounds, allowing them to quickly catalyze activity across a broad spectrum of research areas, assuring a high return for each research dollar and generating significant scientific discoveries. The group has built a collaborative network of over 1,025 scientists spanning 35 TAMU departments, TAMU system partners, 35 countries, 87 academic groups outside TAMU, and a growing number of private sector life science and agricultural companies.

Investments in personnel and equipment have been critical to providing genomics and bioinformatics infrastructure for student training, faculty retention and successful R&D initiatives in the areas of agriculture, life sciences, human health, and veterinary medicine. Over the last six years we have an international reputation for our expertise in genotyping-by-sequencing and have become the go to academic lab for many companies with unusual or difficult sequencing challenges.

Expanding Genomics Research

Texas A&M AgriLife Research created a seed grant program to provide preliminary sequencing data and analysis, through TxGen, to encourage genomics based grants by university faculty. The seed grant program has distributed over \$1.6M in total and reaped a 10-20X return in new research funding for our faculty. Since the founding of TxGen, genomic research funding across A&M has expanded by over \$70M.

Modern DNA Sequencing

Post-Sanger Sequencing, Next Generation Sequencing (NGS), High Throughput, High Output, 2nd Generation Sequencing, 3rd Generation Sequencing, and the names go on, but the song remains the same. The ability to translate chemical information embedded in the composition of deoxyribonucleic acid molecules (DNA), faster and cheaper than was thought to be possible only a few short years ago. Over the last six years we have updated our NGS capabilities a total of ten times, to always provide the latest in sequencing technology to our collaborators. We now have the latest in short read and long read technology. We are one of only a handful of service providers in the world offering access to the PacBio Sequel system. Everything offered on a fee for service basis.

Next Generation Sequencing

- Illumina HiSeq 4000, 2500v4, 2500 rapid, MiSeqv3
- PacBio Sequel (NEW)
- Oxford Nanopore MinION R9

Library Preparation

We offer library preparation using Illumina TruSeq/Nextera, Bioo Scientific, and PacBio.

Libraries for Illumina Sequencing

- Illumina TruSeq DNA
- Illumina TruSeq DNA-PCR Free
- Illumina TruSeq RNA stranded
- Illumina TruSeq small RNA
- Illumina Nextera XT DNA
- Bioo Scientific DNA
- Bioo Scientific RNA
- Bioo Scientific miRNA
- Bioo Scientific ChipSeq

Library preparation from PacBio

- DNA for Whole Genome Sequencing
- RNA ISOSeq for Whole Transcript Sequencing
- Preparations for Epigenetic Sequencing

Bioinformatics

Our quantitative and computational analytical unit sits at the cutting edge of bioinformatics research — we use the latest tools and develop improvements to correct shortcomings with these tools. The Center for Bioinformatics and Genomic Systems Biology (CBGSE) has 15 faculty and over 30 graduate students who work in computational and systems biology and bioinformatics. Nine of those students are dedicated to working plant focused bioinformatics. The CBGSE works in software development, the team is led by an experienced PhD level software engineer who has developed bioinformatics tool for leading genomic technology companies. The LIMS software currently being used at TxGen was developed within AgriLife.

Working with Our Scientists

Our typical engagement begins with an investigator contacting TxGen's director to discuss their research project and desired research outcomes. We have significant experience in experimental design and the application of genomic technology to solve your research problems. Once a project is completed it is then presented to the investigator. From there, our services continue as we provide software and human insights into their projects and help with next steps; publications, grants, follow up studies, etc.

Internal Development

The breadth of genomics research across Texas A&M has necessitated adding an active technology development program to TxGen. This process taps into and supports the rich research programs at Texas A&M for information and ideas. Additionally, new bioinformatics software and methods are constantly being added as our staff are challenged with novel projects.

More About Us

- Conducted 374 projects (YR15-16)
- Median completed project size \$4.2k
- 2016 Quotes in the queue \$2.8M (133)
- 15,000 samples processed in 2016
- Most common project type: Genotyping-by-Sequence and RNASeq
- Supported over 1,025 researchers drawn from over 35 departments, 10 colleges, and multiple agencies across the Texas A&M System.
- Involved in over 350 state and federal grant submissions, resulting in tens of millions in new funding for faculty across the TAMU system (>\$60M to date).
- Launched seven Seed Grant programs- distributing a total of \$1.6M in sequencing and bioinformatics services to faculty across the system to generate preliminary data to facilitate outside grant funding. 398 seed grants submitted with over 800 total participants. 81 funded projects, generating \$8M in new funding from the first \$400k seed grant program.

