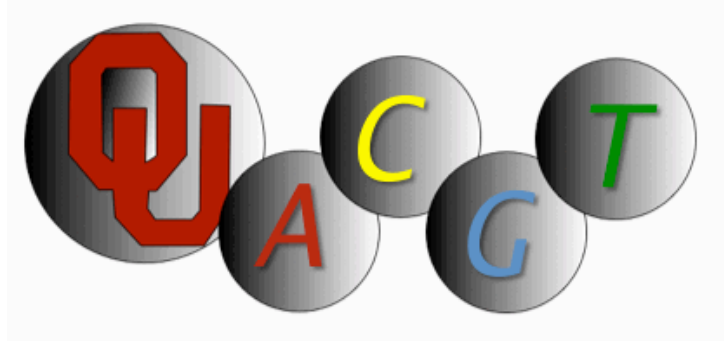


Advanced Center for Genome Technology (OU-ACGT)

Annual Profile January 2011



Overview of the Organization:

Since its inception as a National Institutes of Health Genome Center in 1990, and an OU approved center shortly thereafter, the ACGT has been at the fore-front of DNA high throughput sequencing and state-of-the-art bioinformatics.

The ACGT also is

- One of the first centers incorporated into the Human Genome Project, and was responsible for the sequencing of Human Chromosome 22 and has attracted more than \$60 million in research grants, mainly from the National Institutes of Health and the National Science Foundation
- Home to the Bioinformatics Core Facility (BCF) that houses the E. coli Community's Gene Expression Database (GenExpDB) and funded by the NIH National Institutes of General Medical Sciences
- Actively involved in developing large scale DNA sequencing methods and implementing them in collaborations with individual laboratories both from within and outside Oklahoma.
- Involved in other world-wide, collaborative, high-profile sequencing and gene expression projects, including the mouse genome, and in decoding the genes for various bacteria, fungi, and plants
- Remained at the forefront of investigating microbial communities, microbial gene expression in the mammalian gut and the synergistic relationships between members of microbial ecosystems.
- Partnered with several different departments at the University of Oklahoma, other educational institutions within the state, and universities and scholars in this country and abroad in efforts to improve our understanding of genomes and to explore the potential benefits of such genome projects

2010 Highlights:

- Developed high throughput tagging methods for deep coverage sequencing of microbial and viral community members and for de novo sequencing of genomic including:
- Determined genome-wide DNA methylation maps in follicular lymphoma cells to study gene expression in tumor cells.
- Studied microbial population dynamics in cow rumen during adaptation to a high-grain diet, examined gene expression in the traditional Chinese medicinal plant, *Epimedium sagittatum*, identified of microRNAs and their targets in switchgrass, a model biofuel plant species, used high-throughput sequence analysis of *Ciona intestinalis* SL trans-spliced mRNAs and

discovered alternative expression modes and gene function correlates, determined the microcollinearity between autoploid sugarcane and diploid sorghum genomes, and used comparative DNA sequence analysis to study the detoxification enzymes in *Acyrtosiphon pisum* and *Myzus persicae*.

- Used DNA sequencing to gain insights into evolution of multicellular fungi from the assembled chromosomes of the mushroom *Coprinopsis cinerea* (*Coprinus cinereus*), and to study the genomic island TnSmu2 of *Streptococcus mutans* that harbors a nonribosomal peptide synthetase-polyketide synthase gene cluster responsible for the biosynthesis of pigments involved in oxygen and H₂O₂ tolerance.
- Supported DNA microarray analysis for gene expression (transcriptome) studies of *Drosophila melanogaster*, *Arabidopsis*, *E. coli*, *Enterococcus faecalis*, to name a few. Created related databases for data sharing, analysis, and public data visualization.
- Initiated RNA deep-sequencing (RNA-Seq) for transcriptome analysis and developed web-based computational analysis tools.

Activities Planned for 2010:

- Continue to developing, improving and implementing the research necessary to rapidly and efficiently complete both large and small scale DNA sequencing projects using state-of-the-art instrumentation within the context of sequencing the tomato genome as well as several other microbial genomes and microbial communities..
- Maintain our focus of training the next generation of Oklahoma scientists in the latest techniques for recombinant DNA, genetic engineering, cloning and DNA sequencing,
- Aid collaborators in submission of grant proposals requiring DNA sequencing, computer analysis of DNA sequences, and DNA synthesis by serving as a state-wide resource for this technology,
- Improve our involvement in education and research by continuing to train students at both the graduate and undergraduate levels as well as address the national needs of megabase sequencing,
- Strengthen our role of serving as a magnet to attract additional highly qualified investigators and new faculty for Oklahoma universities, as well as provide in-service training and technology transfer to students and faculty both from other Oklahoma colleges and local industry.
- Expand the user base for the Bioinformatics Core Facility (BCF) that contains the computer programs necessary for genetic research in Oklahoma and the various data bases, i.e. GenBank, EMBL, and NBRF, the programs used to search these data bases. and the programs for DNA, RNA structure and functional analysis at the genome and proteome levels.

Core Competences:

- Developed, maintains and implements both 454/Roche GS-FLX-xl massively parallel automated DNA sequencing technology and ABI-3730 capillary sequencers
- Pioneered, maintains and develops robotic methods for DNA isolation and analysis
- Maintains a state of the art computational genomics facility for analysis of both DNA and gene expression data through the development of interactive relational databases
- Performs advanced research on comparative genomics, microbial community composition dynamics and gene expression

- Develops methods for visualization of genomic, microbial community and gene expression data.

Linkages and Partnerships

- Continue our highly productive research collaboration with numerous OU faculty and staff in mega-microbial sequencing projects from soil, water, gut and feces.
- Maintain our collaborative research grants with external organizations including plant related groups, including for example, the Noble Foundation, Oklahoma State University, University of Minnesota and Cornell University, and others worldwide.
- Continue hosting and supporting national and international visiting students and scientists during our summer internship academic year programs as well as tours of our DNA sequencing, gene expression and computational biology facilities.

Recently Published Results

During 2010, we published over a dozen refereed journal articles including:

- Two papers with with graduate students Simone McMill and Graham Wiley, one on the determination of the bisulfite treated DNA sequence-based genome-wide DNA methylation maps in follicular lymphoma cells and the second on high-throughput sequence analysis of *Ciona intestinalis* SL trans-spliced mRNAs: Alternative expression modes and gene function correlates.
- A paper on rumen microbial population dynamics during adaptation to a high-grain diet and another on a novel conjugative plasmid from *Enterococcus faecalis* E99 enhances resistance to ultraviolet radiation. with postdoctoral fellow Fares Najjar in collaboration with investigators at OSU and OUHSC, respectively.
- A study that showed that streptococcus mutans harbors a nonribosomal peptide synthetase-polyketide synthase gene cluster responsible for the biosynthesis of pigments involved in oxygen and H₂O₂ tolerance with Dr. Robert Cixhewicz in Chemistry and Drs. Joe Fettetti and Fran Qi at the OUHSC.
- Studied evolution of multicellular fungi from the assembled chromosomes of the mushroom *Coprinopsis cinerea* (*Coprinus cinereus*) with postdoctoral fellow Doris Kupfer
- Used comparative DNA sequence analysis to study the detoxification enzymes in *Acyrtosiphon pisum* and *Myzus persicae* with graduate student Simone Macmil
- Microcollinearity between autopolyploid sugarcane and diploid sorghum genomes. BMC Genomics. 11(1): 261 (2010). With postdoctoral fellow Fares Najjar, and graduate students Graham Wiley and Simone Macmil.
- Extensive microarray analysis of “Discretely calibrated regulatory loops controlled by ppGpp partition gene induction across the ‘feast to famine’ gradient in *Escherichia coli*”, authored by Matt Traxler and others in the Conway laboratory, will appear on the cover of Molecular Microbiology in March, 2011.
- The full list of OU ACGT and BCF publications can be found at URLs: http://www.genome.ou.edu/personnel/broe/roe_vitae.html and <http://www.ou.edu/microarray/oubcf/docs/publications.shtml>, respectively.

Impacts and Outcomes of Center

The Advanced Center for Genome Technology is congruent with the State’s goals of increasing the bio-medical industry in the state. The availability of such a unique state-wide accessible

facility allows individual groups to expand their search by providing both the research expertise and the facilities needed to begin addressing larger and more global evolutionary and genomic organization questions. Individual researcher groups in Oklahoma access this facility by either sending samples for sequence analysis or bringing samples for analysis by the individual researcher, with training being provided by the DNA Sequencing Core Staff. Because we have long established relationships with researchers across the nation, we are in a strong position to continue to improve the State's reputation as a leader in biotechnology.

The Bioinformatics Core Facility improves the University's competitiveness for national and private grant funding. As the quality and throughput of life science research tools improve and the size of datasets grows, the funding agencies are asking researchers to have a plan for data management. The BCF can aid in data submission to the international databases and also has the potential for development of software products for public distribution.

Address: Stephenson Research and Technology Center,
101 David L. Boren Blvd.
Norman, OK 73072

Co-Directors: Dr. Bruce A. Roe (broe@ou.edu) ((405) 325 – 4912)
Dr. Tyrrell Conway (tconway@ou.edu) (405) 325 – 1683

Center Web Sites: Advanced Center for Genome Technology
<http://www.genome.ou.edu>
OU Microarray and Bioinformatics Core Facility
<http://www.ou.edu/microarray/>