

Genomics Day highlights breadth of NIEHS resources and research

By Staton Wade

NIEHS and EPA scientists gathered May 1 for the fifth annual Genomics Day. The event increases awareness of the vast array of genomics resources available to NIEHS researchers and promotes discussion about the research those resources support throughout the Institute.

Kevin Gerrish, Ph.D., deputy director of the NIEHS Molecular Genomics Core, organized and moderated the event. Highlights included a keynote address, talks from junior researchers and trainees (see [text box](#)), and a poster session, featuring 29 posters on genomics research by NIEHS and EPA scientists, and 18 posters on genomics services and products available from support groups.

Core facilities provide new genomics technologies

During his opening remarks, Gerrish highlighted new technologies available to researchers through the Molecular Genomics Core, including the NanoString nCounter Analysis System, and new high content arrays for gene expression and DNA methylation analysis.

Greg Solomon, manager of the NIEHS Epigenomics Core, explained that he and his staff have been busy providing next generation sequencing data to NIEHS researchers and maximizing the output of their Illumina MiSeq sequencers. The Epigenomics Core has performed almost 500 runs since this technology became available. "These instruments run basically nonstop in my laboratory," said Solomon.

To analyze the wealth of data generated by the core facilities, David Fargo, Ph.D., head of the Integrative Bioinformatics Group, pointed out that his team supports investigators at multiple levels, from simple analyses to the development of custom bioinformatics tools. "The real goal is to be scientific collaborators, and this involves integration of data for meaningful biological discovery," he explained.

The power of genomics for disease prediction

Steven Kleeberger, Ph.D., head of the NIEHS [Environmental Genetics Group](#) in the Laboratory of Respiratory Biology, gave the keynote address. Kleeberger described how his lab uses both genomic and transcriptomic data to identify gene signatures that predict susceptibility to respiratory syncytial virus (RSV).

RSV causes 160,000 deaths, worldwide, and the hospitalization of 144,000 children in the U.S. every year, explained Kleeberger. By identifying genes associated with RSV susceptibility, he hopes to be able to predict disease severity, prior to infection, and identify patients who would most benefit from preventative measures.

(Staton Wade, Ph.D., is an Intramural Research Training Award fellow in the NIEHS Chromatin and Gene Expression Group.)



Gerrish noted that Genomics Day promotes awareness of available resources, as well as enhances collaboration with local EPA colleagues. (Photo courtesy of Steve McCaw)



In addition to the bioinformatics services his group provides, Fargo described the computing resources available to researchers at NIEHS, which include a new parallel processor, servers that host hundreds of software applications, and nearly a petabyte of storage optimized for big data science. (Photo courtesy of Steve McCaw)



Solomon described the techniques used in the newest core at NIEHS - the Epigenomics Core - which has made powerful next generation sequencing technology available on-site to researchers. (Photo courtesy of Steve McCaw)



Keynote speaker Kleeberger led a research team that used genome-wide association mapping to identify a gene that may make premature infants susceptible to a chronic lung disease called bronchopulmonary dysplasia ([summary](#)). (Photo courtesy of Steve McCaw)



After his talk on oxidative stress and adipogenesis, Karaca, center, took advantage of the poster session to discuss the bioinformatics tools available to NIEHS scientists. (Photo courtesy of Steve McCaw)



Biologist Yin Li, Ph.D., of the NIEHS Receptor Biology Group, was excited to discuss her work with visiting fellow Motoki Takaku, Ph.D., of the Eukaryotic Transcriptional Regulation Group. Li presented a poster on the role of the estrogen receptor in mediating the epigenetic effects of diethylstilbestrol (DES) exposure in reproductive organs. (Photo courtesy of Steve McCaw)

Genomics Day talks by NIEHS fellows and junior researchers

- **Mallikarjuna Metukuri, Ph.D.**, research fellow in the [Metabolism, Genes, and Environment Group](#), used microarray gene expression analysis to demonstrate how the metabolic regulator SIRT1 affects intestinal homeostasis, inflammation, and the gut microbiome.
- **Diana Cruz-Topete, Ph.D.**, research fellow in the [Molecular Endocrinology Group](#), used microarray technology to define a novel role for the glucocorticoid receptor in the electrophysiology of the heart.
- **Daniel Menendez, Ph.D.**, staff scientist in the [Chromosome Stability Group](#), combined microarray analysis and next generation sequencing to identify novel targets of the p53 tumor suppressor involved in innate, or nonspecific, immunity.
- **Li Wang, Ph.D.**, visiting fellow in the [Stem Cell Biology Group](#), used the results of a genomic screen to identify the THO complex as a RNA exporter required for self-renewal of embryonic stem cells.
- **Mehmet Karaca, Ph.D.**, postdoctoral fellow in the [Environmental Genomics Group](#), performed genome-wide expression analysis of both messenger RNA and microRNA to explore the role of transcription factor NRF2 in adipogenesis, or the cell differentiation process leading to adipocytes, or fat cells.
- **Sophia Harlid, Ph.D.**, postdoctoral fellow in the [Molecular and Genetic Epidemiology Group](#), used DNA methylation arrays to study the epigenetic effects of phytoestrogen exposure in infants who are fed soy formula.

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