

NIEHS celebrates core support on Genomics Day

By Eddy Ball

As the data get bigger and the technology grows increasingly sophisticated, it is becoming more critical for NIEHS to maintain its network of core support for genomics research. At this year's Genomics Day, May 7, the institute's scientists gathered to learn about the constantly growing scope of resources available to help research teams explore entire genomes and interpret their findings.

"Every year it gets more and more interesting," observed moderator Kevin Gerrish, Ph.D., in his introduction. He has chaired the event since its beginning in 2009.

Exploring the potential of new tools

Gerrish explained that the cores at NIEHS receive cross-divisional funding to provide equipment and expertise that individual research groups could not supply on their own. These include the latest in instrumentation, such as the newly acquired NanoString Technologies nCounter Analysis System, and specialized assistance in experiment design and data interpretation.

In addition to the overview by Gerrish, who is acting director of the Molecular Genomics Core, attendees heard from lead researcher Paul Wade, Ph.D., who heads the Epigenomics Core, and David Fargo Ph.D., director of the Integrative Bioinformatics Core.

Wade spoke of numbers that ranged as high as 13 billion — the total number of reads performed on sequencing instrumentation over the past two years. Fargo described his group's high performance computing capabilities — 2 terabytes, or nearly two trillion bytes, of random access memory and 1.3 petabytes, or more than one quadrillion bytes, of data storage.

Seeing core support in action

Trainees gave a series of six short talks illustrating outcomes of research supported by the cores. This allowed the trainees, representing NIEHS and the National Toxicology Program (NTP), to present the latest results of their work, ranging from studies of memory storage at the molecular level to explorations of the mechanics of epigenetic modification of gene expression.

The keynote talk was given by distinguished lead researcher [Thomas Kunkel, Ph.D.](#), head of the DNA Replication Fidelity Group. Kunkel presented an overview of the essential process of error correction, which the genome constantly performs in every cell of the body with mind-boggling speed and near perfect accuracy. He also explained what happens when the genome's safety net fails, leading to serious and even life-threatening diseases, including cancer.

Kunkel, who is a leading authority on replication processes, demonstrated how whole genome sequencing of yeast allowed his team to analyze replication error rates in 8 diploid yeast strains over 900 generations. He said he expects the findings from the 12 million base-pair yeast genome to parallel findings anticipated from research underway on the human genome, which is 250 times as large.

The day concluded with a poster session, presented by institute researchers, NIEHS core representatives, and 15 participating vendors.

(Eddy Ball is a contract writer for the NIEHS Office of Communications and Public Liaison)



Gerrish described his group's dedication to providing capacity for start-to-finish genotyping, microarray, and sequencing experiments. (Photo courtesy of Steve McCaw)



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Fargo, left, was a co-author on three studies in the oral presentation segment of the program. He and Wade, right, also co-authored a poster presentation on NextGen sequencing capabilities in the Epigenetics Core. (Photo courtesy of Steve McCaw)



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William Copeland, Ph.D., left, and Steven Kleeberger, Ph.D., were among a number of lead researchers on hand to learn about new resources in genomics at NIEHS. (Photo courtesy of Steve McCaw)



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Nguyen's study of p53 binding and regulation of immune response genes took advantage of resources across the cores. "This is a good example of how entwined research is here at NIEHS," said Gerrish, in his introduction. (Photo courtesy of Steve McCaw)



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Kunkel's presentation illustrated the value of core support in unraveling the mysteries of DNA replication fidelity in health and disease. He and his collaborators demonstrated that the type of errors in replication vary among the three polymerases involved in humans – alpha, delta, and epsilon. (Photo courtesy of Steve McCaw)



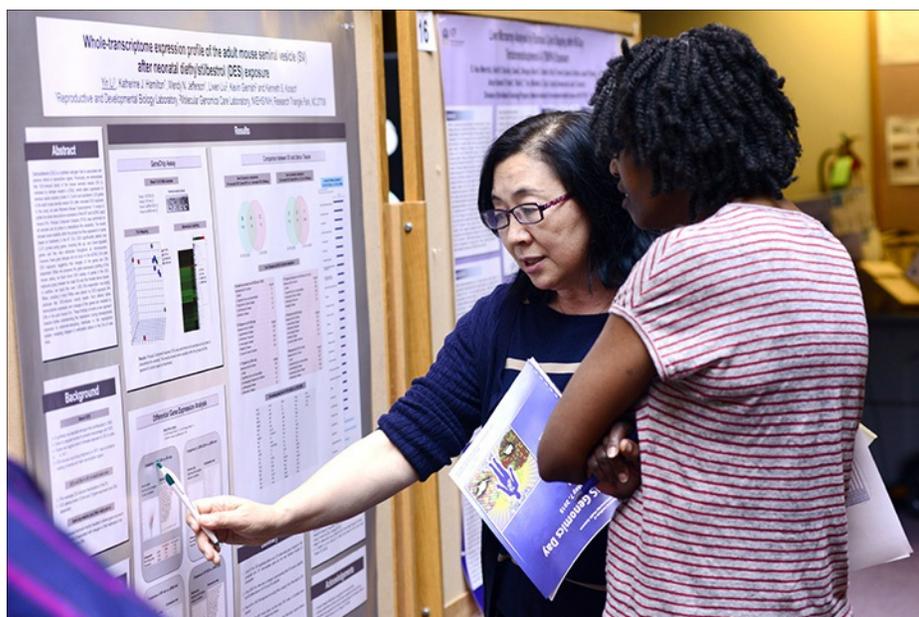
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Chan, left, listened to NTP toxicologist June Dunnick, Ph.D., as she outlined molecular changes in mice exposed to dimethylpropiothetin, a chemical used in medical devices. She said these changes represent candidate markers for nasal cavity environmental toxins linked to cancer progression. (Photo courtesy of Steve McCaw)



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Wade, left, chatted with contractor Ruchir Shah, Ph.D., who is involved in NTP high-throughput screening and co-authored one of the poster studies. (Photo courtesy of Steve McCaw)



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NIEHS biologist Yin Li, Ph.D., left, explains the results of her team's whole-transcriptome expression profiling to staff scientist Harriet Kinyamu, Ph.D. (Photo courtesy of Steve McCaw)

Leveraging institute-wide resources

Although Genomics Day presentations highlighted sequencing and bioinformatics support, several researchers took advantage of other resources from across the institute, including the Flow Cytometry Core and Clinical Research Unit. The trainees who presented are:

- **Shannon Farris, Ph.D.** — Farris S, Wang Y, Ward JM, Dudek SM. "Plasticity in Hippocampal Area CA2: Lost in Translation?"
- **Seddon Thomas, Ph.D.** — Thomas SY, Whitehead GS, Gowdy KM, Ward JA, Nakano K, Nakano H, Cook DN. "Dendritic and Epithelial Cell Crosstalk in the Lung: The Impact of Cell-specific Myd88 Expression on Immune Response to Inhaled Allergens."
- **Thuy-Ai Nguyen, Ph.D.** — Nguyen T-A, Menendez D, Grimm SA, Bushel PR, Ward JM, Freudenberg JM, Jothi R, Fargo DC, Resnick MA. "P53 Binding and Regulation of Immune Response Genes in Human Primary T-lymphocytes."
- **Kin Chan, Ph.D.** — Chan K, Roberts SA, Klimczak LJ, Sterling JF, Saini N, Malc EP, Kim J, Kwiatkoski DJ, Fargo DC, Mieczkowski PA, Getz G, Gordenin DA. "APOBEC3A Is the Primary Mutagenic Cytidine Deaminase in Human Cancers."
- **Janine Santos, Ph.D.** — Lozoya O, Grenet D, Wolfgang T, Santos J, Woychik R. "Crosstalk Between Mitochondrial Function, the Epigenome, and Gene Expression."
- **Benjamin Scruggs, Ph.D.** — Scruggs BS, Gilchrist DA, Nechaev S, Muse GW, Burkholder A, Fargo DC, Adelman K. "Upstream Anti-sense Promoters Are Distinct Hubs of Transcription Factor Binding and Active Histone Modifications."

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