Happenings at HCGS: Summer 2015

The 54th Annual Meeting of the Society of Nematologists, was held July 19-24, 2015 at Michigan State University Campus in East Lansing, Michigan. W. Kelley Thomas was elected to Fellow at the 2015 Society of Nematologists, and Weimin Ye (former HCGS post-doc) received the Sygenta Award. Congrats to both Weimin and Kelley!

Frequently Asked Questions:

Q: How much does a lane of sequencing cost?
A: 2 x 100 high output and 2 x 100 Rapid: $2,000.00 per lane; 2 x 150 Rapid: $2,750.00 per lane; 2 x 250 Rapid: $3,200.00 per lane

Q: How much data would you expect from a single lane of sequencing?
A: Between 130 and 200 million paired end reads (260-400 million reads total for paired-end lanes).

Q: What read lengths do you offer?
A: 100, 150 or 250

Q: What are some of the libraries you sequence regularly?
A: DNA, RNA (RNAseq), Amplicon (16S, 18S, ITS, etc), GBS

Q: What can I send you for sequencing?
A: We work with all sorts of different materials. Some users choose to send us raw tissue for extraction all the through library prep and sequencing. Others will send libraries that have already been pooled and are ready for sequencing. It depends on the need(s) of the users.
**RCN: EukHiTS Bioinformatics and Biodiversity Bootcamp**  
**July 27-30, 2015**

The HCGS just completed its second annual Bioinformatics and Biodiversity Bootcamp in conjunction with the NSF Research Coordination Network grant. We hosted 17 undergraduate students from all over the United States and three mentors: Eyualem Abebe (Elizabeth City State University), Holly Bik (University of Birmingham-UK), and Jo Sharma (University of Texas, San Antonio). The bioinformatics component focused primarily on developing command line skills to run different bioinformatics pipelines. The Biodiversity component focused on marine/estuarine environments and sampling procedures with a field trip to the Jackson Lab in Durham. Several of the attendees expressed interest in our graduate programs. If Eyualem’s and Holly’s names seem familiar, it’s because they were both HCGS post-docs.

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**Publications**

If you have any publications resulting from data generated by the HCGS that you would like to have listed here, please send the citation to Cynthia.Wiggin@unh.edu.

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“In an age of molecular genomics, it is ever more apparent that the fingerprints of evolution are pressed deeply into human DNA, just as they are into the genomes of every other organism. Biologists understand this, and so do students who study the science of life.”  
—Kenneth R Miller