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American Association of Anthropological Genetics (AAAG) News: AGAR Workshop

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American Association of Anthropological Genetics (AAAG) News: AGAR Workshop

Abstract

Early this year, more than 60 molecular anthropologists from across the country gathered in San Antonio, Texas, to hone their technical and analytical skills in the growing field of genomics at the first ever Application of Genomics to Anthropo-logical Research (AGAR) workshop. This two-day workshop, held between January 9th and 10th at the Texas Biomedical Research Institute, was organized by the Education Committee of the American Association of Anthropological Genetics (AAAG) and sought to address the major advantages (and hurdles) related to integration of state-of-the-art genomic data into anthropological studies.

American Association of Anthropological Genetics (AAAG) News: AGAR Workshop

AAAG Education Committee News: Application of Genomics to Anthropological Research (AGAR) Workshop: A Success!

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Over the course of the workshop, attendees were presented with formal lectures from experts in the field of genomics and engaged in informal Q&A and chalk-talk sessions on the intersection of genomics and anthropology. The presentations opened on the first day with an overview on genomic research by AAAG founding member John Blangero. From there, presenters quickly dove into methodological discussions of high-throughput sequencing (Joanne Curran), computational workflow and variant calling (Juan Peralta), genomic structural variation (August Blackburn), longitudinal study design and data collection (Stefan Czerwinski), investigations of genome-wide transcriptional data (Harald Göring), and uncovering adaptive variation through targeted exome sequencing (Abigail Bigham). The first day of the workshop concluded with a keynote lecture by Dr. Lynn Jorde (University of Utah, former president of the American Society of Human Genetics) on disease-gene discovery through pedigree genomics. Workshop attendees were then treated to an authentic Tex-Mex dinner at La Fonda on Main, generously donated by Texas Biomed supporters Cappy and Suzy Lawton.

Day two focused more heavily on the application of genomic technology and analytics into more traditional anthropological studies, such as ancient genomics (Nadin Rohland), population genomics (Krishna Veeramah), pathogen genome evolution (Anne Stone), and comparative primate genomics (Omer Gökçümen). At the conclusion of these lectures, the workshop attendees discussed two potential anthropological genomic projects to optimize how anthropologists can better design genomic research, target alternative sources for funding, and utilize their unique perspectives and data sets to address the big questions surrounding human evolutionary history.

In sum, the workshop was a great success, and all attendees welcomed the chance to participate in similar conferences in the future. As a result, be on the lookout for upcoming training opportunities through the AAAG on topics such as next-generation-sequencing wet-lab training, hands-on bioinformatic instruction, and similarly themed web-based instructional programs.

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