Human Heredity and Health in Africa (H3Africa)

NIH Common Fund Program









H3Africa



Overall vision: To enhance capacity for using contemporary research approaches, in Africa by African scientists, to understand the genetic and environmental factors that determine disease susceptibility and drug responses in African populations.

- Increase the number of internationally competitive African scientists in genomics and population-based research
- Establish collaborative networks of African investigators
- Create and expand infrastructure for genomics research
- Support the ongoing policy development for ethical issues in genomics research, particularly in an African context
 High-risk/high-reward with long-term goals

Current H3Africa Footprint

- ★ H3ABioNet
 - Nodes (32)
- ★ Biorepositories (3)
- Collaborative
 Centers (5 NIH)
 Collection sites
- ★ Independent Research (7)
 - Collection sites
- ELSI Research (6)
 Interview sites

Collaborative Centers (3 WT) Collection sites



Governance



H3Africa: Major Accomplishments

The epigenome of Trypanosoma brucei: A regulatory interface to an unconventional transcriptional machine

Johannes P. Maree, Hugh -G. Patterton 📥 · 🔤

A Call for Policy Action in Sub-Saharan Africa to Rethink Diagnostics for Pregnancy Affected by Sickle Cell Disease: Differential Views of Medical Doctors, Parents and Adult Patients Predict Value Conflicts in Cameroon

Wonkam Ambroise and Hurst Samia

OMICS: A Journal of Integrative Biology.

VIRAL EVOLUTION

Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak

Stephen K. Gire,^{1,2*} Augustine Goba,^{3*} Kristian G. Andersen,^{1,2*} Rachel S. G. Sealfon,^{2,4*} Daniel J. Park,^{2*} Lansana Kanneh,³ Simbirie Jalloh,³ Mambu Momoh,^{3,5}
Mohamed Fullah,^{3,5} Gytis Dudas,⁶ Shirlee Wohl,^{1,2,7} Lina M. Moses,⁸ Nathan L. Yozwiak,^{1,2} Sarah Winnicki,^{1,2} Christian B. Matranga,² Christine M. Malboeuf,² James Qu,² Adrianne D. Gladden,² Stephen F. Schaffner,^{1,2} Xiao Yang,² Pan-Pan Jiang,^{1,2}
Mahan Nekoui,^{1,2} Andres Colubri,¹ Moinya Ruth Coomber,³ Mbalu Fonnie,³ Alex Moigboi,³ Michael Gbakie,³ Fatima K. Kamara,³ Veronica Tucker,³
Edwin Konuwa,³ Sidiki Saffa,³ Josephine Sellu,³ Abdul Azziz Jalloh,³ Alice Kovoma,³ James Koninga,³ Ibrahim Mustapha,³ Kandeh Kargbo,³ Momoh Foday,³
Mohamed Yillah,³ Franklyn Kanneh,³ Willie Robert,³ James L. B. Massally,³ Sinéad B. Chapman,² James Bochicchio,² Cheryl Murphy,² Chad Nusbaum,² Sarah Young,² Bruce W. Birren,² Donald S. Grant,³ John S. Scheiffelin,⁸ Eric S. Lander,^{2,7,9}

The H3Africa policy framework: negotiating fairness in genomics

Jantina de Vries¹, Paulina Tindana², Katherine Littler³, Michèle Ramsay⁴, Charles Rotimi⁵, Akin Abayomi⁶, Nicola Mulder⁷, and Bongani M. Mayosi⁸

Sustainability: leveraging resources and building interest

CAFGen – Gabriel Anabwani, Botswana Distribution of SNVs in Uganda







SAMPLE ID





TrypanoGEN and 1000 genomes SNPs Enock Matovu - Makarare

PC 1 v 2 of SNP on Chromosome 1



TrypanoGEN samples: CDI Côte d'Ivoire DRC Dem. Rep. Congo CUI Guinea UGB SE Uganda UGN N Uganda

TrypanoGEN Bantu samples cluster tightly with 1000 genomes African (quality)

 The Nilo-Saharan (Central Sudanic; Lugbara) cluster very distinct from other African samples



Pilot 2: Transcriptome analyses in Guinea

15 samples per phenotype

Asymptomatic carriers of *T. b. gambiense* have distinct cytokine and transcription profiles (increase in IL-4, decrease in IFNγ.)

QTL: mostly genes of unknown function, 3 SNPs in HLA-A – class 1 MHC

71% prevalence in asymptomatics compared to 29 % in symptomatics, 23% in controls.



B Bucheton, A MacLeod

Christian Happi-Nigeria Advanced Genomics Training – Summer 2015



- MiSeq installation and operation
- Sample preparation and sequencing
- Sequencing analysis
- Independent research











H3Africa: Projected Resources

> Infrastructure

- Pan-African Bioinformatics capacity (physical and human resources)
- Three DNA Biorepositories (East, West, and South)
- Ethical guidelines; best practices for informed consent and community engagement in an African context
- A collaborative community and a culture of data and sample sharing

> 70,000 DNA Samples to be collected with:

- A subset of harmonized phenotypes
- Broad representation of different ethno-linguistic, environmental, cultural and genetic backgrounds and different disease states
- ~55,000 samples with H3Africa genotyping array data
- Genomic data (genotyping, whole genome, exome, microbiome)
- H3Africa Pan-African genotyping array
- Guidelines, policies, and SOPs for African genomics research

H3Africa: Looking Forward

★ You are here 🕂

	FY13	FY14	FY15	FY16	FY17	FY18	FY19	FY20	FY21	FY22
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STAGE I: Capacity Building

STAGE II: Capacity Implementation

H3Africa: Looking Forward

🗶 You are here 💛



The H3Africa Consortium: Stage I



The H3Africa Consortium: Stage II



H3Africa: Synergy and Sustainability

- NIH
 - MEPI
 - BRAD
 - FIC training programs
 - IC Global Health Initiatives
- Other Funding Agencies
 - Wellcome Trust
 - GSK
 - Gates Foundation
 - Government Funding Agencies
 - SIDA
- African Organizations
 - AESA
 - AAS
 - **AU**
 - NEPAD



Challenges



Opportunities

H3Africa NIH Working Group (EC)

*NHGRI:

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NCI:

Elizabeth Gillanders Joe Harford Damali Martin Ben Prickril Vikram Bhadrasain Makeda Williams Jack Welch

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NIDCR: Emily Harris

NIMHD: Irene Dankwa-Mullan

*NIMH:

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<u>*FIC:</u> Ken Bridbord Stacy Wallick

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NIAAA: Peggy Murray

<u>NLM:</u> Julia Royall Dan Gerendasy