HeLa Genome Data Access Working Group

Report to the Advisory Committee to the Director

December 13, 2018

Carrie D. Wolinetz, Ph.D.
Acting Chief of Staff
Associate Director for Science Policy
National Institutes of Health

Spero M. Manson, Ph.D.
Distinguished Professor of Public Health and Psychiatry
Director, Centers for American Indian and Alaska Native Health
The Colorado Trust Chair in American Indian Health
Associate Dean for Research at the Colorado School of Public Health
University of Colorado

The HeLa Genome Data Use Agreement

Per the agreement between NIH and the Lacks family, NIH is requesting that ***all researchers***:

- Apply for access to HeLa whole genome sequence in the database of Genotype and Phenotype (dbGaP)
- Abide by terms outlined in the HeLa Genome Data Use Agreement, such as:
  - Data can only be used for biomedical research only; this does not include the study of population origins or ancestry
  - Requestors are not to make contact with the Lacks family
  - Requestors are to disclose any commercial plans
  - Requestors are to include an acknowledgment in publications and presentations
- Deposit future whole genome sequence data into dbGaP

Role of HeLa Genome Data Access Working Group

- Evaluate requests to access HeLa cell genome data in dbGaP for consistency with the terms of the HeLa Genome Data Use Agreement
  - Evaluation not based on scientific merit
- Report findings to the Advisory Committee to the Director
- Make recommendations to the ACD on changes to the terms specified in the HeLa Genome Data Use Agreement

HeLa Genome Data Access Working Group Roster

Spero M. Mason, Ph.D. (Co-Chair)
Distinguished Professor of Public Health and Psychiatry
Director, Centers for American Indian and Alaska Native Health
The Colorado Trust Chair in American Indian Health
Associate Dean for Research at the Colorado School of Public Health
University of Colorado

Carrie D. Wolinetz, Ph.D. (Co-Chair)
Acting Chief of Staff
Associate Director for Science Policy
National Institutes of Health

Russ B. Altman, M.D., Ph.D.
Professor, Bioengineering, Genetics, & Medicine
Director, Biomedical Informatics Training Program
Stanford University

Ruth Faden, Ph.D., M.P.H.
Philip Franklin Wagley Professor in Biomedical Ethics
Director, Johns Hopkins Berman Institute of Bioethics
Bloomberg School of Public Health
Johns Hopkins University

David Lacks Jr.
Representative, Henrietta Lacks Family

Jeri Lacks-Whye
Representative, Henrietta Lacks Family

Richard M. Myers, Ph.D.
President, Director and Faculty Investigator
HudsonAlpha Institute for Biotechnology

Robert L. Nussbaum, M.D.
Chief Medical Officer
Invitae Corporation

Veronica Spencer
Representative, Henrietta Lacks Family

HeLa Whole Genome Sequence Data in dbGaP

Principal Investigator	Institution	Project Title	Year
John Moran	**University of Michigan**	**RNA Ligation Precedes U6 snRNA/LINE-1 Retrotransposition**	**2018**
John Moran	**University of Michigan**	**Examination of Engineered LINE-1 Integration Events in HeLa Cells**	**2018**
David Gilbert	**Florida State University**	**Bacterial Artificial Chromosomes Establish Replication Timing and Sub-nuclear Compartment de novo as Extra-chromosomal Vectors**	**2018**
Wataru Yoshida	Tokyo University of Technology, Japan	Identification of G-quadruplex Clusters by High-throughput Sequencing of Whole Genome Amplified Products with G-quadruplex Ligand	2018
Andrew Adey	Oregon Health and Science University, USA	Construction of Thousands of Single Cell Genome Sequencing Libraries using Combinatorial Indexing	2017
Jay Shendure	University of Washington, USA	Massively Multiplex Single-cell Hi-C	2016
Xun Xu	BGI-Shenzhen, China	Full-length Single-cell RNA-seq Applied to a Viral Human Cancer: Applications to HPV Expression and Splicing Analysis in HeLa S3 Cells	2016
Erez Aiden	Baylor College of Medicine, USA	A 3D Map of the Human Genome at Kilobase Resolution Reveals Principles of Chromatin Looping	2016
Jay Shendure	University of Washington, USA	Chromosome-scale Scaffolding of de novo Genome Assemblies Based on Chromatin Interactions	2014
Jay Shendure	University of Washington, USA	The Haplotype-resolved Genome and Epigenome of the Aneuploid HeLa Cancer Cell Line	2013
Lars Steinmetz	European Molecular Biology Laboratory	The Genomic and Transcriptomic Landscape of a HeLa Cell Line	2013

Working Group Evaluation Criteria

- Is the proposed research focused on health, medical, or biomedical research objectives?
  - Is the proposed research related to determining the ancestry or population origins of HeLa cells?
- Are there any plans to develop intellectual property? Specifically:
  - Does the requestor anticipate or foresee IP or developing commercial products or services from the proposed research?
  - Has the requestor agreed to notify NIH if their plans for IP or commercial products change?
- Are there any plans to publish or present findings?

Types of Findings Reported by the Working Group

In evaluating a Data Access Request, the Working Group will report a finding as:

- **Consistent** with the Data Use Agreement
- **Inconsistent** with the Data Use Agreement
- **Conditional** (will be consistent with the Data Use Agreement if NIH staff find that additional information obtained from the Requestor is satisfactory)
- **Pending** (will require a re-evaluation from the Working group once additional information is obtained from the Requestor)

Status of Data Access Requests

Number of Requests	Status
80	Evaluated by the HeLa Genome Data Access Working Group
72	Approved by NIH Director
1	Disapproved by NIH Director
7	Disapproved by NIH staff (requestors did not respond to requests for clarifications regarding publication plans, IP, and/or the non-technical summary)
Number of New Requests	**Status**
2	Being reported to ACD today

Working Group Findings: Evaluation of Access Requests

Since the last ACD meeting, the Working Group has found 2 requests to be consistent with the HeLa Genome Data Use Agreement:

Project Title	Requestor's Affiliation	Project Overview	Working Group Findings
Integrative Structural Variant Profiling for Individualized Cancer Therapies	**TRON - Translational Oncology GGMBH**	**• Immune cells are dispersed throughout the body and work together to defend the body against infection. The body's immune cells can also defend against cancer cells but only if the immune cells are "taught" which genomic changes are specific to cancer cells and should be targeted. • The investigator proposes to use the HeLa genome sequencing studies, whose cancer-specific genomic changes have been well-characterized, to develop cancer-specific prediction software that characterizes which genomic changes are specific to cancer and should be targeted.**	**CONSISTENT WITH DATA USE AGREEMENT**
Nonsense mediated decay sub-pathways	**University of Edinburgh**	**• Nonsense-mediated decay is a pathway, which exists in every cell, that functions to reduce errors in gene expression and protein assembly. It is of continued interest to better understand where and how this pathway is controlled in cells. • To investigate where and how the nonsense-mediated decay pathway operates, the investigator proposes to compare the HeLa cell genome sequence to the genomic changes previously identified in the investigator's lab.**	**CONSISTENT WITH DATA USE AGREEMENT**

ACD Discussion, Vote, and Recommendations

Working Group Findings: Evaluation of Access Requests

Project Title	Requestor's Affiliation	Working Group Findings
Integrative Structural Variant Profiling for Individualized Cancer Therapies	TRON - Translational Oncology GGMBH	CONSISTENT WITH DATA USE AGREEMENT
Nonsense mediated decay sub-pathways	University of Edinburgh	CONSISTENT WITH DATA USE AGREEMENT