NIH Advisory Committee to the Director
June 9, 2016

Summary of HeLa Genome Data Access Request

1. Project # 11065, Chromatin Dynamics Related to its Structure
   European Molecular Biology Laboratory

National Institutes of Health
Advisory Committee to the Director
HeLa Genome Data Access Working Group

HeLa Genome Data Access Request: Project 11065

Working Group Finding	Consistent with the Data Use Agreement
Project Title	**Chromatin Dynamics Related to its Structure**
Date Received	4/08/2016
Project Summary (Provided by NIH)	• The research team has used time-lapse microscopy methods to identify chromatin movements in HeLa cells in an effort to better understand genomic function and regulation • The research team will compare its microscopy data with sequencing-based structural information obtained from the HeLa data in dbGaP, to better understand how structure and dynamics of the genome influence genes and cellular functions
Institution	European Molecular Biology Laboratory
Research Use Statement (Provided by Requestor)	The three-dimensional organization of chromosomes of eukaryotic interphase cells is emerging as an important parameter for the regulation of genomic function. Beyond the mere storage of genetic information, the spatial structure of chromatin fosters its compaction, replication and transcription on all scales ranging from the single DNA base pair (bp) to ~100 Mbp of a whole chromosome. Chromatin dynamics can be studied using time-lapse microscopy methods, e.g., we could identify local chromatin movements in HeLa cells in interphase in a recent study (Wachsmuth et al., Nature Biotechnology 33, 384-389). However, details of the organization and especially of dynamic properties of chromatin in single living cells are elusive. We intend to study the interplay of chromatin organization and dynamics in HeLa cells using our time-lapse microscopy data of chromatin globally as well as of specific genomic sites. Using quantitative biophysical modelling of chromatin organization, we intend to compare our experimental data of dynamics and our simulations of structure and dynamics with structural information extracted from Hi-C data obtained in HeLa cells, too, by Rao et al. (Cell 159, 1665-1680, 2014) and deposited in dbGaP. The purpose of our study is to obtain basic knowledge about the structural organization of the human genome. We do not expect the results to be of commercial interest, and we also do not foresee that our study will generate intellectual property. If, against our expectations, such intellectual property will be generated, we agree to notify the National Institutes of Health under the terms of the HeLa Genome Data Use Agreement. If our study will generate novel scientific knowledge we plan to publish our results in peer-reviewed scientific journals.
Non-Technical Summary (Provided by Requestor)	The human genome consists of a large amount of DNA which is assembled with proteins to higher-order structures referred to as the chromatin fiber and chromosomes. Details of structural and dynamic aspects thereof are elusive, however, they are essential for cellular function, with defects resulting in diseases, including cancer. We aim to better understand the interplay of structural and dynamic aspects of the genome by comparing microscopy data that we have obtained and will obtain from HeLa cells with sequencing-based structural information that can be derived from data

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	deposited in the dbGaP. Using a physical model to describe both types of experimental data, we aim at a better understanding how structure and dynamics of the genome influence genes and cellular functions.