

NIH Advisory Committee to the Director  
December 11, 2014

### **Summary of HeLa Genome Data Access Requests**

1. HeLa Cells: Repetitive Elements  
*Institut de Genetique et de Biologie Moleculaire et Cellulaire*

National Institutes of Health  
 Advisory Committee to the Director  
 HeLa Genome Data Access Working Group  
**HeLa Genome Data Access Request: Project 7811**

<b>Working Group Finding</b>	<b>Conditional (will be approved pending receipt of satisfactory non-technical summary)</b>
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Project Title	<b>HeLa Cells: Repetitive Elements</b>
Date Received	November 17, 2014
Project Overview	<ul style="list-style-type: none"> <li>• Retrotransposons, fragments of DNA sometimes called “jumping genes,” are capable of copying and reinserting themselves throughout the genomes of plants and animals, altering the expression of important genes and which sometimes leads to cancer. More than 40% of the human genome consists of these elements.</li> <li>• The requestor plans on comparing retrotransposon insertion locations in the genomes in several human cell lines, including HeLa cell lines, with the aim of gaining insight regarding the mechanisms by which these elements are regulated by cells.</li> </ul>
Requestor’s Organization	Institut de Genetique et de Biologie Moleculaire et Cellulaire, Illkirch, France
Research Use Statement (Supplied by Requestor)	<p>Repetitive elements are forming a major part of the human genome. Some retrotransposons can still be transcribed, translated and integrate into novel genomic positions. This novel integrations are one of the hallmarks of cancer and can be a major cause of genome instability but also of the misexpression of neighboring genes. Our aim is to compare retrotransposons between different human cell lines, both their sequences as well as their genomic locations (clarification provided by requestor regarding other human cell lines to be included: “we will include MCF7, HT1080 and HCT116 cells. In the future we might extend this to other cells especially lung and colon cancer cells where activation of repetitive elements had been shown”). We will develop and apply computational methods for genomic annotations. HeLa cell lines are among the best characterized cell lines to date, and can therefore provide a valuable resource for the study of transposable elements and their evolution. Comprehensive study of repetitive elements repertoire in various cell lines will help us to get insight into co-evolution between various families of retrotransposons and repressive mechanisms that work to keep such elements silenced in variety of cell types. We will complement these in silico study with biochemical experiments to access impact of retrotransposones on genome architecture and gene expression. All the results from these studies will be published in peer-reviewed journals and/or presented at scientific conferences. We have no plans to commercialize or file intellectual property any results arising from the research.</p>
Addendum to Research Use Statement (Clarifications received from Requestor)	<ul style="list-style-type: none"> <li>• We are not seeking IP or any commercialization. If this plan should change we would of course inform NIH.</li> <li>• At the moment we are also looking at MCF7, HT1080 and HCT116 cells. In the future we might extend this to other cells especially lung and colon cancer cells where activation of repetetive elements had been shown.</li> </ul>
Non-Technical Summary (Supplied by Requestor)	The data will be used to compare endogenous transposable elements between human cell lines.