

Project Title:

Predicting 3D structure of the human genome

Name:

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<p>1. Background and purpose of the project, the relationship of the project with other projects</p> <p>Viral infection results in alterations in the transcriptome landscape of the infected cells. This may result due to changes in the chromatin conformation of the infected cells, therefore changing their promoter-enhancer regulatory network. For our project, we are using the three-dimensional structure of the genome to identify the potential changes in the regulatory elements network due to viral infection in human cell lines. Also, we will be comparing the changes among different viral strains.</p> <p>2. Specific usage status of the system and calculation method</p> <p>Processing deep-sequenced Hi-C data is a computationally intensive process, and the supercomputer facility was used extensively to process the generated Hi-C libraries. The server was used to process the Hi-C data generated using human cells transfected with different viral strains.</p> <p>3. Result/Conclusion</p> <p>Hi-C data is processed and is now being used to generate the genomic interaction tables. This will help deduce the commonality and differences in response to viral infections.</p> <p>4. Schedule and prospect for the future</p>	<p>We will use the server in the next FY for downstream analysis of the processed Hi-C data.</p> <p>5. If no job was executed, specify the reason.</p> <p>Not applicable</p>
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