平成２７年度　京都大学化学研究所　スーパーコンピューターシステム　利用報告書

NGS を用いた転写制御および細菌叢の研究

Study of transcriptional regulation and microbiomes by NGS technologies

京都大学化学研究所　バイオインフォマティクスセンター　化学生命科学研究領域

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1.Analysis of intestinal bacteria:

This research was conducted in collaboration with Prof. Okazazki of Kinki University Medical School. Ulcerative colon (UC) is a form of inflammatory bowel disease. Case studies reported by Higashi-Osaka-Shiritsu-Higashi hospital (東大阪市立東病院), have shown patients recovering from UC by treatment with elemental diet (ED). ED is also known to be effective for Crohn's disease (CD), and a change of intestinal microbiota has been observed in CD patients when compared to other patients who have not received ED.

In our research we will be seeing whether or not Lipacreon, a treatment given to patients of pancreatitis for better food digestion, will have the same effect on intestinal microbiota as ED had. We will be examining three types of mouse: Lipacreon treated mouse, Elental (elemental diet) treated mouse, and control mouse. Bile and various parts of intestine were taken from each mouse and its microbiota was examined by Next Generation Sequencer (NGS). We are currently analyzing the NGS data and are planning to continue the research.

2.Characterization of *Arabidopsis thaliana* ARR1 Binding Sites:

This research was conducted in collaboration with Prof. Aoyama of Kyoto University Institute of Chemical Research. Cytokinins promote the growth of *Arabidopsis thaliana* (*At*) by sending a signal through the His-Asp phosphorelay. This causes Arabidopsis response regulator 1 (ARR1) to activate a group of plant growth related genes.

5'-GAT(C/T)-3' (core motif) is essential for ARR1 to bind to DNA strands, and it has been discovered that the extended version of the motif, 5'-AAGAT(C/T)TT-3' (extended core motif), appears more frequently in the promoters of 23 genes that are known to be directly regulated by ARR1 when compared to randomly chosen promoters [4][5]. Chromatin immunoprecipitation sequencing (ChIP-Seq) data of non-treated (control), water treated (negative control), and benzyl adenine (BA, activator of ARR1) treated *Arabidopsis thaliana* (*At*) plants were used to identify the bindings sites of ARR1.

By analyzing the relationship between the occurrence of the core motif and the ChIP-Seq scores, we have found that ARR1 binding regions of BA treated *At* with a score $\geqq 30$ tended to have a higher density of core motif than randomly chosen sequence regions. This study is planned to be continued in the next year.