2016年03月23日 臨床醫學研究所演講照片 醫學院201教室

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題　目 :The Investigation of Genome-wide DNA Methylation

The Investigation of Genome wide DNA Methylation

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The focus of our research is on the development of both experimental and computational methods to interpret genomic and epigenomic data from plants, animals and human. By integrating data produce from the next-generation sequencing technologies, we would like to implement novel analytical strategies to solve problems in genetics and molecular biology.

Next generation genetics:

Next-generation or massively parallel DNA sequencing technologies have the potential to markedly accelerate genetics research. In our lab we perform and analyze mRNA-seq for transcriptome studies, and BS-seq for DNA methylation profiling (WGBS and RRBS). Our goal is to integrate both experiments and statistical methods and software to address biologically relevant questions.

DNA Demethylation Dynamics in the Human Prenatal Germline

It is known that the genetic information for the next generation is formed in germ cells during the pregnancy of the previous generation. However, very little is known about how prenatal germline cells are made in the body. A biochemical process that is crucial for protecting human genetic information is called methylation. All healthy cells in the human body are methylated. Methylation acts as a protective coat on the genome that safeguards cells from mutations. If cells are not methylated, the genome is vulnerable to damage. Methylation removal, called demethylation, happens very infrequently in the human body. One such time is during a short period of time in prenatal life during pregnancy. This period of germ cell demethylation was the focus of

this research, which mapped the amount, duration and location of demethylation in prenatal germ cells from 53 to 137 days of development. The study found that the human germline erases almost all evidence of genome methylation by 113 days of prenatal development. Importantly, while a large amount of demethylation did occur, some areas of the germ cells retained a small amount of methylation. The result implies that living in a healthy life environment is extremely important for the development of germ cells during the pregnancy, particularly during the first 3 to 4 months.

DNA methylation landscape in plants, animals, and human:

The genomes of many animals, plants and fungi are tagged by methylation of DNA cytosine. To understand the biological significance of this epigenetic mark it is essential to know where in the genome it is located. We are investigating the genome wide DNA methylation pattern on human prenatal germ cells. In addition, we are studying the impact of maternal diet on methylation landscape of the offspring. Also we are examining the impact of IVF (in vitro fertilization) on human and mice by studying the methylation status of fetus. New techniques are making it easier to map DNA methylation patterns on a large scale and the results have already provided surprises. We aimed to develop tools to understand the impact of this highly dynamic DNA methylation pattern and its function.

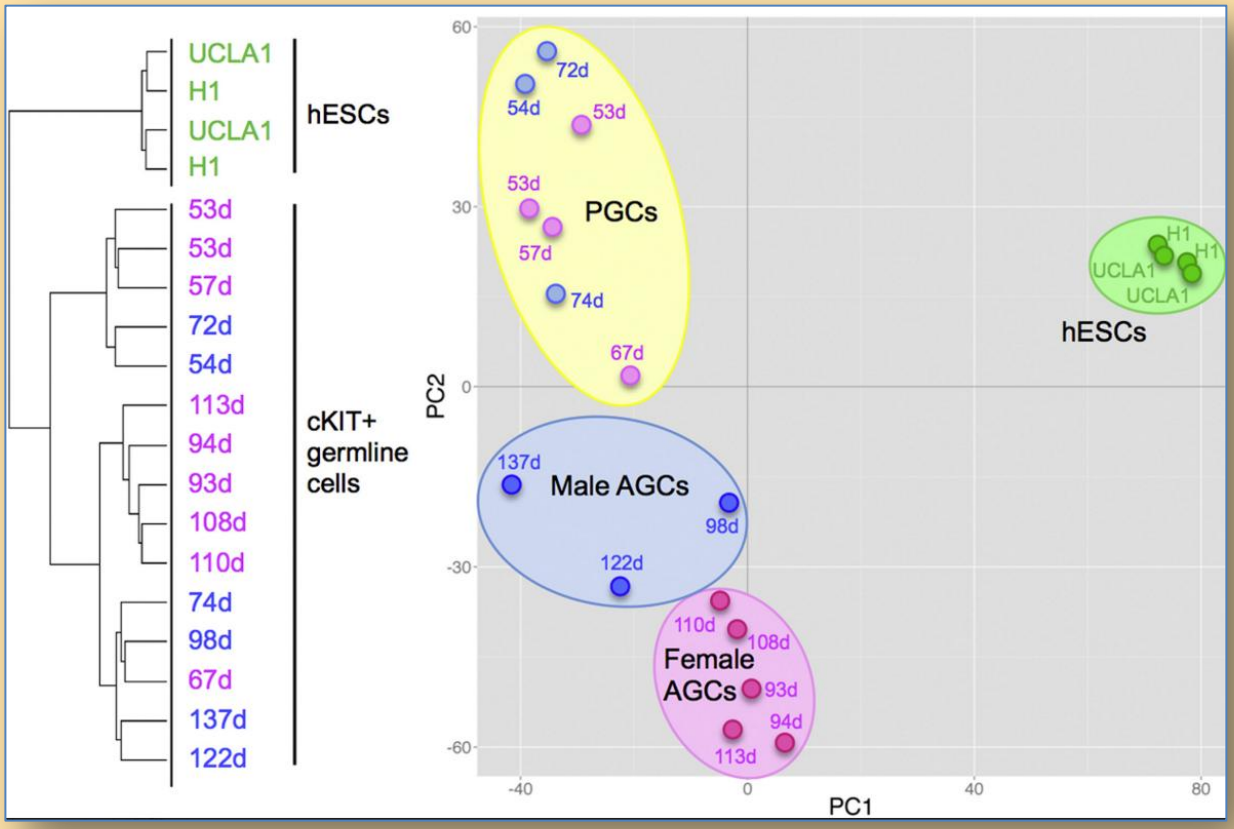
人類胚胎內生殖細胞DNA去甲基化過程探究

Sofia Gkountela, Kelvin X. Zhang, Tiasha A. Shafiq, 廖玟崴, Joseph Hargan-Calvopin, 陳柏仰*, and Amander T. Clark*
***Cell*, 161, 6, 1425–1436 (2015)**

研究貢獻：

- 完成人類胚胎內生殖細胞全基因體DNA甲基化圖譜
- 提供人類胚胎內生殖細胞基因表現量資訊
- 驗證人類生殖細胞不同於內細胞團及多功能幹細胞
- 發現人類多功能幹細胞特定DNA區域不易受去甲基化影響

生殖細胞基因表現特徵



胚胎內生殖細胞DNA去甲基化程度