Microfluidic-Based Epigenetic Studies for Precision Medicine: An Application to *BRCA1* Mutation-Related Breast Cancer

Abstract:

Epigenetics, which refers to changes in gene expression without altering the DNA sequence, has become increasingly significant in recent years for the study of cancer and human diseases. However, traditional research methods that require a large number of cells as the source of research limit the use of clinical patient samples. With the advancement of technology, the design and development of microfluidics have become more mature, enabling the use of microscale devices to study epigenetic changes. By utilizing the physical properties of microfluidics, the required number of cells for experiments can be greatly reduced. Subsequently, through software applications, low input and high-throughput requirements can be achieved.

In this study, we used microfluidic-based epigenetic studies to investigate the histone modifications (H3K27ac and H3K4me3) in *BRCA1* mutation pre-cancer human breast tissues. Our findings revealed that basal and stromal cells showed the most extensive epigenomic differences between mutation carriers (*BRCA1*mut/+) and non-carriers (*BRCA1*+/+), while luminal progenitor and mature luminal cells remained relatively unchanged with the mutation. Furthermore, the epigenomic changes in basal cells due to *BRCA1* mutation appeared to facilitate their transformation into luminal progenitor cells. Together, these results suggest that epigenomic regulation plays a crucial role in shaping the molecular landscape that facilitates tumorigenesis in the context of *BRCA1* mutation.

Overall, this microfluidic-based epigenetic study approach offers great potential for the development of precision medicine in breast cancer and other diseases. The ability to study epigenetic changes with a reduced number of cells could help overcome the limitations of traditional research methods and provide new insights into disease pathogenesis and potential therapeutic targets.