論 文 要 旨

Direct next-generation sequencing analysis using endometrial liquid-based cytology specimens for rapid cancer genomic profiling

赤羽　俊章

Abstract

Background

Genomic examination of cytology specimens is often performed on cell blocks or conventional smears rather than on liquid-based cytology (LBC) specimens. Since LBC specimens preserve high-quality DNA, cancer genome profiling using next-generation sequencing (NGS) is also attainable from residual LBC specimens. One of the advantages of using LBC specimens for NGS is that it allows direct extraction of DNA from residual specimens, avoiding a sacrifice of smear slides and minimizing genomic profiling processing time.

Methods

Endometrial LBC specimens were subjected to NGS analysis to validate the practicality of rapid cancer genomic profiling in a pathology laboratory. The extracted DNA was subjected to NGS using a customized cancer gene panel comprising 56 genes and 17 microsatellite regions. The workflow strategy was defined, and the processing time estimated for specimen sampling, cell counting, NGS run, and genome profiling.

Results

NGS analysis of most LBC specimens revealed somatic mutations, tumor mutation burden, and microsatellite instability, which were almost identical to those obtained from formalin-fixed paraffin-embedded tissues. The processing time for direct NGS analysis and cancer genomic profiling of the residual LBC specimens was approximately 5 days.

Conclusion

The residual LBC specimens collected using endometrial cytology were verified to carry a high tumor fraction for NGS analysis and could serve as an alternate source for rapid molecular classification and diagnosis of endometrial cancers, as a routine process in a pathology laboratory.