It’s a Small (-scale assay) World:  
Limited sample analysis in Tsukuba Genomics Platform  
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Recent advances in high-throughput sequencing technologies transformed genomics research. Rapid expansion of research applications of these technologies are strongly promoted by availability of useful kits and analysis software. However, it is still challenging to perform genomics analysis in individual research projects as sample format and analysis goals may not fit exactly to commercially available assays. It is also too expensive and time-consuming to go through many rounds of assay optimizations using 2nd generation sequencing. To fill the gap, we started a ‘one-stop genomics platform’ in Tsukuba, which helps timely implementation of genomics analysis for high-priority projects.

Sample limitation is a major bottle neck. Biologically interesting cell populations are often available at low quantity and quality. For example, to understand early cell specification, it is important to analyze native cells from early embryos. In clinical research, primary tissue samples from cancer patients typically provided by biobank is less than 20 mg. These small frozen tissues are shared for a panel of assays, including Exome-seq, RNA-seq, ChIP-seq and targeted validation. Furthermore, native tissue contains large portion of non-cancer cells. It usually takes several hours from surgical operation to freezing samples – compromising tissue quality. In collaboration with Diagnostic Pathology Laboratory and Tsukuba Human Tissue Biobank Centre, we are developing technological solutions to obtain high-quality ChIPseq and RNAseq data from these difficult samples. Initially, we thought this is a process to simply translate our small-scale assay workflow into clinical research. But, in reality, we often find important know-how in clinical practice to reverse-translate into basic research projects. In this talk, I will introduce some of the ongoing research in Tsukuba and would like to explore opportunities for potential collaborations.