Biobanks and future emerging technologies: new approaches, new pre-analytical challenges

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Establishing a Biobank is a major long-term commitment and samples collected today must be relevant for next generation techniques far into the future.

It is therefore crucial for biobanks to be "future compatible" and rely on sampling and storage methods to maximize the future value of the collections. In it's most basic form such future compatibility may be limited to careful sample management such as a strict adherence to quality management and best practices as laid down by authoritative sources such as ISBER (International Society for Biological and Environmental Repositories, 2012) guidelines and BRISQ (Moore *et al.*, 2011; 2012; 2013), among others.

This approach will be sufficient, if adhered to, for most current generation sequencing techniques where read-lengths are limited to 150-500 bp and if biobank samples intended for sequencing carry an abundance of RNA or DNA. But single cell sequencing of circulating tumor cells, DNA methylation analysis and proteogenomic studies, where DNA, RNA and protein from the same sample is analysed (Nesvizhskii, 2014), require new standards for sample collection and storage.

Therefore, and looking at the future, it would be very desirable to run studies similar to SPIDIA-RNA (Malentacchi *et al.*, 2014) and SPIDIA-DNA (Malentacchi, 2013) to ensure that samples can be used for proteogenomics and other applications where proteomics and nucleic acid based assays are combined. But to achieve this it is necessary to create biobank cohorts with sufficient collection, quality and storage conditions.

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