Archival Bone Marrow Samples: Suitable for Multiple Biomarker Analysis?

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Archival samples represent a significant potential for genetic studies, particularly in severe diseases with risk of lethal outcome, such as in cancer. In this pilot study, we aimed to evaluate the usability of archival bone marrow smears and biopsies for DNA extraction and purification, whole genome amplification (WGA), multiple marker analysis including 10 short tandem repeats, and finally a comprehensive genotyping of 33,683 single nucleotide polymorphisms (SNPs) with multiplexed targeted next-generation sequencing. A total of 73 samples from 21 bone marrow smears and 13 bone marrow biopsies from 18 Danish and Norwegian childhood acute lymphoblastic leukemia patients were included and compared with corresponding blood samples. Samples were grouped according to the age of sample and whether WGA was performed or not. We found that measurements of DNA concentration after DNA extraction was dependent on detection method and that spectrophotometry overestimated DNA amount compared with fluorometry. In the short tandem repeat analysis, detection rate dropped slightly with longer fragments. After WGA, this drop was more pronounced. Samples stored for 0 to 3 years showed better results compared with samples stored for 4 to 10 years. Acceptable call rates for SNPs were detected for 7 of 42 archival samples. In conclusion, archival bone marrow samples are suitable for DNA extraction and multiple marker analysis, but WGA was less successful, especially when longer fragments were analyzed. Multiple SNP analysis seems feasible, but the method has to be further optimized.

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