COMPARISON OF SHORT-READ AND LONG-READ NEXT-GENERATION SEQUENCING APPROACHES FOR HIGH RESOLUTION HLA TYPING

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The field of DNA sequencing is constantly evolving, with various techniques developed to decode genetic information. Nowadays, the main focus is on Next-Generation Sequencing (NGS), which has become the dominant approach. Since it first became available, at the beginning of 21st century, until today two main NGS methods are available, short read and long read sequencing. Considering the importance of obtaining results rapidly for patient and donor HLA typing, we aimed to compare this two approaches for high resolution HLA typing. We analyzed DNA samples *(n=12)* with Nano-TYPE™ assay (Omixon, Hungary) based on long read sequencing protocol and NGS-Pronto® (GenDx, Netherlands), which use third generation sequencing technology from Oxford Nanopore Technologies (ONT). The data obtained from ONT sequencing was compared with previously analyzed results of these samples using All type™ - FASTplex™ NGS 11 Loci Flex kit and NGS-go®-MX6-1 kit on Illumina platform, as short read sequencing protocol. What we found useful for ONT technology is the simplified workflow for library preparation and the possibility for performing only one sample or one locus, in short period of time. Oxford Nanopore Technology exhibits good performance when compared to other, well established NGS technology for HLA typing, particularly in resolving phasing and ambiguous genotypes. However, some discrepancies were found in DRB1 locus, sequenced with NanoTYPE™ assay. Both approaches have their own benefits and flaws, depending on what the assay is aiming to accomplish. With continuous improvement in the nanopore design, base calling method and novel bioinformatics tools, nanopore sequencing may fulfill the promise of a fast and robust platform for HLA typing.

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