Protocols from "Comparative performance of the BGISEQ-500 vs Illumina sequencing platforms for palaeogenomic sequencing"

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Abstract

Ancient DNA research has been revolutionized following the development of 'Next Generation' Sequencing platforms. Although a number of such platforms have been applied to ancient DNA samples, the Illumina series are the dominant choice today, mainly because of high production capacities and short read production. Recently a potentially attractive alternative platform for palaeogenomic data generation has been developed, the BGISEQ-500, whose sequence output are comparable with the Illumina series. In this study, we modified the standard BGISEQ-500 library preparation specifically for use on degraded DNA, then directly compared the sequencing performance and data quality of the BGISEQ-500 to the Illumina HiSeq2500 platform, on DNA extracted from eight historic and ancient dog and wolf samples.
 The data generated was largely comparable between sequencing platforms, with no statistically significant difference observed for parameters including level (p=0.371) and average sequence length (p=0718) of endogenous nuclear DNA, sequence GC content (p=0.311), double-stranded DNA damage rate (p=0.309), and sequence clonality (p=0.093). Small significant differences were found in single strand DNA damage rate (δS, slightly lower for the BGISEQ-500, p=0.011) and the background rate of difference from the reference genome (θ, slightly higher for BGISEQ-500, p=0.012). This may result from the differences in amplification cycles used to PCR amplify the libraries. A significant difference was also observed in the mitochondrial DNA percentages recovered (p=0.018), although we believe this is likely a stochastic effect relating to the extremely low levels of mitochondria that were sequenced from three of the samples with overall very low levels of endogenous DNA.
 Although we acknowledge our analyses were limited to animal material, our observations suggest that the BGISEQ-500 holds the potential to represent valid and potentially valuable alternative platform for palaeogenomic data generation, that is worthy of future exploration by those interested in the sequencing and analysis of degraded DNA.

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PROTOCOLS

1. Extraction method A

CONTACT: GigaScience Database

2. Extraction method B

CONTACT: GigaScience Database

3. Extraction method C

CONTACT: GigaScience Database

4. Illumina library construction Protocol

CONTACT: GigaScience Database

5. BGISeq-500 library construction Protocol

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