Comparative performance of the BGISEQ-500 versus Illumina HiSeq2500 sequencing platforms for palaeogenomic sequencing - DTU Orbit (01/01/2019)

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Background: Ancient DNA research has been revolutionised following 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.

Results: 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 \( (p = 0.718) \) 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 \( (\delta S, \text{slight lower for the BGISEQ-500, } p = 0.011) \) and the background rate of difference from the reference genome \( (\theta, \text{slightly higher for BGISEQ-500, } p = 0.012) \). 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.

Conclusions: 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.

General information
State: Published
Organisations: Department of Bio and Health Informatics, Metagenomics, University of Copenhagen, BGI-Shenzhen, Barcelona Institute of Science and Technology, Royal Belgian Institute of Natural Sciences, University of Tübingen, North-Eastern Federal University, Institute of Evolutionary Biology (UPF-CSIC)
Number of pages: 14
Publication date: 2017
Peer-reviewed: Yes

Publication information
Journal: GigaScience
Volume: 6
Issue number: 8
Article number: gix049
ISSN (Print): 2047-217X
Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2017): CiteScore 6.81 SJR 5.022 SNIP 1.784
Web of Science (2017): Impact factor 7.267
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 4.87 SJR 5.068 SNIP 1.738
Web of Science (2016): Impact factor 6.871
Scopus rating (2015): CiteScore 8.64 SJR 4.727 SNIP 1.679
Web of Science (2015): Impact factor 7.463
Web of Science (2015): Indexed yes
Scopus rating (2014): CiteScore 9.35 SJR 5.565 SNIP 2.471
Scopus rating (2013): CiteScore 3.56 SJR 1.561 SNIP 0.849
Original language: English
Keywords: Ancient DNA, BGISEQ-500, Illumina HiSeq 2500, Comparative performance
Electronic versions:
gix049
DOIs:
10.1093/gigascience/gix049

Bibliographical note
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