



Conference Abstract

Amplicon Sequencing in the Era of Highly-Accurate Long Reads

Benjamin J Callahan ‡

‡ North Carolina State University, Raleigh, United States of America

Corresponding author: Benjamin J Callahan (benjamin.j.callahan@gmail.com)

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Abstract

An important advance in DNA sequencing has been the development of long-read sequencing technologies that produce sequencing reads of tens to hundreds of kilobases in length. However, these technologies typically have high (~8%) per-base error rates. Recently, an effectively new technology I call highly-accurate long-read sequencing has been developed, that allows for the generation of multi-kilobase reads with extremely high per-base accuracies (>99.9%). I will present and evaluate two such technologies, PacBio HiFi and LoopSeq SLR sequencing, and discuss potential metabarcoding applications of highly-accurate long-read amplicon sequencing in general.

Keywords

amplicon sequencing, long reads, DNA sequencing, metabarcoding, NGS

Presenting author

Benjamin Callahan, North Carolina State University, Department of Population Health and Pathobiology, USA

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