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Protocols for " Efficient and stable metabarcoding sequencing data using DNBSEQ-G400 sequencer validated by comprehensive community analyses"

Xiaohuan Sun[1], Yuehua Hu[2], Zewei Song[1]

[1]BGI-Shenzhen; [2]CAS Key Laboratory of Tropical Forest Ecology

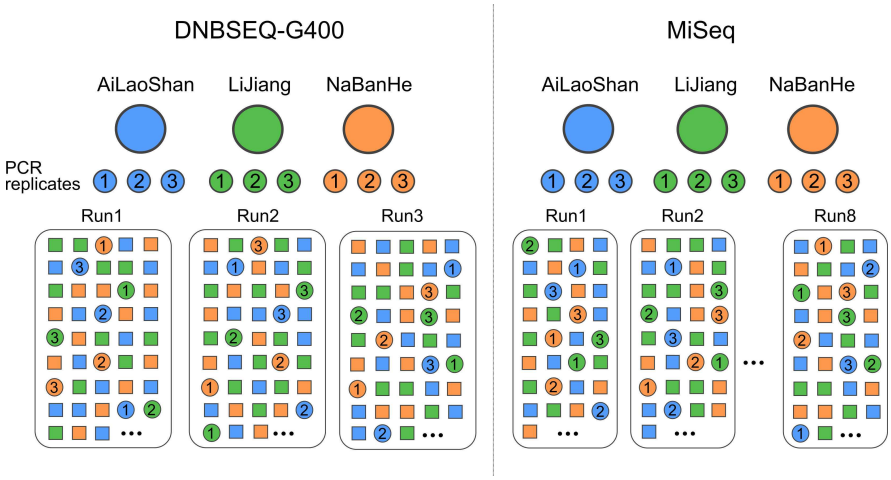
1 *Works for me* dx.doi.org/10.17504/protocols.io.brtpm6mn

Xiaohuan Sun

ABSTRACT

Sequencing in DNBSEQ-G400 of this study was carried out in BGI-Shenzhen. Amplicons from 1276 soil samples were randomly and equally distributed into 3 DNBSEQ runs for both 2×200 paired-end (PE200) and 400 bases single-end sequencing (SE400). The left libraries of total 1276 samples were repetitively sequenced two more times by SE400 using different DNBSEQ-G400 machines. Three randomly chosen soil samples from each forest plot (ALS268, LJ105 and NBH217) were all amplified 3 times separately as PCR replicates. The corresponding 9 sequencing libraries were sequenced repetitively by 3 DNBSEQ runs.

Sequencing was carried out using the entire lane of the Illumina MiSeq platform in the University of Minnesota Genomic Center. Amplicons of the 1276 forest soil were normalized and pooled randomly in equal molar ratios into 8 parallel sequencing runs on MiSeq platform. Again, three randomly chosen soil samples from each forest plot (ALS268, LJ105 and NBH217) were all amplified 3 times separately as PCR replicates. The corresponding 9 sequencing libraries were sequenced repetitively by 8 MiSeq runs.



Schematic representation of sequencing strategy at DNBSEQ-G400 and Illumina MiSeq platforms.

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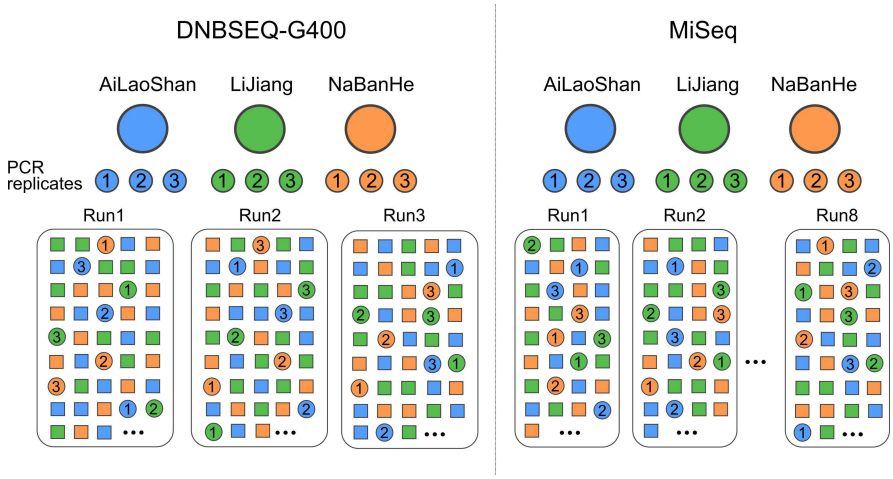

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FILES

High-throughput microbial metabarcoding amplification Protocol sequenced by DNBSEQ-G400
Version 1
by Xiaohuan Sun

Library construction of metabarcoding at DNBSEQ-G400 with MGIEasy universal DNA library prep Kit
Version 1
by Xiaohuan Sun

Sequencing at DNBSEQ-G400 platform with PE200 and SE400 modes
Version 1
by Xiaohuan Sun

Sample preparation for Illumina MiSeq Dual Index metabarcoding
Version 1
by Xiaohuan Sun

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