DeCodi-Fi

High-Fidelity Polymerase Kits

OXFORD NANOPORE 16S SEQUENCING

of soil samples from the Atacama Desert

GOAL

Compare Blikka Genomics' DeCodi-Fi™ High Fidelity Polymerase and NEB's LongAmp® Taq DNA Polymerase for microbial diversity assessment in soil using 16S-targeted ONT sequencing.

METHOD

4 soil samples were sequenced in a single MinION run. Libraries were prepared using either DeCodi-Fi or LongAmp Taq and barcoded for simultaneous sequencing.

PCR was performed based on the thermal cycling protocol recommended by ONT for LongAmp Taq with 16s primers with barcodes, which was not optimized for DeCodi-Fi:

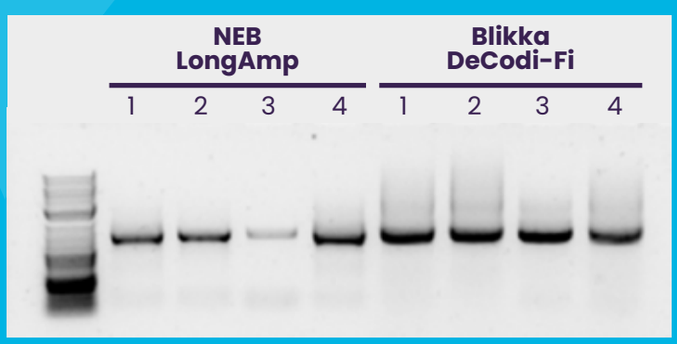
Initial denaturation: 95°C for 3 minutes
35 cycles of:
- 95°C for 20 seconds
- 57°C for 1 minute
- 65°C for 1 minute

Final extension: 65°C for 10 minutes

Despite not being optimized for it, DeCodi-Fi showed robust amplification and full compatibility with the 16S library prep workflow, outperforming LongAmp and highlighting its potential for integration into ONT workflows.

RESULTS

DeCodi-Fi™ High Fidelity Polymerase produced more reads and higher total yield. Due to this increased output, **it consistently outperformed NEB LongAmp,** detecting **2–3X greater microbial diversity.** Read length and quality scores were comparable between methods. Samples 1–4 correspond to four different soil samples analyzed using each polymerase.



These results were generated by Alexis Gaete Silva, Postdoctoral Researcher, Pontificia Universidad Católica de Chile.

QC data		Sample 1		Sample 2		Sample 3		Sample 4	
		Blikka DeCodi-Fi	NEB LongAmp	Blikka DeCodi-Fi	NEB LongAmp	Blikka DeCodi-Fi	NEB LongAmp	Blikka DeCodi-Fi	NEB LongAmp
Yield, Mb		**26.0**	11.2	**24.5**	12.0	**29.4**	3.1	**20.0**	13.8
Q score	**Mean**	13.5	14.2	13.6	14.1	13.7	14.2	13.8	13.9
	Median	13	14	13	14	13	14	14	14
Read Length	**Mean**	1382	1364.4	1388	1399.3	1409.7	1410	1393.9	1368.7
	Median	1404	1399	1419	1422	1422	1414	1418	1416