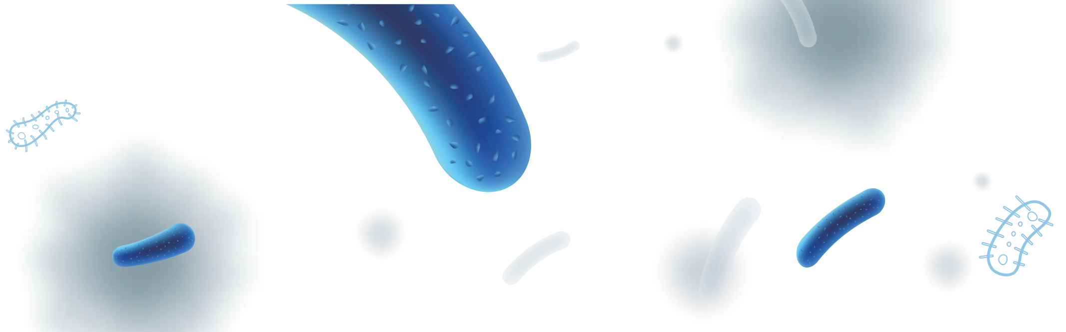

MGI pathogens metagenomic sequencing products package based on DNBSEQ-G99

A fast and accurate sequencing solution that provides a powerful tool for the identification of unknown pathogens and epidemiological research.

Highlights

- **Fast turnaround time throughout the entire process**
  With the DNBSEQ-G99ARS sequencer, library preparation, sequencing, and analysis can be completed in 14.5 hours.
- **Excellent data quality**
  The unique DNBSEQ sequencing technology provides high-quality sequencing data for downstream analysis.
- **High level of automation**
  Combined with the MGISP-100 and data analysis software, automated library preparation and data analysis can be achieved, reducing manual labor.
- **Comprehensive analysis capabilities**
  The self-developed software meets the needs of pathogen identification, genome assembly, mutation monitoring, and traceability requirements.

Introduction

Based on MGI's reagents, automated sample preparation systems, high-throughput sequencing platforms and data processing systems, the entire process from sample to result is covered. This enables fast and accurate high-throughput sequencing of samples, allowing for pathogenic microbiome typing, genome assembly, prediction of virulence and drug resistance genes, and systematic evolutionary analysis, provides tool for the precise identification, monitoring, early warning, tracing of epidemics.

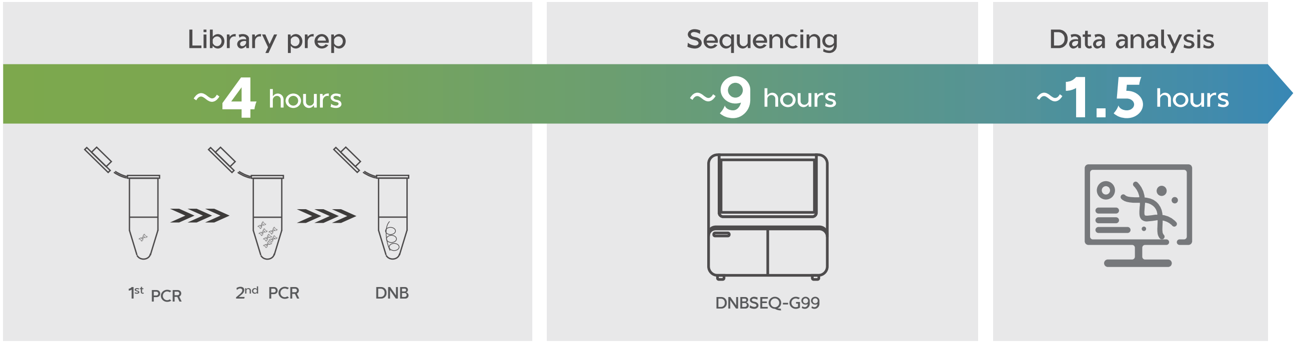

Fig 1. Flowchart

DNBSEQ-G99ARS is one of the fastest models among global mid-sized sequencer, capable of completing PE150 sequencing in 12 hours. It provides efficient and high-quality data output. With built-in computational modules, it achieves integration of sequencing and bioinformatics analysis. It can be used with the BBS (Bioanalysis By Sequencing) to perform data analysis in SE40, SE100, and PE100 formats, enabling rapid identification of pathogens.

Table 1. Parameters

Intended use	Reads length	Reads number	Samples/FC
DNA pathogens sequencing	Identification：SE50	Identification：20M	Identification：4 samples/FC
	Genome assemble：PE100	Genome assemble：80M	Genome assemble：1 samples/FC

The MGAP is based on MPS and genomics technology, which enables the assembly of genomes, systematic evolutionary analysis, and automatic calculation of variation detection results from sequencing data. It also allows flexible selection of analysis modules according to specific needs. The Pathogen Fast Identification software (PFI) is a microbial rapid identification system developed based on the DNBSEQ sequencing platform. It enables fast and accurate identification of microorganisms in the original specimens, automatically generating analysis results, and providing reference for the study of infectious diseases.

Performance

The library preparation, sequencing, and analysis were performed on four simulated pathogen samples (NA12878 standard + microbial DNA). The results after sequencing are as follows: total reads > 110M, Q30 > 95%, split rate > 96%. The data output and quality are excellent.

Table 2. Data QC

Total reads (M)	Q30 (%)	SplitRate (%)
110.17	95.22	96.95

The pathogen identification results of the four simulated samples are consistent with expectations, and the abundance of reads detected for each bacterial species is close to the theoretical abundance, as shown in Table 3.

Table 3. Identification results

Species	Sample1	Sample2	Sample3	Sample4	theoretical abundance	Mean	SD	CV
Salmonella enterica	15.87%	15.60%	15.72%	15.87%	12.00%	15.77%	0.13%	0.008
Pseudomonas aeruginosa	14.12%	14.00%	13.83%	14.12%	12.00%	14.02%	0.14%	0.010
Bacillus subtilis	13.30%	13.14%	13.46%	13.30%	12.00%	13.30%	0.13%	0.010
Escherichia coli	11.75%	12.32%	11.90%	11.75%	12.00%	11.93%	0.27%	0.023
Enterococcus faecalis	11.13%	11.30%	11.24%	11.13%	12.00%	11.20%	0.08%	0.008
Listeria monocytogenes	11.12%	11.02%	11.12%	11.12%	12.00%	11.10%	0.05%	0.005
Staphylococcus aureus	10.18%	10.23%	10.30%	10.18%	12.00%	10.22%	0.06%	0.006
Limosilactobacillus fermentum	9.52%	9.48%	9.46%	9.52%	12.00%	9.50%	0.03%	0.003
Cryptococcus neoformans	1.49%	1.49%	1.52%	1.49%	2.00%	1.50%	0.02%	0.010
Saccharomyces cerevisiae	1.47%	1.42%	1.45%	1.47%	2.00%	1.45%	0.02%	0.016

Taking one of the samples as an example, the PFI software was used to identify the species and subspecies levels. The identification results are shown in Table 4 and Table 5, and they are consistent with expectations.

Table 4. species identification results

Type	Scientific Name	Real Reads	Estimated Reads	Relative Abundance
Bacteria	*Salmonella enterica*	16,432	30,820	15.96%
Bacteria	*Pseudomonas aeruginosa*	1,340	26,947	13.96%
Bacteria	*Bacillus subtilis*	12,406	25,682	13.30%
Bacteria	*Escherichia coli*	653	22,875	11.85%
Bacteria	*Enterococcus faecalis*	20,022	21,947	11.37%
Bacteria	*Listeria monocytogenes*	13,728	21,183	10.97%
Bacteria	*Staphylococcus aureus*	10,950	19,885	10.30%
Bacteria	*Limosilactobacillus fermentum*	16,331	18,025	9.34%
Fungi	*Cryptococcus neoformans*	2,736	2,894	1.50%
Fungi	*Saccharomyces cerevisiae*	2,191	2,798	1.45%

Table 5. subspecies identification results

Type	Scientific Name	Real Reads	Estimated Reads	Relative Abundance
Fungi	*Saccharomyces cerevisiae S288C*	2,187	3,158	52.10%
Fungi	*Cryptococcus neoformans var. grubii*	988	1,517	25.03%
Fungi	*Cryptococcus neoformans var. neoformans*	1,365	1,384	22.84%

Our software also performed analysis and annotation of virulence and resistance factors for this sample. The results are shown in Table 6 and Table 7. The analysis results can provide reference for studying the pathogenic mechanisms and drug resistance of microorganisms.

Table 6. virulence genes analysis result

Virulence Factor	Microorganism	Virulence Protein	Coverage	Depth
ospC4	*Shigella boydii Sb227*	VFG012785(gi:3776756)	57.00	5.58
ycbV) putative fimbrial-like protein [E. coli YcbQ laminin-binding fimbriae (ELF	*Escherichia coli O157:H7 str. EDL933*	VFG042403(gi:15800803)	84.90	2.49
pilV	*Pseudomonas aeruginosa PAO1*	VFG001207(gb|NP_253241)	78.82	2.15
vgrG2	*Pseudomonas aeruginosa PAO1*	VFG041012(gi:15596708)	74.92	1.97
fliS	*Escherichia coli O157:H7 str. EDL933*	VFG043104(gi:15802360)	86.34	1.94
sfaB	*Staphylococcus aureus subsp. aureus str. Newman*	VFG044275(gi:151222292)	88.28	1.94
sbnG	*Staphylococcus aureus subsp. aureus str. Newman*	VFG044260(gi:151220278)	81.90	1.93
fliI	*Escherichia coli O157:H7 str. EDL933*	VFG043110(gi:161367587)	90.82	1.89
fss1	*Enterococcus faecalis V583*	VFG043508(gb|NP_813892)	83.63	1.78
cheY	*Salmonella enterica subsp. enterica serovar Typhimurium str. LT2*	VFG043037(gi:16765258)	93.32	1.77

Table 7. Resistance genes analysis results

Group	Gene	Class	Mechanism	Type	Coverage	Depth
TETL	MEG_7095	Tetracyclines	Tetracycline resistance MFS efflux pumps	Drugs	98.76	15.26
ANT4-PRIME	MEG_978	Aminoglycosides	Aminoglycoside O-nucleotidyltransferases	Drugs	98.57	12.72
TETL	MEG_7093	Tetracyclines	Tetracycline resistance MFS efflux pumps	Drugs	82.49	10.17
QACG	MEG_5846	Drug and biocide resistance	Drug and biocide SMR efflux pumps	Multi-compound	99.38	4.29
ANT4-PRIME	MEG_981	Aminoglycosides	Aminoglycoside O-nucleotidyltransferases	Drugs	86.36	4.29
ANT4-PRIME	MEG_983	Aminoglycosides	Aminoglycoside O-nucleotidyltransferases	Drugs	52.04	2.63
ZUPT	MEG_7865	Biocide and metal resistance	Biocide and metal resistance protein	Multi-compound	82.56	2.26
SITB	MEG_6514	Biocide and metal resistance	Biocide and metal ABC efflux pumps	Multi-compound	87.09	1.71
MEXE	MEG_3909	Drug and biocide resistance	Drug and biocide RND efflux pumps	Multi-compound	79.42	1.69
ACRA	MEG_399	Drug and biocide resistance	Drug and biocide RND efflux pumps	Multi-compound	86.84	1.68

Ordering information

Products	Specifications	Item No.
Sequencer		
DNA Sequencing Library Preparation System MGISP-100RS	Standard	900-000206-00
DNBSEQ-G99ARS	With server	900-000609-00
Reagent		
MGIEasy Fast FS DNA Library Prep Set	96 RXN	940-000027-00
MGIEasy Fast FS DNA Library Prep Set	16 RXN	940-000029-00
DNBSEQ OneStep DNB Make Reagent Kit	4 RXN	1000026466
High-throughput Sequencing Set (G99 SM FCL PE150)	1 Test / Kit	940-000410-00
Software		
Platform of microorganisms Fast Identification software	——	970-000208-00
MGI MGAP	——	970-000109-00

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