



PMseq病原微生物高通量基因检测报告单

PMseq[®] Pathogenic Microorganism Sequencing Result

Name	Fengyao Bi
Sample ID	19B0204676

Name: Fengyao Bi

Sampling Date: 2020-12-29 00:00:00.0

Sample No.: 19B0204676

● Basic Information

Patient Information

Name: Fengyao Bi

Gender: Male

Age: 23 days

Admission No.: 909269

Bed No.: 12

Original Sample No.:-

Clinic Description

Clinical Symptoms: Fever, Convulsions for 1 day

Laboratory testing Results:

Blood WBC: $20.38 \times 10^9/L$ CSF WBC: $283 \times 10^6/L$ Pleural/Ascitic fluid WBC: - CRP: 10.9 mg/L

PCT: 102 μ g/L Culture Result: - Identification Result: - Microscopy Result: -

Clinical Diagnosis: Intracranial Infection, Neonatal Sepsis

Suggestive Pathogenic Agent: Fungi, Bacteria, Mycobacteria, Mycoplasma/Chlamydia, Parasites, Viruses

Anti-infection Agents History: Ceftriaxone, Penicillin, Meropenem, Ceftizoxime, Ampicillin

Sample Information

Applicant: Kunming children's Hospital

Department: Neonatology

Physician: Tingting Liu

Sampling Date: 2020-12-29 00:00:00.0

Received Date: 2020-12-31 10:59:50.0

Reported Date: 2021-01-01 13:59

Sample ID: 19B0204676

Sample Type: Blood

Sample Status: Pass

Test No.: DX1818

Test items : PMseq-DNA Pathogenic Microorganism Sequencing in
Bloodstream Infections

Name: Fengyao Bi

Sampling Date: 2020-12-29 00:00:00.0

Sample No.: 19B0204676

● Sequencing data and theoretical sensitivity of pathogen

Total Reads	Human cell content (6GB) (cells/mL)	Bacteria (4MB) theoretical sensitivity (copies/mL)	Fungi (100MB) theoretical sensitivity (copies/mL)	Virus (10KB) theoretical sensitivity (copies/mL)	Parasites (1GB) theoretical sensitivity (copies/mL)	Internal Reference (Yes/No)
215,106,808	4.60E+04	1.00E+00	1.00E+00	1.30E+02	1.00E+00	Yes

Notes:

Total Reads: The total number of nucleic acid sequences detected by high-throughput sequencing.

Human cell content (cells/mL): The theoretical value of the number of human cells detected through quantitative of human genomic DNA.

Theoretical sensitivity: The number of microorganisms in the unit volume is required when a sequence of pathogenic microorganism was detected and determined as positive.

The number of microorganisms = (human cell content × human genome size) / (total reads × microbial genome size).

In the report, the human genome (diploid) size was 6GB, assumed about 4 MB for the bacteria genome, about 100MB for fungi genome, 10KB for the virus genome, and 1 GB for the parasite genome, respectively. Note: The pathogen genome was determined using the common pathogen size of the Pathogen Microbial Public Database rather than actual size.

Detection Sensitivity: The detection sensitivity was correlated positively with the total reads and negatively correlated with the human cell content per volume of specimen. Due to sequence homology among species, the actual sensitivity is slightly lower than theoretical sensitivity.

Internal Reference: The sequence of internal control added to testing sample.

● Sequencing Results

1) List of detected Bacteria

Type	Genus		Species		Relative abundance
	Name	SMRN	Name	SMRN	
Not found					

2) List of detected Fungi

Name	Genus	Name	Species	Relative abundance
	SMRN		SMRN	
Not found				

3) List of detected DNA Viruses

Type	Species		Type/Subtype		Relative abundance
	Name	SMRN	Name	SMRN	
Not found					

Name: Fengyao Bi

Sampling Date: 2020-12-29 00:00:00.0

Sample No.: 19B0204676

4) List of detected RNA Viruses

Type	Species		Type/Subtype		Relative abundance
	Name	SMRN	Name	SMRN	
Not found					

5) List of detected Parasites

Genus		Species		Relative abundance
Name	SMRN	Name	SMRN	
Not found				

6) List of detected Mycobacterium tuberculosis

Species Complex		Species		Relative abundance
Name	SMRN	Name	SMRN	
Not found				

7) List of detected Mycoplasma/Chlamydia/Rickettsia

Genus		Species		Relative abundance
Name	SMRN	Name	SMRN	
<i>Orienti</i>	25	<i>Orientia tsutsugamushi</i>	23	0.43

8) list of suspected background microorganisms

Type	Genus		Species		Relative abundance
	Name	SMRN	Name	SMRN	
<i>G⁻</i>	<i>Acidovorax</i>	88	<i>Acidovorax delafieldi</i>	24	0.63
			<i>Acidovorax spKKS102</i>	8	0.35
<i>G⁺</i>	<i>Cutibacterium</i>	66	<i>Cutibacterium acnes</i>	41	0.85
			<i>[Propionibacterium] humerusii</i>	7	0.10
<i>G⁻</i>	<i>Acinetobacter</i>	54	<i>Acinetobacter johnsonii</i>	17	0.19
			<i>Acinetobacter junii</i>	14	0.23
<i>G⁻</i>	<i>Dyella</i>	43	<i>Dyella jiangningensis</i>	40	0.80
<i>G⁻</i>	<i>Caballeronia</i>	30	<i>Caballeronia sordidicol</i>	12	0.48
Virus	Not found				
Fungi	<i>Malassezia</i>	7	<i>Malassezia restricta</i>	3	1.67
Parasite	Not found				

Notes:

1) **Type:** Refers to the type of pathogenic microorganism detected including bacteria, viruses, fungi and

Name: Fengyao Bi

Sampling Date: 2020-12-29 00:00:00.0

Sample No.: 19B0204676

parasites. Bacteria includes G+ (gram-positive bacteria) and G- (gram-negative bacteria), and viruses includes single-stranded DNA virus (ssDNA), double-stranded DNA virus (dsDNA), single-stranded RNA virus (ssRNA) and double-stranded RNA virus (dsRNA). -: Unknown; *: indicates that only the genus name could be interpreted.

- 2) **SMRN**: Stringently mapped reads number of a specific microorganism at Genus/Species.
- 3) **Relative abundance**: Refers to the percentage of microorganisms at the lowest level detected in same type of microorganisms (bacteria/fungi/viruses/parasites).
- 4) **Suspected background microorganisms**: Refers to the normal commensal/colonizing microorganism present in the human body, or the microorganism by contamination, the possibility of infection is not ruled out.

Name: Fengyao Bi

Sampling Date: 2020-12-29 00:00:00.0

Sample No.: 19B0204676

● Result Interpretation

The microorganisms detected in the delivered sample was listed by bacteria, viruses, fungi, parasites, mycobacterium tuberculosis complex, mycoplasma/chlamydia/rickettsia and suspected background microorganisms in order of the number of unique reads from high to low. The interpretation of testing results in clinical practice should be made by the clinician integrating the patient's clinical situation and other examination results.

The following was brief information of the detected microorganisms (excluding suspected background microorganisms) listed in the tables. (If no microorganism was listed in above table, the following will be empty):

Orientia tsutsugamushi: It is an obligate intracellular bacterium, the pathogen of tsutsugamushi disease, which is transmitted by the bite of infected chigger mites (primarily *Leptotrombidium* spp.) to humans[1-2].

References

- 1 PMID: 23589529. Ikegaya S, Iwasaki H et al. Tsutsugamushi disease caused by Shimokoshi-type *Orientia tsutsugamushi*: the first report in Western Japan. *Am J Trop Med Hyg.* 2013 Jun;88(6):1217-9.
2. PMID: 24647257. Im JH, Baek JH et al. A case series of possibly recrudescent *Orientia tsutsugamushi* infection presenting as pneumonia. *Jpn J Infect Dis.* 2014;67(2):122-6.

Name: Fengyao Bi

Sampling Date: 2020-12-29 00:00:00.0

Sample No.: 19B0204676

● Detection technology

1) Methods

PMseq® Pathogenic Microorganism High-Throughput Sequencing is based on metagenomics technology. The nucleic acids of all microorganisms in the testing samples are extracted and sequenced unbiasedly on BGI's high-throughput sequencing platform. The generated data was analyzed using dedicated bioinformatic pipelines with curated high-quality and high-standard pathogen database PMDB to detect the pathogens in testing specimens. The curated database PMDB includes about 17,500 pathogens composed of bacteria, fungi, viruses, and parasites. The technology significantly improves the positive rate of pathogen intending to provide information for clinical diagnosis, infection control and management and precise treatment of infections.

2) Assay procedures

The detection process includes sample collection, sample reception, nucleic acid extraction, DNA enzyme hydrolysis + bead-milling /RNA enrichment, library construction, high-throughput sequencing, bioinformation analysis, and result interpretation and release.

3) Microbial species

The PMDB database includes 10989 bacteria (incl. 196 mycobacteria and 159 mycoplasma/chlamydia/rickettsia), 5050 viruses (incl. DNA viruses and RNA viruses), 1179 fungi and 282 parasites.

4) Limitation

- a) The test results are only for reference in clinical practice for assessing infection situation and cannot be solely used for the final clinical decision.
- b) The results in the report are only responsible for the delivered and testing samples. The interpretation of the results must be consulted by the clinician;
- c) The assay cannot guarantee the detection of microorganisms below the limit of detection in the delivered sample. Specific microorganism absent in the testing results does not exclude the possibility of infection, such as in the case of an infection caused by a microorganism outside PMDB.

Tested by:

Reviewed by:

Reported Date: 2021-01-01 13:59