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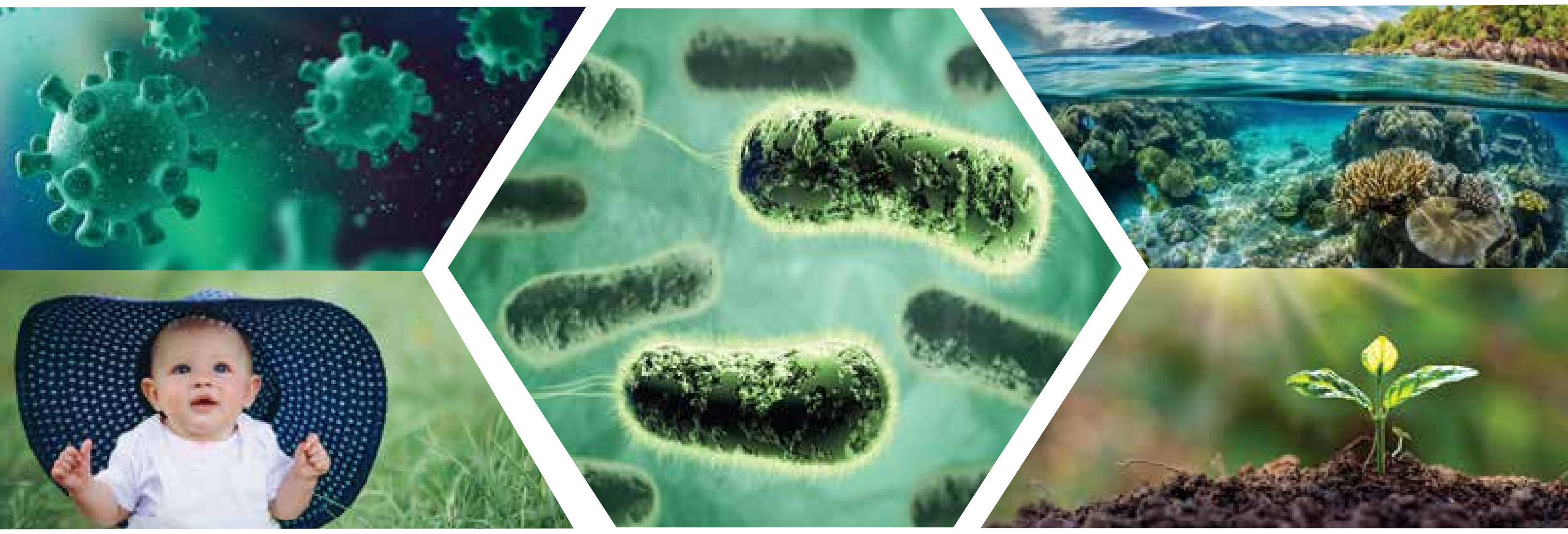
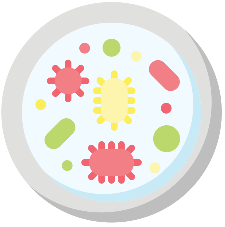


Unlocking the Microbial Universe Exploring Diversity with

SHOTGUN METAGENOMIC SEQUENCING

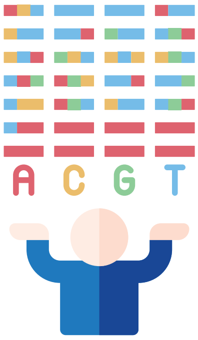
Shotgun Metagenomic Sequencing is a powerful tool for exploring the structure and function of certain organism communities allowing novel discoveries and new insights by analyzing the sequence of genomes present in the community.

It is a robust and a high-throughput method that is applicable to bacterial, fungal, and any microbial as well as eukaryotic communities. A genome holds such dense information that can be harnessed to help researchers better understand their subject and metagenomic further builds upon this by offering information not limited from one organism but all organisms in the environment of interest at the same time.



Why should we use shotgun metagenomic sequencing than the traditional microbial culture techniques?

The metagenomic sequencing technique is not limited by any culture media limitation as in the microbial culture techniques. So long as the genomic DNA of an organism exists within the sample, that organism will be detected using the metagenomic sequencing technique.

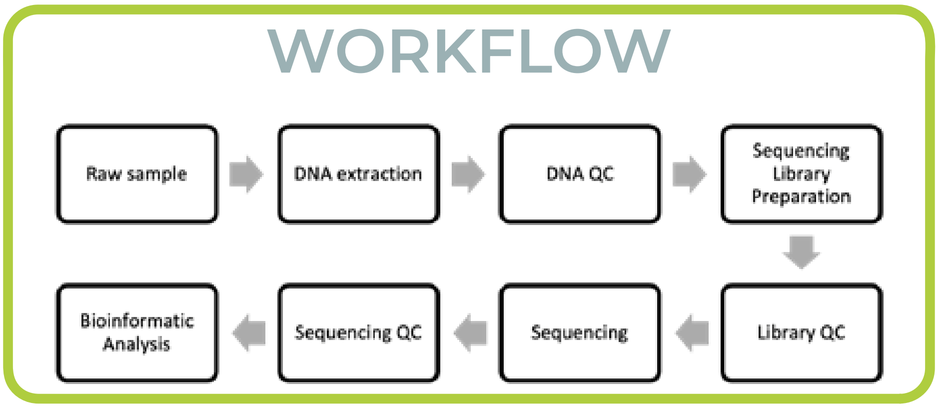


Why should we use shotgun metagenomic sequencing instead of amplicon metagenomic sequencing?

Unlike amplicon metagenomic sequencing, there is no PCR amplification biases introduced in shotgun metagenomic sequencing such that this method is best-suited for discovering have-not-yet-discovered organisms.

Even more, this method offers much richer data compared to the ordinary amplicon metagenomic sequencing by showing the annotated functional genes present in the community as well.

Genetika Science Indonesia is Offering
Shotgun Metagenomic Sequencing using Next Generation Sequencing (NGS) with Illumina Platform.



WORKFLOW

Raw sample
DNA extraction
DNA QC
Sequencing Library Preparation
Library QC
Sequencing
Sequencing QC
Bioinformatic Analysis

Sample Requirements:

- Platform: Illumina NextSeq 500
- Sample type: Raw sample or genomic DNA
- gDNA amount: minimum 100 ng (Nanodrop)
- gDNA Volume: minimum 30 µL
- gDNA Purity: OD 260/280 = 1.8 -2.0

Note:

- ○ Use aseptic technique when taking any samples to prevent any unwanted cross-contamination, especially environmental samples.

- ○ For endophytic microbes or microbes inside a host, avoid extracting the host gDNA as well.

- ○ If the microbial composition data is time-sensitive (e.g samples involving fermentation) extract the genomic DNA immediately after sampling or keep the sample in -20 °C or below.

- ○ When applicable, consider concentrating any liquid sample with low or sparse abundance using either filtration or centrifugation to improve species detection.

Some of the key deliverables for shotgun metagenomic sequencing:

- Raw sequencing data in fastq format.
- Sequencing data QC
- Bioinformatic analysis, includes:
  - Completeness of assembled genomes.
  - Taxonomy annotation and species abundance.
  - Functional profiling and analysis (KEGG, eggNOG, and CAZy).
  - Alpha diversity indices calculation and statistical analysis
  - Beta diversity statistical analysis.
  - Various diagrams and charts (such as Krona, Ternary, Venn, Sankey & PCoA).

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