

**2010****Environmental DNA**

Schmidt et al. first reported environmental genomics by isolating and cloning environment DNA

**2005 ★****NGS sequencer**

First NGS sequencer released by Roche 454. Metagenomic study of human gut virome

**1998****Metagenome**

Handersman proposed the terms metagenomics

**1991****EMP project**

The Earth Microbiome Project (EMP) is an initiative founded

**2024+****More expectations +****2011 ★****PacBio RS sequencer**

PacBio RS sequencer was released, read length beyond 10 kb

**2014****PacBio metagenome project**

Wichmann et al. were the first to report the Exploring ARGs in dairy cow manure with PacBio RS sequencer

**2014 ★****ONT MinION sequencer**

ONT released the MinION sequencer

**2015****ONT metagenome project**

Greninger et al. were the first to report the utilization of real-time metagenomic detection for identifying viral pathogens in clinical specimens via MinION sequencing technology

**2015****PacBio Sequel sequencer**

PacBio releases Sequel system, enhancing long-read metagenomic studies

**2019****ONT Flongle, PromethION sequencer**

ONT released Flongle (small-scale sequencing applications) and PromethION (high throughput long-read sequencing). The R9.4.1 flowcell achieved average accuracy of 92%

**★2022 ONT R10.4.1 Flowcell****★2014 ONT**

1998

**★**

2005

NGS

1991

2010

2019

2024

**Big deals in metagenome studies****2024****BASALT Long-read binners**

BASALT (Binning Across a Series of Assembly Toolkit) released, which can binning and optimize short- or long-read metagenomic

**2023****metaSVs tool**

metaSVs (A pipeline combining long- and short-read to analyze structural variants in metagenomes) released

**2023****Long-read metagenomics — a new milestone**

Comment "Long-read metagenomics paves the way toward a complete microbial tree of life" was published in Nature Method

**2022 ★****ONT R10.4.1 Flowcell Q20 chemistry**

Nanopore released Q20 chemistry and R10.4.1 flowcell. Long-read only metagenomics allows high quality genome reconstruction without Illumina correction

**2020****metaFlye assembler**

The long-read metagenomic assembly software "metaFlye" was published in Nature Methods

**2022****PacBio Revio sequencer hifi-sm-meta assembler**

PacBio Revio upgrade increases throughput and guarantees that HiFi reads attain an accuracy surpass Q30. Then "hifi-sm-meta" was published in Nature Method