Projects for END Course:
1)16S (Phan Tấn Phát và Nhật Trường)   2) Shotgun
(Phúc)

Metaproteomics, metagenomics and 16S rRNA sequencing provide different perspectives on the aerobic granular sludge microbiome

Hugo B.C. Kleikamp [a][1] 👤 ✉, Denis Grouzdev [b], Pim Schaasberg [a], Ramon van Valderen [a], Ramon van der Zwaan [a], Roel van de Wijgaart [a], Yuemei Lin [a], Ben Abbas [a], Mario Pronk [a], Mark C.M. van Loosdrecht [a], Martin Pabst [a] 👤 ✉

Data availability
The mass spectrometry proteomics raw data have been deposited in the ProteomeXchange consortium database with the dataset identifier PXD030677. Whole metagenome sequencing raw data are available through the NCBI Sequence Read Archive (SRA) under accession numbers SRX13522658– SRX13522660, and the 16S rRNA amplicon sequencing data under the accession numbers SRX21486087–SRX21486101. The BioProject accession number is PRJNA792132. The developed python codes for formating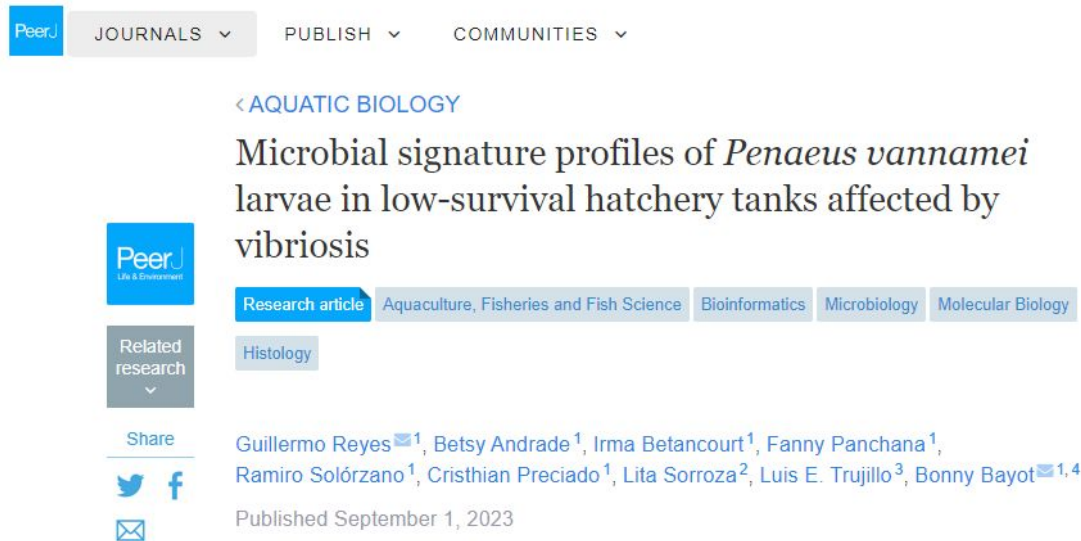 GTDB for the use with Diamond and QIIME are available via https://github.com/hbckleikamp/GTDB2DIAMOND and https://github.com/hbckleikamp/GTDB2QIIME.

https://www.sciencedirect.com/science/article/pii/S0043135423011405

Projects for END Course:

Microbiome Sequencing and Analysis (Project 3: Nguyễn Hữu An and Trần Thị Vũ)

Biopsy specimens were analyzed at the Department of Microbiology and Infection Control, Statens Serum Institut, Copenhagen, Denmark. DNA was extracted using a kit (QIAamp DNA Mini Kit; Qiagen) according to the manufacturer's instructions for tissues. For each batch of DNA extraction, a "negative" control was included containing buffers but no sample material for downstream analysis. DNA was amplified using a 2-step polymerase chain reaction using custom 341F/806R primers targeting the V3-V4 16S regions, as well as 3 primer sets targeting the hypervariable regions V3-V4 of the *18SrDNA* gene, and amplicons were sequenced on a desktop sequencer (MiSeq; Illumina, Inc) using the v2 reagent kit. For details concerning primer design and library preparation, see the eAppendix in the Supplement. Sequence data are available at the European Nucleotide Archive (accession number **PRJEB15266**).

Projects for END Course:

4)16S tôm/cá (Ng T Anh Thư và Khải)

(A260/280 = 1.8−2.0) were examined through a NanoDrop One Microvolume UV-Vis Scanning Spectral Spectrophotometer (Thermo Fisher Scientific, Waltham, MA, USA). The gDNA of all 45 samples was then submitted to Novogene Incorporation (Beijing, China) for amplification of the V3–V4 region of the *16S rRNA* gene using the 341F/806R primers (Takahashi et al., 2014), amplicon library construction, and paired-end sequencing with the Illumina NovaSeq 6000 P250 platform. The DNA sequences of the 20 samples from the five tanks affected by zoea 2 syndrome were deposited at the National Center for Biotechnology Information (NCBI) Sequence Read Archive (SRA) under accession number PRJNA870476. The sequences of the 25 samples from the seven tanks affected by AHPND are available under accession number PRJNA800805 (Reyes et al., 2022).

https://peerj.com/articles/15795/   https://www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA870476

Projects for END Course:

5) Shotgun bệnh (Ng Kỳ Phát, Trương Anh Tú, Trần Quang Minh và cô Diệp)

Research Paper

Preterm infants at low risk for early-onset sepsis differ in early fecal microbiome assembly

Sagori Mukhopadhyay ✉ iD, Jung-Jin Lee iD, Erica Hartman, Emily Woodford, Miren B. Dhudasia iD, Lisa M. Mattei iD,

...show all

The shotgun metagenomic sequencing data supporting the conclusions of this article is deposited at the NCBI Sequence Read Archive (PRJNA872399) and can be accessed at the URL https://www.ncbi.nlm.nih.gov/bioproject/PRJNA872399.

https://www.tandfonline.com/doi/full/10.1080/19490976.2022.2154091

Projects for END Course:

6) 16S bệnh (Hoàng Anh, Hoàng Sơn và Ngô Đại Phú)

Các bạn điền vào giúp, cảm ơn các bạn!