Microbiome Protocols eBook Initial: Fill the Gaps between Methods and Actual Operation

微生物组实验手册启动：填补方法与实操间的空白

Yong-Xin Liu, Haiyan Chu, Yongguan Zhu, Shuangjiang Liu, Baoli Zhu, …. Yang Bai

题纲

本领域很重要，。在分析上发表了一系列的标准化流程QIIME、USEARCH等极大的加速了本领域了发展，但复杂的实验对象、个性化的实验和分析仍然困扰着广大同行进入本领域。而且非标准的实验和分析方案也让同行间的结果难以整合分析与比较。为解决存在的很多问题，我们发现的微生物组实验手册项目。

本项目简介。

本项目的主题

本项目的意义。

图. 微生物组实验手册，架起各领域通过微生物组学世界的桥梁。

<https://bio-protocol.org/bio101/Special_Issue_info.aspx?siid=48>

Protists are a highly diverse group of microscopic eukaryotic organisms that are not fungi, animals, or plants. Protists were some of the microbes first visualized and described by Anton van Leeuwenhoek using the microscope in the seventeenth century. After that, the description and cataloging of these diverse microbial eukaryotes was pursued by microbiologists throughout the following centuries.1 So far, more than 60,000 protist species have been recorded in the NCBI taxonomy system, but many have yet to be identified. Protists have long been considered important models in fundamental biological studies, such as cell biology, genetics, ecology and evolution, toxicology, and applied fields, including biofuels, nutritional supplements and aquaculture feed production, environmental monitoring and pollution treatment, protozoan parasitic disease treatment and prevention, as well as agriculture.

In 1969, Robert Whittaker proposed the popular five-kingdom scheme2 (Figue 1). The protists, which made up the Protista, was regarded as one of the five kingdoms of life (Monera, Protista, Fungi, Plantae, and Animalia). As one of four kingdoms of eukaryotes, only 1,246 (1.9% of total) sequencing projects were performed for 1,151 (3.5% of total) Protista organisms according to the statistics of Genomes Online Database (GOLD). The extreme biased distribution of the current sequencing projects in different kingdoms indicates that there is a huge gap in the understand of the origin, evolution, and diversity of protists.3 Large-scale genome projects have been presented for all the kingdoms of life except the Protista, including the 10,000 Plant Genomes Project (10KP) for plants; the 1000 Fungal Genomes Project (1KFG) for fungi; the 5,000 Arthropod Genomes Project (i5K), Dog 10K Genomes Project (Dog10K), Bird 10,000 Genomes Project (B10K), and Fish 10,000 Genomes Project (FISH10K) for different clades of animals; and the Chinese Academy of Sciences (CAS) Initiative of Microbiome (CMI) and Earth Microbiome Project (EMP) for prokaryotes.

Considering the extremely unbalanced distribution of sequenced eukaryotic genomes and the under-representation of Protista genomes, scientists in six institutions in China, including the Institute of Hydrobiology (IHB), CAS, Tibet University (UTIBET), Henan Agricultural University (HAU), Lanzhou Veterinary Research Institute (LVRI) – Chinese Academy of Agricultural Sciences (CAAS), the Beijing Institute of Genomics (BIG) – CAS, and Huazhong University of Science and Technology (HUST), jointly launched the Protist 10,000 Genomes Project (P10K, Figure 1) on Dec 30, 2019, in Wuhan, China, and thus the P10K consortium was established. The IHB does excellent work in phycology and protozoology, and runs the National Aquatic Biological Resource Center (NABRC) in China, which contains more than 3,000 strains of protist. The UTIBET conducts long-term research of protozoa with special interests in Qinghai-Tibet Plateau. The HAU and LVRI mainly focuses on the parasitic protists, especially for livestock and poultry, and run part of the National Parasitic Resource Center (NPRC) in China. The BIG is an excellent institution in genomics and runs the National Genomics Data Center (NGDC) of China, which supports data analysis and management. The HUST has excellent teams in metagenomics and supports protist genomic data mining from metagenomics data.

The primary goals of P10K are to generate the whole-genome sequences (WGSs) of 10,000 protists and create new reference genomes for the representative species of different lineages of protists. The rapid development of genome sequencing technologies (in particular, single-cell sequencing of protists that are not amenable to laboratory culture) combined with bioinformatic technologies on algorithms (in particular, data mining of metagenomes) and databases has made it feasible to decipher the genome sequences of protists, reconstruct their phylogenetic trees, and accordingly address fundamental scientific questions of broad interest, such as the origin of eukaryotes and multicellularity, the diversification of eukaryotes, the adaptive evolution of protists toward the extreme conditions, microbe interaction, and genetic resources mining.

P10K will be the first international genome sequencing initiative focusing on the kingdom of Protista. P10K will run as an open initiative. We invite teams worldwide that could contribute the samples, sequencing, and bioinformatics analysis to join P10K. At the time of this writing, a team from Jilin Agriculture University focusing on slime molds, and a team from Southwest University focusing on microsporidia, have joined this project.