

The Chinese Microbial Type-strain Genome Project

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Microorganisms, generally comprising archaea, bacteria, and fungi, are the most diverse and widely distributed life forms on Earth. As the most primitive organisms, they play pivotal roles in unraveling the enigmas of evolution and harnessing their capabilities offers one of the most promising avenues to tackle forthcoming human challenges.

Type strains are fundamental in taxonomy as they act as reference points for characterising the traits of various species. Typically, these strains are extensively characterised regarding their phenotype, genotype, isolation source, geographical distribution, and other criteria defined by governing bodies such as the International Code of Nomenclature across various king-

doms.^{1,2} They act as a benchmark for evaluating and describing newly identified microorganisms, and their genomic data have the potential to enhance our comprehension of the relationship between existing species, as evidenced by a plethora of recent research studies.^{3,4} Therefore, the large-scale generation of type-derived genomes is of immense importance in the era of "Big Data".

Efforts such as the Genomic Encyclopedia of Bacteria and Archaea (GEBA) and the Global Catalogue of Microorganisms (GCM) 10K prokaryotic type strain sequencing project, have made over 12,000 prokaryotic genomes from type strains publicly accessible. However, fungal genome sequencing lags

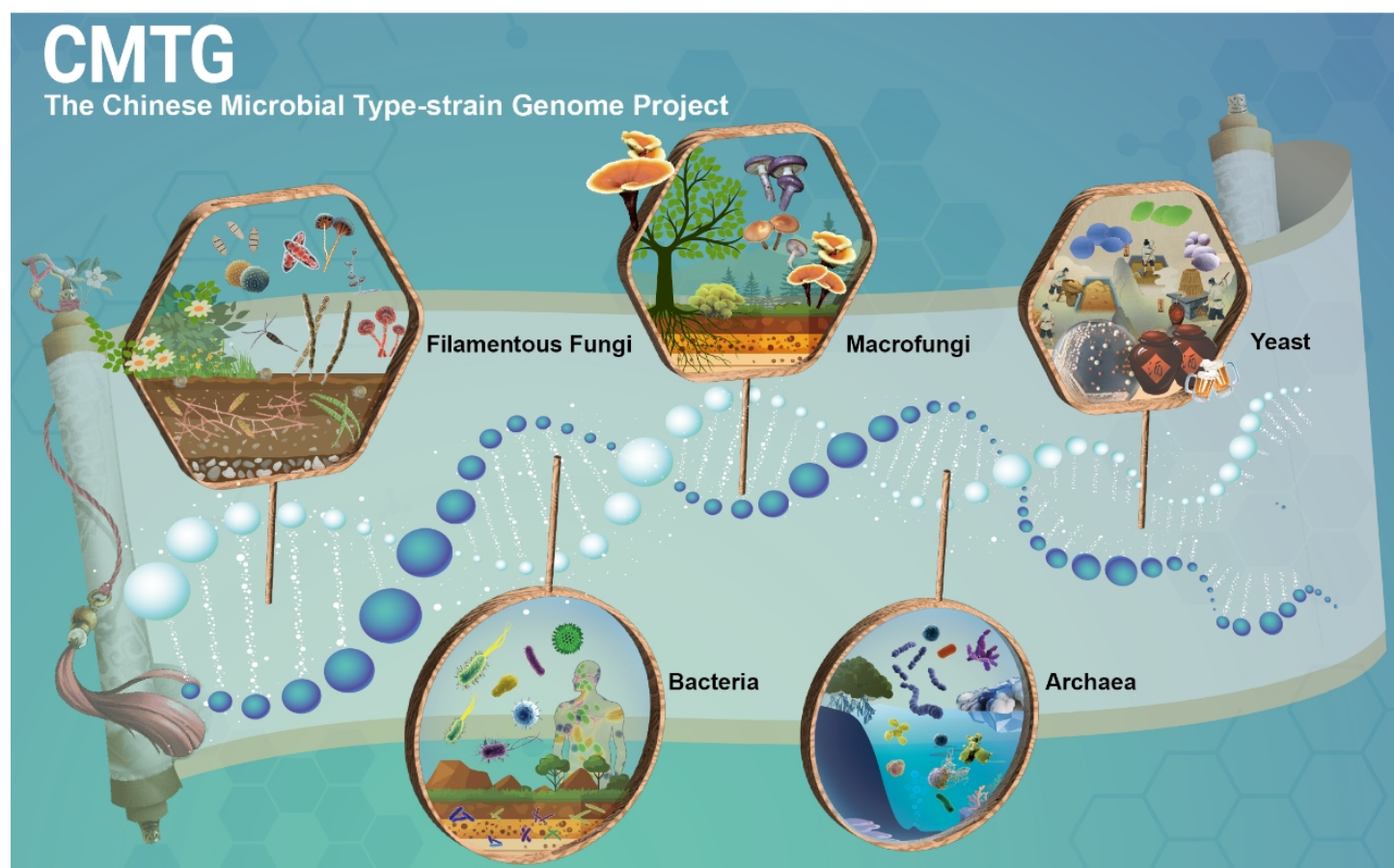


Figure 1. The Chinese Microbial Type-strain Genome Project (CMTG).

largely behind, with only a few projects initiated. The 1000 Fungal Genomes Project (1KFG) is amongst these, as well as other small-scale sequencing which are largely biased towards economically important groups in *Penicillium*, *Aspergillus*, yeast, and human or plant pathogens. In the past two decades, significant progress has been made in mycological research in China. For example, in the last three years (2020-2022), Chinese mycologists have described 3,039 new fungal species, accounting for 37.63% of the global total.

Unfortunately, unlike newly introduced prokaryotic species that require storage in at least two different culture collections, there is no mandatory requirement to store fungal type strains according to the code. This leads to many of these fungal type strains being kept in private collections. Therefore, there is a pressing need to collect, preserve and establish a high-quality genomic database of Chinese fungal resources. This project has the potential to strategically improve the preservation of fungal biological resources in China.

With support from the Chinese Ministry of Science and Technology, Chinese scientists from eight institutes (including Institute of Microbiology, Chinese Academy of Sciences (IMCAS), Wuhan University, the Second and the Third Institute of Oceanography, Ministry of Natural Resources, Chinese Center for Disease Control and Prevention, Hebei University, and Xinjiang Institute of Ecology and Geography, CAS), in collaboration with additional 15 research groups in the fields of mycology and microbiology initiated the Chinese Microbial Type-strain Genome Project (CMTG) on Sep 01, 2021. The project will run for three years and aims to produce comprehensive and high-quality genome sequences for a minimum of 1,200 fungal and 3,500 archaeal and bacterial species, sampled from Chinese type strains. This will result in a greatly expanded genome catalogue for a variety of prokaryotic and fungal taxa, particularly those that are under-represented. A high-quality database for archiving and managing all sequenced genomes will be established by China National Microbiology Data Center. The CMTG is not only the first microbial genome sequencing project involving fungi in China but also the largest-scale type microbial sequencing project worldwide. "The vast amount of genome data will provide scientists with new opportunities to investigate crucial topics such as understanding the origins of various microbial life forms and their functional roles in the environment. Additionally, it will facilitate the utilization of microbes in diverse fields, including the development of medical products, agriculture, and industrial applications." stated Professor Lei Cai, the Principal Investigator of the project.

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DECLARATION OF INTERESTS

The authors declare no competing interests.