

Asian mycology toward global contribution

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ABSTRACT:

Few people have a doubt that the biodiversity of fungi in most of Asian countries are enormous, probably exceeding those in Europe. However, the evidence for the occurrence may be scattered. In addition, there are still a number of fungi remained unsearched or undescribed. Contribution of mycological knowledge from Asia is greatly expected. The speaker has worked on the taxonomy of Helotiales for the last 35 years, and also served as the Node Manager of Global Biodiversity Information Facility (GBIF) for 9 years. Nowadays, we have new technology for global contribution. In the present talk, I would like to present some examples and possible way for the further contribution to understand and elucidate the fungal diversity in Asia.

1) Advance inventory. Inventory is a list of all known organisms in the given area. In Japan, Katamoto (2009) revised the previous inventory of fungi. The data have been digitized and followed up by the current activity in the Mycological Society of Japan. These data are available from the website (<https://www.mycology-jp.org/html/checklist.html>). The cumulated information is the basis to understand the fungal diversity in the given place, and makes further strategic collection possible.

2) Advance sequence-based approach (barcoding). Today, sequence-based approach is essential in both systematics and ecology. Occurrence can also be described using the barcoding data (<https://docs.gbif.org/publishing-dna-derived-data/1.0/en/>). When think about the biodiversity of fungi in Asia, this kind of approach is very important, because we have to describe a number of undescribed fungi, and conventional procedure for the description may be too time consuming. Adopting sequence-based concept has been already accepted and being standardized in world database such as UNITE (<https://unite.ut.ee/>) which shows more realistic approach compared to the conventional one. Culture collection will provide the voucher for the genomic data, and sequences obtained from specimens provides another supplementary data. Sequence data link the specimens and the data obtained from metagenomic approach, and expands our knowledge for fungal diversity.

3) Advance databases following global standards. We now have occurrence data based on literature, specimens, culture collection, and metagenomic approach. These may result in independent database. To exploit the data, we should follow FAIR principle (<https://www.go-fair.org/fair-principles/>). Namely, the data should be findable, accessible, interoperable, and reusable. Darwin Core is a global standard to describe the biodiversity (<https://dwc.tdwg.org/terms/>) applicable for the occurrence of fungi. The accumulated data would be exploited for reverse taxonomic approach to understand the fungal biodiversity or biological interactions. Together with search for underutilized fungi, the above three approaches would maximize our knowledge and provides the clue toward the exploitation of fungal bioresources.

KEYWORDS:

Barcoding; bioresource; databasing; Darwin core; FAIR principle; inventory.