

Short notes on Indian Glomeromycota

Manju M Gupta and Prabhat Kumar

Affiliations: University of Delhi, Department of Botany, Sri Aurobindo College, Delhi 110017 India

Abstract

Indian Glomeromycota, the complete checklist (*iAMF*) available online at a subdomain of Delhi University (www.amfungi.aurobindo.du.ac.in), is a first of its kind digital database on arbuscular mycorrhizal (AM) fungal diversity and distribution from majority of states of India. It reports occurrence of at least 161 species of Glomeromycota in India along with comprehensive information on distribution, taxonomy, phylogeny, culture collection, molecular sequence and bibliographic data on these fungi. The database is based on the primary data through on going survey in Northern India and secondary data from 99 earlier studies spread over 23 states of India during 2008–2016. The present database would prove useful to elucidate region specific information about Indian Glomeromycota.

Key words: Arbuscular, AM fungi, database, bioinformatics, phylotaxonomy, biodiversity

Onset of the present decade has seen a shift in focus from individual species to community, ecosystem, country and global level (Davison et al. 2015; Opik et al. 2016 ;). Country wide AM fungal distribution databases are recently launched for Germany and USA (Menzel et al. 2016; Swaty et al. 2016). The Indian Glomeromycota distribution and phylogeny database (*iAMF*) is being reported in the present study available online both at amfungi.aurobindo.du.ac.in and amfungi.in with ~ 11000 hits as on date (figure1). This is first digital database of its kind which has evolved as result of pressing changes in the world of arbuscular mycorrhizal fungi (AMF) in the recent times in terms of its phylogeny, taxonomy distribution and occurrence.

The Glomeromycotean fungi form intimate and mutualistic symbioses with the vast majority of land plants and have been major drivers in almost all terrestrial ecosystems for more than 450 million years. The eponymous feature of this symbiosis is presence of tree-like structures called arbuscules, which are formed during fungal colonization of the plant root and are site present in the state of active bidirectional nutrient transfer between the plant and the fungal partner. The symbiotic fungal partner of this association provides phosphorus, nitrogen and other nutrients to the host plant. The plant partner, in exchange, supplies up to 20% of the photosynthetically fixed carbon to the fungus (Smith and Read 2008). Arbuscular mycorrhizal fungi (AMF) are ecologically and economically important as they can improve pathogen resistance; mitigate different kinds of plant stresses such as drought or heavy metal toxicity which leads to better growth and productivity of plants. Government of India vide their notification no 2304 in the Gazette of India has included mycorrhiza as a biofertiliser. Proper management of this environmentally friendly technology could lead to million dollars.



Figure 1

Radical changes have come improved our understanding of biodiversity and morpho-phylogeny identification of these fungi by application of DNA sequencing and computational analysis methods. The classical work of Krüger et al. (2012) where they resolved phylogeny on the basis of small subunit (SSU) rRNA, internal transcribed spacer (ITS) and large subunit (LSU) rRNA sequences for 109 named species. This also led to a major reshuffling of the names of AM fungi specially those belonging to genus *Glomus* for example 'The model AM fungi' was known as *Glomus intraradices* when the first genome sequencing project for the Glomeromycota began in 2012 and when the project finished, it was changed to *Rhizophagus irregularis* (Tisseran et al. 2013). Present database was built to substantiate the Indian Glomeromycota as a unit in context of changes in the following direction in the international scenario:

1. The consensus classification –The families, genera and species not accepted in consensus classification (Redecker et al.2013) should be unambiguously dropped in our studies.
2. One name-one AMF- The online linkAmfphylogeny (<http://schuessler.userweb.mwn.de/amphylo/>; updated Oct 2015) gives an exhaustive list as one name to one taxon of AM fungi in order to resolve the synonyms paradox.
3. To have an updated and consolidated biodiversity data and the number of species figure for Indian Glomeromycota.
4. Software database websites which keep updating the data but Indian data is missing. Some of these databases include: *MaarjAM*(environmental sequences), *Phymyco-DB* (SSU rRNA and EF-1- α gene sequences from all fungal phyla), *Amf-phylogeny* (all phylogenetic information) and *INVAM*(culture collection).

The present web based *iAMF* is based on data generated from rhizosphere soil collected across three Indian states namely HP, Delhi and UK from 2013 onwards under Delhi University innovation project and UGC major project. Apart from this, secondary data from 99 references reporting occurrence of AM fungi across 23 states of India from 2008-2016 is also included. The search engine in the database provides information for 164 species on occurrence in different states whether studied by culturing using morphological or molecular methods and which with barcode sequence used in case of molecular methods. It gives full reference to the study which mentioned its occurrence in India and also provides a link to original description through amf phylogeny web site

(<http://www.amfphylogeny.com>). It also provides taxonomic information and also whether the live culture is available or not (figure 2) along with the other popular names for this fungus in India with one accepted name to be used in the studies.

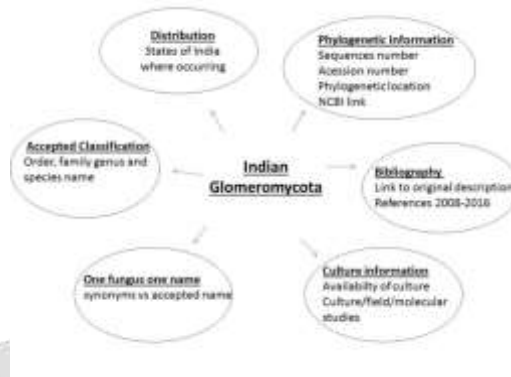


Figure 2

The data base also provides a collection of 335 sequences curated from NCBI which had partial or full sequences which were identified to species level covering the consensus sequence as marker (small subunit (SSU) rRNA, internal transcribed spacer (ITS) and large subunit (LSU) rRNA region). Mostly the fragments were >1000 bp in length but about 20% of the sequences were shorter or partial sequences. It also included *Corymbioglomus* (1), *Sclerocystis* (2), *Entrophospora* (1). Details about genera and species for which the sequences could be curated is given in table 1. We failed miserably as only 25% (41/164) of our genera are sequenced and that mostly in other studies. These sequences were rechecked for clean sequence data were expected be useful in taxonomic studies. Multiple sequence alignment was done using both clustal and MAFFT and were used in building the correct phylogenetic tree using Raxmlat cyperus web site (figure 3) to check the utility in further phylogenetic and taxonomic studies.

	#Sequences	#Species
<i>Purnelliformis</i>	35	2
<i>Septoglomus</i>	4	1
<i>Glomus</i>	29	5
<i>Rhizoglyphus</i>	1	1
<i>Pactispora</i>	2	1
<i>Acutispora</i>	43	6
<i>Glomerispora</i>	4	1
<i>Phosphaera</i>	4	1
<i>Oligospora</i>	73	4
<i>Dactyloctenium</i>	19	1
<i>Chlorospora</i>	0	0
<i>Rhizocetra</i>	18	4
<i>Scutelliospora</i>	8	2
<i>Clavarioglyphus</i>	34	2
<i>Parasporium</i>	3	1
<i>Arctosporium</i>	11	2
<i>Arctospora</i>	34	2
<i>Glomopsis</i>	5	1

Table 1

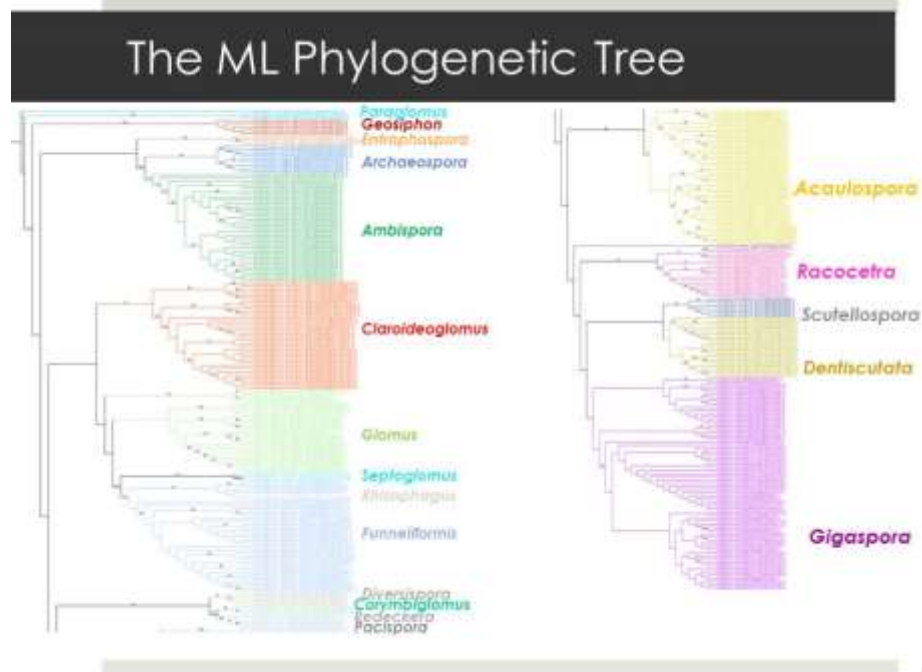


Figure 3

Database is developed using MS access and visual basic applications initially and finally uses php admin on web in such a way that it would be possible to always have a dynamic complete consolidated list of species available. In the first attempt to estimating regional species, number of AM fungi in India (Gupta et al.2014) suggested a figure of 148 species belonging to 21 genera were found to be present across 18 states of India. *Funneliformis mosseae* was reported to be the most commonly occurring species followed by *Rhizophagus fasciculatus*. *Glomus* was the most diverse genus represented by 48 species, followed by 27 and 10 for *Acaulospora* and *Scutellospora*, respectively. The upgradation of data in 2016 however revealed 161 species to be occurring in 23 states of India. New species added to the list are *Acaulospora colombiana*, *Diversispora eburnean*, *Diversispora spurca*, *Glomus albidum*, *Glomus pallidum*, *Glomus pustolatum*, *Glomus tortuosum*, *Glomus versiforme*, *Rhizophagus diaphanous*, *Sclerocystis liquidambaris*, *Scutellospora armeniaca*, *Scutellospora pellucida* and *Scutellospora reticulata*. Several interesting other facts which were very prominent during building of the database were:

1. Majority of the biodiversity studies conducted in India are based on field samples. Very few studies are including the molecular sequences characteristics. Morphological characters are usually lost in field filed sample which that might be leading to wrong identification.
2. Despite the availability of species and we still prefer to use our conventional names; for example *Glomus fasciculatus* which is based on molecular studies has been renamed to *Rhizophagus fasciculatus*(references).???
3. Molecular sequence data is available for very few of our species. This emphasizes on the need for more molecular sequencing studies to be done from well characterized Glomeromycota spores occurring in India.

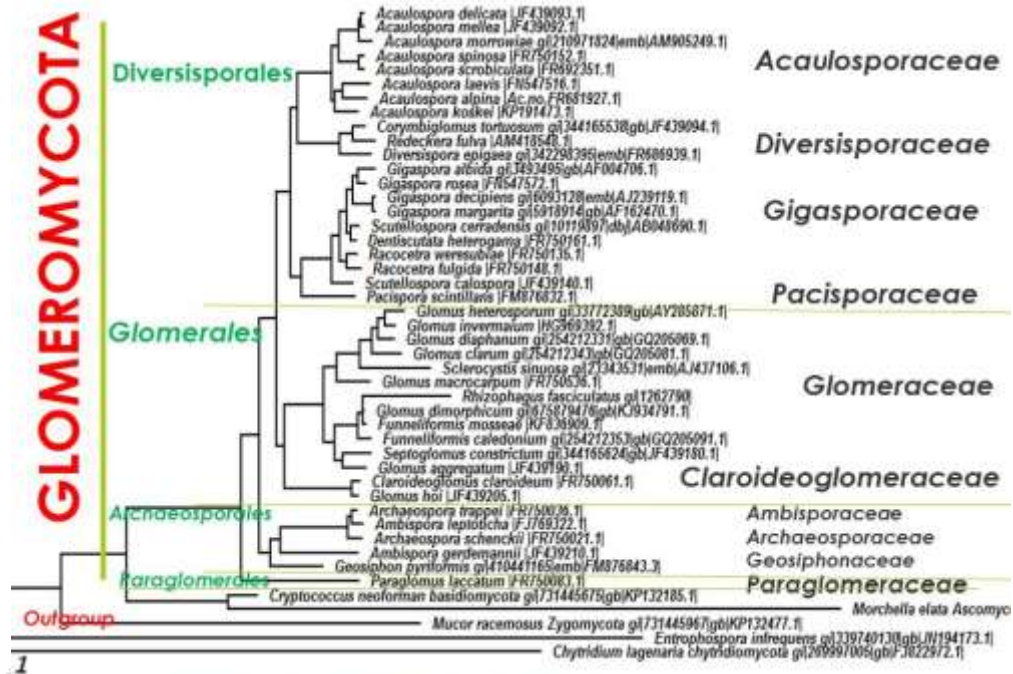


Figure 4

Much more field- verified data is required needed to improve the current estimates of biodiversity of AM fungi and this can be speeded up by involving more biologists to accomplish the goal. All AMF biodiversity data should be interconnected and made easily accessible to public so that it can be best used for human welfare. However, it would be ideal and in the interest of those who are working on AM fungi to have central database which reflects all changes occurring in taxonomy, phylogeny and biodiversity of Glomeromycota at one place.

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