

those patterns. Meanwhile it is quite difficult, or even practically impossible, to complete such studies, because there is no images of studied individuals (herbarium or live specimens) in most caryological reports. By my opinion, the World Database of image files of Herbarium specimen and their karyotypes, made by high resolution, is very much necessary and should be obligatory for any chromosome researches.

Creation of these image files (scanograms) and access for scientists could help in solving of a number of problems. This will afford an unimpeded drawing of cytotaxonomic collections into scientific use. Their availability in WWW or on a CD-ROM will afford to study these specimens by a number of taxonomists. Digital replicas help to avoid irretrievable losses as a result of natural disasters, military conflicts, fires, etc. Such accidents unfortunately were not so rare during the history of taxonomic botany. Digital replicas minimize expenditures of time and budget spent on scientific trips and shipping of specimens, and for sure none could lose, destroy, make wet or steal a digital image.

Undoubtedly, a digital image could not replace real herbarium specimens completely. Nevertheless, it is also correct, that it is possible to substitute in several cases a remote herbarium specimen with a digital images of high resolution and depth, which could be made with the help of some types of scanners. One can observe on these images tiny morphological characters important

for taxonomy such as details of hairs, features of surface texture of some organs, etc. It is possible to make scaling of image fragment using software on a CD. This helps to study a specimen without traditional optical instruments. A label, as an important element of an authentic herbarium specimen, is reproduced ideally in this case.

That is why a number of Herbaria start their projects on digitalizing and placing in the Internet the most valuable collections (historic collections, authentic specimens etc.). The specimens which confirm chromosome numbers reports should be digitalized either.

Experimental project on digitalizing of rare herbarium specimens from MW Herbarium was started by a group of botanists in Moscow State University several years ago. Published CD-ROM* is a first result of this project, which could be easily demonstrated on a request.

* Balandin, S.A., Gubanov, I.A., Jarvis, C.E., Majorov, S. R., Simonov, S.S., Sokoloff, D.D. and Sukhov, S.V. The Linnaean Collection of the Herbarium of Moscow State University: digital images, comments, historical review. [Electronic resource]. — Moscow, Dehlia Co., Ltd., 2001. — 1 CD-ROM. — System requirements: IBM PC or Apple Macintosh; CD-ROM drive; Microsoft Internet Explorer 5.0 or better with Java support; Microsoft Windows 95/98/Me/NT/2000 or Mac OS 8.1; 64 MB RAM or videdmore.

Re-assessing orchid mycorrhizae : The promise of DNA phylogenetic methods, and taxonomic and geographic sampling biases

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The orchid mycorrhiza has been a central theme of mycorrhizal biology from its inception as a specialized field. Descriptions of orchid mycorrhizal morphology and hypothesized symbiotic relationships cover over a century. However, understanding this symbiosis requires a robust, natural system of identification. DNA phylogenies have revolutionized evolutionary thinking in the last two decades, nowhere more so than in microbial biology, where morphological characters are inadequate to characterize evolutionary relationships

adequately. The result is a continuing re-structuring of Kingdom Fungi, with only two of the four generally recognized divisions now recognized as natural and monophyletic. Orchid mycorrhizal fungi, previously described as Rhizoctonia species, are now also being re-assessed and re-classified primarily throughout Division Basidiomycota, but with some taxa even in Division Ascomycota. Molecular phylogenetic re-assessments of genus Rhizoctonia have been conformed through ultra-structural analysis of fungal morphology via electron

microscopy. As such, Rhizoctonia is no longer a useful taxon, and further re-analysis of the molecular data is needed to re-define our current understanding of orchid mycorrhizae.

To understand orchid mycorrhizal associations, purported mycorrhizal fungi must be identified through DNA phylogenies. Ideally, these phylogenies must be based on genomic regions proven useful for this purpose, in particular the nuclear small and large subunit genes and internal transcribed spacers, and should include taxa from common sequence databases, such as the Bruns *et al.* (1998) mitochondrial large subunit database. I searched the literature and found 12 papers that met this condition, excluding papers that further analyzed finer-scale data from previous papers, all of which were published since 1997. These twelve papers represent a complete literature search including ONLY those papers that: 1) used a reasonable method to separate potential mycorrhizal fungi from other, non-mycorrhizal endophytic fungi, and 2) used proven DNA methodologies for identification, necessarily including PCR with established fungal primers, sequencing, and phylogeny reconstruction.

At first glance, these twelve papers seem to represent a diverse grouping of orchid taxa, suggesting that at last we may have enough knowledge to understand the evolutionary history of this symbiosis. However, of these, five deal exclusively with epidendroids; the orchidoids are dealt with exclusively by only one study, although three other papers include orchidoid taxa; the cypripedioids, apostasioids, and spiranthoids are tackled by only one study each; and the cymbidioids are only included in two studies, never exclusively. These studies are very limited in scope because they generally only choose a few species, including an average of 3.5 species per study though attempting to generalize to a family of over 20,000 plant species. Geographically, five of the twelve studies use taxa exclusively from North

America, while a further three exclusively focus on European locations. Only one study included Asian taxa, only two included taxa from Australia and Oceania, while none included African or South American taxa. Furthermore, most studies dealt with taxa from only one locality. Otero *et al.* (2002) surveyed nine orchid species, more than any other study, but all were collected from Puerto Rico, and seven were epidendroids. The only study dealing with Asian orchids, Ma *et al.* (2003), included eight taxa, but all were epidendroids from Singapore.

Phylogenetic reconstruction is highly sensitive to sampling effort and biases. Taxon biases are not surprising in the orchid literature, and in part may reflect the distribution of orchid species throughout the orchid family. For example, although more studies focused on epidendroids than other subfamilies, subfamily Epidendroideae includes over 80% of orchid species. However, in order to re-construct the evolutionary history of the orchid mycorrhizal interaction, studies must include taxa distributed throughout the Orchidaceae, and a synthetic phylogeny must at some point in the future include at least a simple majority of species. Otherwise, evolutionary events occurring at the tips of the orchid phylogeny may be misconstrued as having occurred more ancestrally, and many events may be missed altogether.

Geographic bias and taxonomic bias appear mutually exclusive, as the sheer scale of sampling required for a full, detailed re-analysis of the evolutionary history of the orchid mycorrhizal requires greater effort, time, and money than any single group is likely to be capable of. I therefore propose that an international study group be formed to tackle this issue in a more efficient way. Special priority should be given to parts of the world with less resources and less representation. Asia and Africa are particularly important in this regard, and special attention should be given to far eastern Russia.