# Release 7.0 of Mendel database

Following the recent correspondence by Jens Stougaard *et al.*[1], we would like to draw the attention of your readers to the latest release of the *Mendel* database for the nomenclature of sequenced plant genes. *Mendel* provides common designations for gene families across the plant kingdom, as recommended by the Commission on Plant Gene Nomenclature (CPGN). We are pleased to report the mounting of the latest release of the database, *Mendel 7.0*, in the traditional ACeDB format, on the USDA-ARS Center for Bioinformatics and Comparative Genomics at Cornell University's Genome Web site (http://genome.cornell.edu/cgi-bin/WebAce/webace?db5Mendel/), and at Stanford's Genomic Resources site (http://genome-www.Stanford.edu/Mendel/).

*Mendel 7.0* is more than twice the size of its predecessor and is contemporary with EMBL/GenBank sequence databases up until February 1999. *Mendel 7.0* retains the model of sorting proteins by sequence similarity that was introduced by the John Innes group under the direction of David Lonsdale. Unfortunately the John Innes group (Norwich, UK) announced in February that it could no longer support the CPGN's *Mendel* database, but the CPGN wishes to express its gratitude to David and to his associates, in particular Benedict Arnold, for automating accessions to *Mendel*.

The new release contains all protein sequences from Swiss-Prot (release 37) and includes the complete accessions of non-green algae and cyanobacteria, in addition to the ongoing coverage of higher plants and green algae. *Mendel 7.0* lists many new gene family names, including those related to alcohol dehydrogenase, methyl transferases, transporters, and additional gene families of light-harvesting proteins and chloroplast open-reading frames of undetermined function.

Recognizing that function does not always correspond to simple sequence similarity, we have renamed the alignment sets derived through automation as 'product families'; the term 'gene family' is reserved for sets that share similarity of sequence and function, as determined by working groups. The CPGN endorses, and indeed promotes, the importance of integrating hand curation with automated sorting.

With the rush to automation, several important features of the original *Mendel* had become lost or obscured in recent releases. A number of gene families that had been omitted from *Mendel 6* include families encoding RNAs, catalase, sucrose synthase, and subunits of RNA polymerase. These are being reinstated in *Mendel 7.0*, along with other features, including the fields defining alleles, subgenomes and links to other databases. In addition to all other search parameters that were available in recent releases (such as plant species, gene synonyms and accession numbers from EMBL/GenBank and Swiss-Prot) another restored feature of *Mendel 7.0* is the ability to search directly by gene product. Additionally, dialog boxes will be available for comments and suggestions.

The CPGN is also committed to the ongoing development of the nomenclature guidelines. Within the past few months we have identified names for >200 new gene families, including a new category of temporary gene families, which are identified by a caret (e.g. Aladh1^). Some of these temporary names have been proposed by working groups or by individual scientists, whereas others are based on traditional gene names. All names will need to be reviewed publicly on the CPGN's Web site. Names for gene families encoding components of acetyl-coenzyme A carboxylase, for example, are currently under discussion at http://mbclserver.rutgers.edu/CPGN/FattyAcid.group.html. Those names that survive will be presented for approval by the CPGN's associated scientists.

Interested members of the scientific community are invited to propose gene family names for as yet unnamed product families; suggestions should be addressed to the e-mail address below. Discussions will be posted on the CPGN Web site (http://mbclserver.rutgers.edu/CPGN/Conversations.html), and contributors whose proposals for gene family names are adopted by the CPGN will be identified in *Mendel 7.1*.

Finally, we are currently in discussion with the manufacturer of an excellent relational database whose web-based format has proved too slow and tedious under our test conditions. We hope to mount a later release of *Mendel* that will be fast, flexible and totally user friendly.

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# An age-old problem

We read with interest the Perspective article on the age of tropical rain forest trees[1]. Although the piece is well written and informative, there are a number of points that we think need to be clarified. First, the authors state that 'for time estimates of between 1000 and 2000 years this technique (natural radiocarbon dating) has a 25–50% precision', and cite an article by K.M. Goh[2]. On consulting this article, the figure turns out to have a precision of 0.25–0.50% and is for rounding off $^{14}C$ ages. This is two orders of magnitude less than the cited value[1]. Second, the authors appear to confuse what they refer to as 'natural radiocarbon dating' and 'human-induced radiocarbon dating'. To our knowledge 'bomb' $^{14}C$ has only been used to estimate the age of trees by extrapolating growth rates[3]. In their section 'Estimates using radioactive indicators' the authors incorrectly cite an article on radiocarbon ages[4] as being derived from bomb $^{14}C$ tracer methods. They also refer to a 1060-year-old rain forest tree and cite the same report[4]. In fact, this tree was a conifer in an Australian transition rain forest, and 1000-year-old conifers are common throughout the world.

In their abstract, the authors also state that 'it is not clear how accurate the technique (radiocarbon-based dating) is compared with other methods'. For trees that are less than ~350-years old, historic changes in atmospheric radiocarbon, combined with measurement precision, result in relatively inaccurate dates (~±100 years). However, for trees that are >500-years old, atmospheric radiocarbon is more stable, and dates are accurate to ~±50 years. In the absence of annual rings, radiocarbon dating is the only way to directly determine the age of a tree. The indirect methods that Miguel Martínez-Ramos and Elena Alvarez-Bullya refer to are useful for understanding the mean behavior of a cohort of trees. However, these techniques cannot account for trees that remain suppressed for many decades (i.e. there is no stem diameter increment), or respond to numerous canopy openings over a period of centuries, and eventually become ancient giants.

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# Reply...Tropical rain forest tree life-history diversity calls for more than one aging method

Jeffrey Chambers and Susan Trumbore[1] correctly clarify some inaccurate statements concerning the $^{14}C$ dating methods that we made in our paper[2] on methods to estimate tropical rain forest (TRF) tree ages. We appreciate and accept their corrections on these technical issues for which we are not experts and had to rely on secondary sources. However, we would like to stress the main point of our paper, namely, that given the great diversity of life-history strategies and life-spans found among tropical tree species, $^{14}C$-based and demographic dating methods are complementary, rather than mutually exclusive. An interesting result emerging from our review was that in TRF tree communities there is a fascinating variation in longevity among tree species, ranging from less than ten to ~2000 years[2]. We also found that most age estimates fall below 400 years. We have already stated[2] that the dynamic nature of TRF tree community regeneration is involved in the evolution of this diverse array of species' life histories and successional traits.

In our opinion, $^{14}C$-based dating methods are useful for aging long-lived species and old trees (>500 years), whereas demographic methods are needed for aging short-lived species and young trees. Hence, the usefulness of these two methods depends on the species' successional traits and the life-stage of an individual (Fig. 1)[3,4]. Chambers and Trumbore[1] indicate that radiocarbon dating trees that are <~350-years old yields relatively inaccurate estimates (about ±100 years) but that it yields more accurate estimates for trees >500-years old (about ±50 years). Thus, radiocarbon dating is more useful (accurate) when applied to late (climax) rather than early successional (pioneer) trees. Late successional trees grow slowly and survive for long periods (perhaps centuries) at the equilibrium phase (Fig. 1). Whereas, demographic methods might be more accurate and useful when applied to early life stages and to tree species of early and mid-successional stages. These grow fast at early life cycle stages (Fig. 1)[2] and survive for short periods (some decades) at the equilibrium phase. Yet, the use of demographic methods has also enabled the discovery of ancient TRF trees of ~2000-years old[5]. We, therefore, disagree with the statement of Chambers and Trumbore[1] that radiocarbon dating is the 'only way to directly determine the age of a TRF tree'. Rather, this is the most direct and accurate method to date ancient trees, but other methods might be better for other trees.

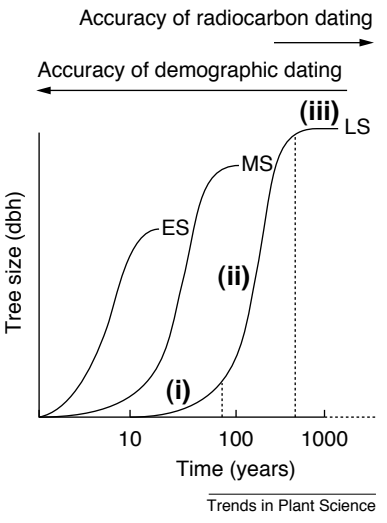


**Fig. 1.** Oversimplified logistic growth trajectories for hypothetical trees of different successional status: ES, early successional (pioneer); MS, mid-successional; LS, late successional (climax) species. In each curve, growth trajectories are divided into three life cycle stages: (i) slow growth; (ii) rapid growth; and (iii) equilibrium. At the equilibrium stage, when photosynthetic carbon gains and respiratory costs are in balance, trees do not experience any additional growth. Time is shown in a logarithmic scale, and tree size (diameter at breast height; dbh) in a relative scale. Arrows at the top of the figure indicate the increasing usefulness of the dating approaches.

Furthermore, ancient trees might not represent the major component of a TRF tree community. Indeed, from the 20 big trees that Chambers *et al.*[6] dated with $^{14}C$, nine were >500-years old. The remainder were younger, including five of ~200-years old. Wood density, which is inversely related to growth rate, could be used to select candidate trees for dating with $^{14}C$. The current high cost, and technical complexities of the $^{14}C$ dating method, limit its use as a standard method, especially in population-level ecological studies. Long-term monitoring, the length of which (few years to several decades) will depend on species life history characteristics, might provide not only a complementary way to estimate ages in TRF trees, but can also generate rich data sets to explore and understand the underlying biological basis of inter-tree age variation.

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