

References

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

Jeffrey Chambers and Susan Trumbore¹ correctly clarify some inaccurate statements concerning the ¹⁴C dating methods that we made in our paper² 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, ¹⁴C-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 years². We also found that most age estimates fall below 400 years. We have already stated² 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, ¹⁴C-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 Trumbore¹ indicate that radiocarbon dating trees that are <~350-years old yields relatively inaccurate estimates (about ±100 years) but that it yields

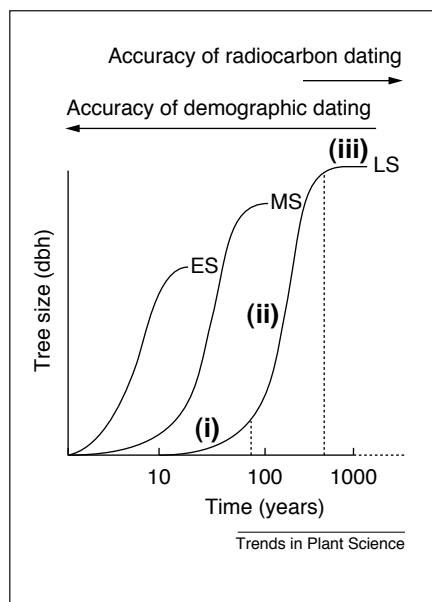


Fig. 1. Oversimplified logistic growth trajectories for hypothetical trees of different successional status: ES, early successional (pioneer); MS, mid-successional; LS, late successional (climax) species. In each curve, growth trajectories are divided into three life cycle stages: (i) slow growth; (ii) 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.

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 old⁵. We, therefore, disagree with the statement of Chambers and Trumbore¹ 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.

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 ¹⁴C, 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 ¹⁴C. The current high cost, and technical complexities of the ¹⁴C 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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