Vegetation Diversity after Logging in the Southern Appalachians

We read with great interest the article by Duffy and Meier in *Conservation Biology* 6:196–201. Only limited information is available on the impact of forest management activities on vegetation diversity in the southern Appalachians, and forest managers need information to help plan, modify, or eliminate future management options. Duffy and Meier's article has received considerable attention by land managers and the media in the southern Appalachian region, as well as nationally. Hence, our science is directly influencing the policy makers, land managers, and public. In this instance, accurate collection, analysis, and interpretation of data goes beyond "good science"—major changes in policy are based in part on these data. We have some serious concerns with the methods and interpretations presented in Duffy and Meier. Our purpose is to identify these concerns in hopes of improving the scientific data and knowledge base so critical to forest management issues.

Our specific concerns are as follows:

(1) Decisions regarding the choice of both the size and number of sample plots are critical to any analysis of vegetation diversity. There is no discussion regarding the rationale used by Duffy and Meier. Species-area curves are required to develop a sampling regime sufficient to derive species diversity estimates (richness, density, etc.) suitable for valid comparisons. Reporting species richness results on a *per-plot* basis (as was done by Duffy and Meier) can result in sampling artifacts when plot size and number are chosen arbitrarily.

To illustrate, assume that in one stand plant population density is 100,000 per ha, with individuals randomly distributed. A random sample using, say, twenty 1-m^2 plots would yield a mean of 10 plants per plot. Assume that in another stand plant population density is 50,000 per ha, again with plants randomly distributed. A random sample of 20 1-m^2 plots would yield a mean of 5 plants per plot. Now, say that in both stands the total population of plants contains 10 species. In the stand with 100,000 plants per ha, the number of species in each sample (mean species richness) can approach 10 species per plot—if there are 10,000 individuals per species and each species is randomly distributed. In the stand with a total population of 50,000 plants per ha, however, the mean number of species can only approach 5 species per plot. The obvious result is that even though both stands contain 10 species, species richness per plot is a function of population size and the plot size used to sample the population.

(2) Reporting species richness on a per-plot basis can result in even further misinterpretation of the data if species are not randomly distributed. To illustrate, Duffy and Meier found an average of 9 to 14 species per plot in primary forests and 2.75 to 8.75 in secondary forests. If species are randomly distributed, then the species per plot would equal the

stand total (in other words, the same 9 species would occur in every plot). At the other extreme, however, each plot could contain 9 different species. In this case, the average per plot would equal 9 but the stand total would equal 216 (9 species × 24 plots). Obviously, this would result in very different interpretations of the data. In Duffy and Meier's article, we have no way of knowing the significance of the "per-plot" versus "per-stand" comparisons.

(3) Not sampling the entire community *will* bias the sample. Our experience (and data) clearly shows that the floristic community beneath *Rhododendron maximum* is either extremely sparse or nonexistent. The impact of this artifact on Duffy and Meier's analysis depends on the differences in *R. maximum* composition (percent of area occupied, density, etc.) between the communities compared. Based on our experience, this can vary tremendously both between and within forest stands.

(4) Floristic comparisons need to be made in other seasons as well. For example, secondary sites may have greater species richness in the summer or fall. A more complete sample could have changed the results substantially.

(5) The age gap of 84 years (secondary sites) to 200 years (primary sites) invalidates the statement in the conclusion that "the data presented here strongly suggest that recovery requires at least several centuries." Assuming that the methods used were correct (we contend they were not), the data *only* show that recovery had not occurred by 84 years.

These are what we consider to be major methodological flaws severely limiting the usefulness of the data and of subsequent comparisons and interpretations. We consider this issue to be extremely important, and we fully support research efforts in the area of management impact on biodiversity. These studies must,

however, be carefully conducted to avoid methodological errors that invalidate the research results.

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