References and Notes

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Response

IN CONTRAST TO MATURE SCIENTIFIC FIELDS, understanding of the global environmental impact of humans is still in its infancy. Haberl *et al.* note the need to develop a means to reduce uncertainty in estimates of human appropriation of NPP. We concur and stated this in our report. As they note, some reduction in uncertainty is possible by making changes in the model we used. In our report, we explicitly borrowed and did not modify the model of Vitousek *et al.* (*1*) because it is well known and we feel that it is a good starting point for attempting a worldwide assessment of NPP using more contemporary data.

As noted by Haberl *et al.*, this model can and should be improved. We agree, but significant reductions in uncertainty will not come about through modifications of this globally averaged model. Rather, major reductions in uncertainty will only be realized with more accurate estimates of the basic parameters governing human appropriation of NPP.

Haberl *et al.* suggest that by using Food and Agriculture Organization (FAO) data, we can get accurate estimates on the productivity of agricultural lands. It should be noted, however, that our estimate of uncertainty in productivity of agricultural land is less than the estimate of mean uncertainty of all the parameters in the model. We disagree with Haberl *et al.* that our estimates of uncertainty in this parameter are inflated.

FAO data sets are useful for estimating components of human appropriation of NPP, and we used them extensively in our analysis. FAO estimates, as noted by Haberl *et al.*, depend on data supplied by individual countries. With regard to developed, democratic nations (such as Austria), FAO data are of high quality. But the preponderance of the world's population lives in countries where government-based estimates of agriculture are poor or are modified for political purposes. Also, FAO data describe the edible mass produced and not the productivity of the land itself. Given these limitations, an FAO-based estimate of global agricultural productivity cannot be expected to provide an improvement over our estimate. Shortcomings like these point to the difficulty of measuring the human footprint on biological resources with current data sets.

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Fungal Diversity and Plant Roots

PHILIPPE VANDENKOORNHUYSE *ET AL.* ("Extensive fungal diversity in plant roots," Brevia, 15 March, p. 2051) report on various new and unusual fungi from roots of the grass plant *Arrhenatherum elatius*. I won't quibble about the putative identification and taxonomic grouping of the fungi involved, but the authors strongly suggest a necessary relationship between the fungi recovered and the plants themselves. I contend that it is just as likely that these fungi were associated with the plants simply by accident. Root sampling and cleaning techniques were not well described, but plant roots commonly have wounds associated with them even before sampling. Many organisms may become passively associated with such wounds or may even be drawn up into the nonliving root xylem if this is exposed to soil and soil water. Polymerase chain reaction techniques are so powerful that even traces of accidental associations would be detected. Thus, I contend that many of the novel organisms detected by the authors could simply be passive associations of soil organisms that have no necessary involvement directly with the roots of these plants. On the basis of DNA extractions from soil directly, we are all aware that most soil microorganisms have yet to be identified because they fail to culture easily on common growth media. The ones described by Vandenkoornhuyse *et al.* could simply be from that great array.

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Response

IN OUR BREVIA, WE CHARACTERIZE FUNGAL diversity in a mundane ecological niche, the roots of a plant. Sequences from roots of *Arrhenatherum elatius* revealed an unexpected diversity, with all known fungal phyla represented. The diversity within these phyla is very high, with a large proportion of fungi that could not be related to any known SSU rRNA gene sequence. The cleaning procedure of the root surface was designed to remove the mineral and organic particles. With this strategy, it is impossible to clean the inner root structures such as xylem. However, observations of stained roots under microscope showed only arbuscular mycorrhiza (Glomales) and septate endophytic fungal structures within or between the root cortical cells and a network of septate fungal filaments on the root surface. These external hyphae did not form the typical structures of ectomycorrhiza, nor did we observe any symptoms of plant pathology.

Crowe addresses, in part, the question of the ecological functions of these fungi associated with roots. One fungal group that we certainly did expect to find represented in roots was the arbuscular mycorrhizal (AM) fungi (*1*, *2*). These ubiquitous biotrophic zygomycetes in the order Glomales form symbioses with more than 80% of land plants (*3*). The co-occurrence of different symbiotic AM fungal phylotypes within the roots of a plant species is in agreement with previous work (*1*, *2*). However, our results show clearly that the Glomales correspond only to a small fraction of the fungal diversity in these roots.

We can only speculate on the possible roles of the other 94% of the root fungal diversity found here. Further studies are required to know which part of root fungal diversity interacts actively with host plant. A better knowledge of the diversity of the fungal world and a better understanding of fungal ecological functions in ecological niches and ecosystems are likely to become important issues.

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CORRECTIONS AND CLARIFICATIONS

SPECIAL ISSUE ON SUPRAMOLECULAR CHEMISTRY AND SELF-ASSEMBLY—NEWS: "Chemists look to follow biology lead" by J. Alper (29 Mar., p. 2396). The name in the photo credit for organic molecules appearing on page 2397 should have appeared as Sone *et al.*

PERSPECTIVES: "Of predators, prey, and power laws" by P. A. Marquet (22 March, p. 2229). In the figure, the y axis should have been labeled as "Log density/km^2."