

to $\pm 3|V_{pp\pi}|d/D$ when $\frac{2d}{D} \ll 1$.

All of these predictions are consistent with the numerical results shown in Fig. 1c. Because the semiconducting and metallic SWNTs studied experimentally all have $d/D \approx 0.1$ and $V_{pp\pi} \approx -2.7$ eV, these predictions explain the observed peak spacing in the SWNT DOS^{2,3}, further confirming the band structure theory of these nanowires⁴⁻⁹.

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A more reliable design for biodiversity study?

Naeem and Li¹ present the results of a microcosm study in which species diversity of organisms within trophic groups was varied. They conclude that the existence of multiple species within these groups enhanced the “reliability” of these systems, that is, the increased likelihood of a consistent level of performance over a given unit of time. But there are problems with their study. For the least diverse communities, one predator species was randomly selected from a selection of two, one autotroph from a selection of three, one consumer of bacteria from a selection of five, and one omnivore from a selection of six. Meanwhile, with the most diverse communities, both predator species and all three autotroph species were used, three consumer bacteria were chosen from the five and three omnivores from the six.

Thus, for the most diverse communities, the species composition of the individual

replicates was identical for three of the five functional groups considered (when the non-manipulated functional group, decomposers, is also considered) and, for the least diverse communities, the composition was identical across replicates for only one of the functional groups. Even for the remaining two groups, there is a greater probability of the species compositions being more similar to each other across replicates in the more diverse treatment (Table 1).

Therefore, the observation that biomass variation of the non-manipulated functional group (decomposers or bacteria) across replicates was less in the more diverse microcosms (used by Naeem and Li as evidence that enhanced diversity increased “ecosystem reliability”) could be explained simply in terms of the individual replicates of the more species-rich microcosms being more similar to each other than those of the less diverse microcosms at the start of the experiment, in terms of both the composition of food sources and the consumers of bacteria.

Similarly, the observation that algal density was most closely associated with the number of functional (trophic) groups in the more species-rich microcosms could be attributed to lower variability in starting conditions across replicates of these microcosms, resulting in a tighter and more consistent relationship across replicates within treatments that is less likely to be obscured by within-treatment variation.

The hypothesis tested by Naeem and Li could only be investigated reliably by using a sufficiently large species pool to enable non-overlapping species compositions across replicates of the most species-diverse microcosms. Such an experiment could consist of, for example, four different groups (with non-overlapping compositions) of ten sets of identical high-diversity communities and four different groups of ten sets of identical low-diversity communities.

The variability is then calculated for each group of ten, and the variability across each group of ten is used as one datum. The result is four replicate measures of variability for each of the high- and low-diversity situations. But even with a larger species pool, caution is needed in the interpretation of results when the causative effects of biodiversity are being investigated²⁻⁵. A more robust experimental design is needed to justify claims such as “provision of

adequate redundancy may be one reason for preserving biodiversity”.

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Naeem and Li reply — Wardle’s concerns arise from conflating biodiversity loss within an ecosystem (our study¹) with biodiversity loss among ecosystems. To examine biodiversity loss within an ecosystem experimentally, a community is compared with more depauperate versions of itself^{2,3}. This design mimics the pattern observed in nature and sheds light on theory and mechanisms. Our experiment followed this approach to test predictions of reliability theory based on the mechanism of compensatory growth among redundant species.

In contrast, to examine biodiversity loss among ecosystems, communities of similar biodiversity but with unique species composition are compared across different diversity levels. (So far, only the European Union’s recent BIODEPTH experiment follows such a design.) So what Wardle calls a “more robust” design would actually be addressing a different question.

Wardle’s concerns arise because he believes that variability in initial community composition will be correlated with variability in final measures of ecosystem functioning, but he does not provide any theory or mechanism for this hypothetical correlation. Trivially, communities of non-overlapping composition may show less variability within communities than among them (Wardle’s design) but there is no ecological foundation for the belief that variability within replicates of a diverse community will be lower than variability among depauperate versions of itself (our design).

Factors such as local extinction, variation in nutrients or energy output, and increases in density and standing biomass by several orders of magnitude over many generations (all characteristics of replicate communities in our experiment) generate a wide variety of production and dynamic responses in communities. Contrary to Wardle’s claim, our findings clearly support the possibility that preserving an ecosystem’s biodiversity might provide more reliable functioning.

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Table 1 Expected proportion of total number of species in common between any two replicates for each diversity treatment at the start of the experiment conducted by Naeem and Li

Functional group	Lowest diversity treatment	Intermediate diversity treatment	Highest diversity treatment
Autotrophs	0.333	0.667	1.000
Decomposers	1.000	1.000	1.000
Omnivores	0.167	0.333	0.567
Consumers of decomposers	0.200	0.400	0.667
Top predators	0.500	1.000	1.000
All species	0.368	0.579	0.776