BIODIVERSITY

Remote responsibility

International trade is the underlying cause of 30% of threatened animal species extinctions, according to a modelling analysis of the impact of global supply chains and consumption patterns on biodiversity. SEE LETTER P.109

EDGAR HERTWICH

Biodiversity loss has just become a little more personal. Your freshly brewed cup of coffee is implicated in causing a significant number of threats of animal extinctions, according to a study by Lenzen *et al.*[1] on page 109 this issue. The authors present an analysis of species threats associated with internationally traded commodities, based on a detailed model of the global supply chains that connect final consumption to economic activities — and thus, for example, coffee drinking to species vulnerability.

If you buy a set of chess figures carved from ivory, you can suspect that you have contributed to killing an elephant. But if you buy a sausage, you cannot know whether the pig that was turned into the sausage was fed soy meal sourced from a farm that had just expanded into elephant habitat. The effects on species diversity, however, are similar. Understanding the complete causality chains leading to animal species extinctions has proven an intractable problem. Although the causes of individual threats to species are routinely identified when these species are 'red-listed' as vulnerable, endangered or extinct, the driving forces behind these immediate causes have until now escaped quantification. This incomplete understanding has hindered us from seeing the big picture and appropriately identifying the importance of different drivers.

The difficulties in linking proximate causes, such as the consumption of specific goods by identifiable groups of people, to immediate threats to biodiversity, such as habitat change, arise from both the sheer complexity of causal relationships that run through interconnected environmental and human systems, and from a lack of adequate indicators. Lenzen and colleagues present two significant advances in making such connections. The first is their model, the most detailed yet to describe the economic relationships between production and consumption. The second is their use of the threat causes recorded by the International Union for Conservation of Nature's Red Lists to identify direct links between threatened species and economic production activity.

Multiregional input–output models trace the multiple inputs required by manufacturing industry and other producing sectors, even across international borders, and have become the tool of choice for analysing the environmental pressures of consumption activities[2,3]. For example, such models have linked greenhouse-gas emissions from production activities in emerging economies to consumption in affluent countries[3], and shown that the emissions resulting from importation to affluent countries are increasing at a faster rate than the emissions associated with exported goods[4]. Lenzen *et al.* present a new multiregional input–output model, which they constructed 'from the bottom up' using a wide range of data sources — primarily national input–output tables and trade data. Their modelling combines powerful computation with novel approaches for reconciling conflicting data and estimating data points for which no primary data exist.

The authors then used their model to link economic activity to biodiversity (Fig. 1). Conventionally, this type of assessment links economic activity to individual environmental pressures that have been identified[5] as threats to biodiversity, such as land use, water use, or the over-fertilization of land and water. This approach allows the contribution of consumption to different environmental pressures to be quantified[6]. Impacts are then assessed using mechanistic models that connect the environmental pressures with an intermediate or final indicator of ecosystem impact, such as species threats. There are many such mechanisms, however, and some are highly site-dependent, so that this assessment approach is not able to provide a satisfactory picture of global biodiversity impacts[7]. An alternative approach is to link biodiversity models to environmental pressures[8], but such analysis has not yet, to my knowledge, been connected to models of global supply chains.

Pragmatically, Lenzen *et al.* circumvent any attempt to model the causal relationship between environmental pressure and ecosystem impact, and rely instead on threat causes provided in the Red Lists, such as 'smallholder farming' and 'logging and wood harvesting'. These causes are thereby connected in the input–output tables to specific industries, such as farming and forestry. When more than one industry can be connected to a cause, the responsibility is distributed in proportion to the economic importance of the industry. The fundamental unit of measurement in the authors' system is thus national species-threat

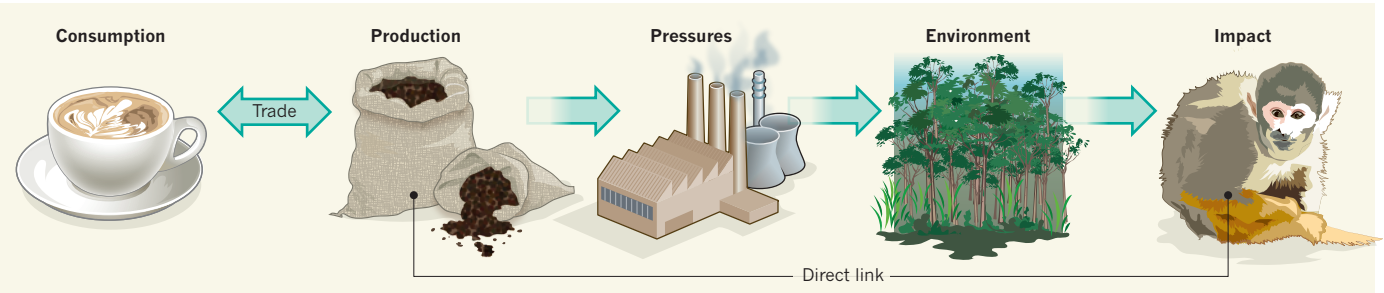

Figure 1 | Exporting species threats. The causal link between consumption and biodiversity loss involves the driving forces of economic activities (production, trade and consumption); the pressures exerted by these activities (such as resource extraction, pollution and land use); and the environmental processes, such as habitat change, that link these pressures to impacts, which include species threats. Impact-assessment methods typically trace causality from pressure to impact, but Lenzen *et al.*[1] have used established causes of observed species threats to link biodiversity loss directly to economic activity.

records; in other words, the instances of a species being put on a Red List in a given country. In the model, fractional responsibilities are then redistributed, using the input–output calculations, to final consumers all over the world. An example from the study is the Central American spider monkey *Ateles geoffroyi*, the red-listing of which is specified as resulting from habitat loss linked to coffee and cocoa plantations (Fig. 1).

Lenzen and colleagues' results indicate that 30% of instances of red-listed species worldwide are caused by internationally traded commodities, and that the United States, Japan and European countries are the main net 'importers' of species threats, whereas southeast Asian countries are the main net 'exporters'— the region in which the most species threats arising from trade occur. The authors show that the contribution of trade to biodiversity threats is similar to its contribution to global carbon dioxide emissions[3,4], although it is China, Russia and South Africa that are the largest emissions exporters.

There is some risk that this research overemphasizes the effect of international trade because, in developing countries, the production of cash crops for export results in a higher added value than subsistence agriculture, so that species threats may be disproportionally allocated to exported crops. Starting a cause–effect analysis from the effect side, as Lenzen and colleagues have done, is a novel and interesting approach. However, their results should be corroborated by further research exploring the linkage of pressures on biodiversity through global trade to consumption.

This study provides an indication of which areas of consumption need to be targeted to reduce biodiversity threats, which is a valuable contribution. The fundamental question that remains is whether the current (and increasing) scale of consumption will inevitably cause these threats, or whether ways could be found to satisfy this consumption but allow affluent consumers to reduce their impact, such as improved labelling systems and lower-impact production methods. ■

Edgar Hertwich *is in the Department of Energy and Process Engineering, Norwegian University of Science and Technology, 7941 Trondheim, Norway.*
e-mail: edgar.hertwich@ntnu.no

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CELL BIOLOGY

High-tech yeast ageing

A method commonly employed to study replicative ageing in yeast is laborious and slow. The use of miniaturized culture chambers opens the door for automated molecular analyses of individual cells during ageing.

MICHAEL POLYMENIS & BRIAN K. KENNEDY

Similarly to many cells in our body, the cells of budding yeast cannot replicate indefinitely. On division, a yeast cell gives rise to a mother cell and a 'fresh' daughter cell. The mother cell can produce, on average, only about 25 daughters before it dies. A test that measures the replicative lifespan of yeast cells has become a popular way to study ageing processes, and researchers have used it to identify genes and pathways that were later confirmed to have roles in longevity in animals[1–4]. However, such an assay is labour intensive and cannot be implemented in a high-throughput fashion[5]. Two studies, one by Lee *et al.*[6] in *Proceedings of the National Academy of Sciences* and another by Xie *et al.*[7] in *Aging Cell*, offer modified versions of the assay that are amenable to automation and that allow the study of ageing processes in yeast cells to be made in unprecedented detail. The techniques use tiny chambers to retain mother cells and wash away daughters, coupled to powerful microscopes capable of time-lapse photography.

In the conventional replicative ageing assay, the experimenter must look through a microscope and painstakingly remove each daughter cell after division using a small needle on the surface of thick, solid culture media (Fig. 1a). Moreover, just as with other organisms, there is significant variation in lifespan between individual yeast cells, even when they are genetically identical. This means that a minimum of 40 cells have to be interrogated to generate a reliable lifespan data set, which necessitates the manual removal of approximately 1,000 daughter cells.

Lee *et al.* and Xie *et al.* replaced the manual approach with transparent microfluidic devices that consisted of submillimetre-scale channels and tunnels through which nutrient broth flows in a controlled manner (Fig. 1b). Such a set-up allowed the authors to apply high-resolution microscopy techniques for tracking individual cells and molecular markers.

Subtle differences exist between the two systems, however. Lee and colleagues suspended the yeast cells between silicone micropads and thin cover glass. The micropads were slightly lifted by the hydrostatic pressure of the broth during loading of a cell suspension, and they held the mother cells after release of the pressure. Daughter cells were washed away because of their smaller size.

By contrast, Xie *et al.* trapped the cells in 'micro-jails' from which the daughters could escape through gates. The researchers also attached biotin molecules to the mothers' cell walls, causing these cells to adhere to the chambers' surfaces, which had been coated with avidin (a protein that binds biotin with high affinity). This ensured that only mother cells remained trapped, as the synthesis of new cell wall in yeast is confined to daughter cells, and no biotin was supplied after the initial labelling of the mother cells.

Interestingly, both groups of authors studied

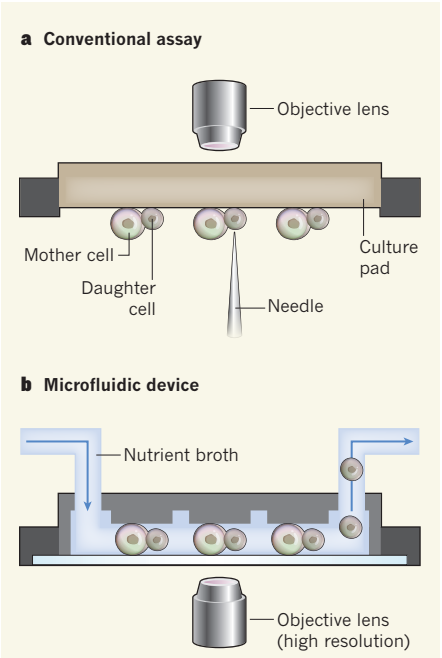

Figure 1 | Watching how cells age. Budding yeast divides by forming a bigger mother cell and a smaller daughter cell. As a measure of lifespan in yeast, researchers count the number of daughters produced by each mother. **a**, In a conventional assay, yeast cells are grown on the surface of thick culture media, and the researcher removes daughter cells — one by one — using a needle and a microscope. **b**, Lee *et al.*[6] and Xie *et al.*[7] developed transparent microfluidic devices that trap mother cells in small chambers, whereas daughters are washed away by a controlled flow of nutrient broth. The authors used high-resolution microscopes to track changes associated with ageing in individual cells. (Figure modified from ref. 6).