Life after GE Nightmare

Mae-Wan Ho

European Parliament Briefing
20 October 2004 Brussels

GM Crops

Global Stats. 2003

	mHa	%
World	67.7	100.0
USA	42.8	63.2
Argentina	13.9	20.5
Canada	4.4	6.5
China	2.8	4.1
S. Africa	0.4	0.6

	mHa	%
Soya	41.4	61.2
Maize	15.5	22.9
Cotton	7.2	10.6
OSR	3.6	5.3

	mHa	%
Herb. tol.	49.7	73.4
Insect. res.	12.2	18.0
Both	5.8	8.6

GM Crops

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Both	5.8	8.6

GM crops occupy just **1.3%** of the world's 5019.6 mHa agricultural land

Nearly **84%** are confined to the USA and Argentina

Sources: www.fao.org; www.isaaa.org

Biotech Investment Busy Going Nowhere

***Claire Robinson** exposes the financial woes of the biotech industry*

Biotechnology is the answer to problems ranging from hunger in Africa and Asia to obesity in the West. This was the upbeat message from the industry's promotional showcase, the BIO 2004 conference, which took place in San Francisco in June. In launching the conference, BIO (the Biotechnology Industry Organisation) trumpeted, "the biotechnology industry is performing

in its falling bottom line. As the *New Zealand Herald* said, "Investment in genetically modified food is drying up in the world's biggest GM market, the United States, because consumers in the rest of the world are not willing to buy its products."

Roger Wyse of Burrill and Company, the biggest investment firm focused on life sciences, said the consumer backlash against GMOs had forced a lull in projects aimed at modifying food. "We are probably looking at three, four or five years before the GMO issue subsides sufficiently that we will feel comfortable investing in it," he said.

Lack of investment has led to massive losses. Back to Ewing: "Last year, this industry lost $5.4 billion, and has lost a staggering $57.7 billion since BIO last held its annual conference in San Francisco in 1994, according to an Ernst and Young study. Only a few companies have been consistently profitable in the 30 years since biotech was born - a few, such as Amgen and Genentech, fantastically so. Remove

up of its products, selling stocks has become a biotech industry lifeline. In 2003, US biotech firms raised almost $4 billion by selling new stock to investors, according to Burrill & Co. The same year, US biotechs as a group posted almost that much in losses. Only 12 of the 50 largest biotechs turned a profit in 2003.

Meltdown continues

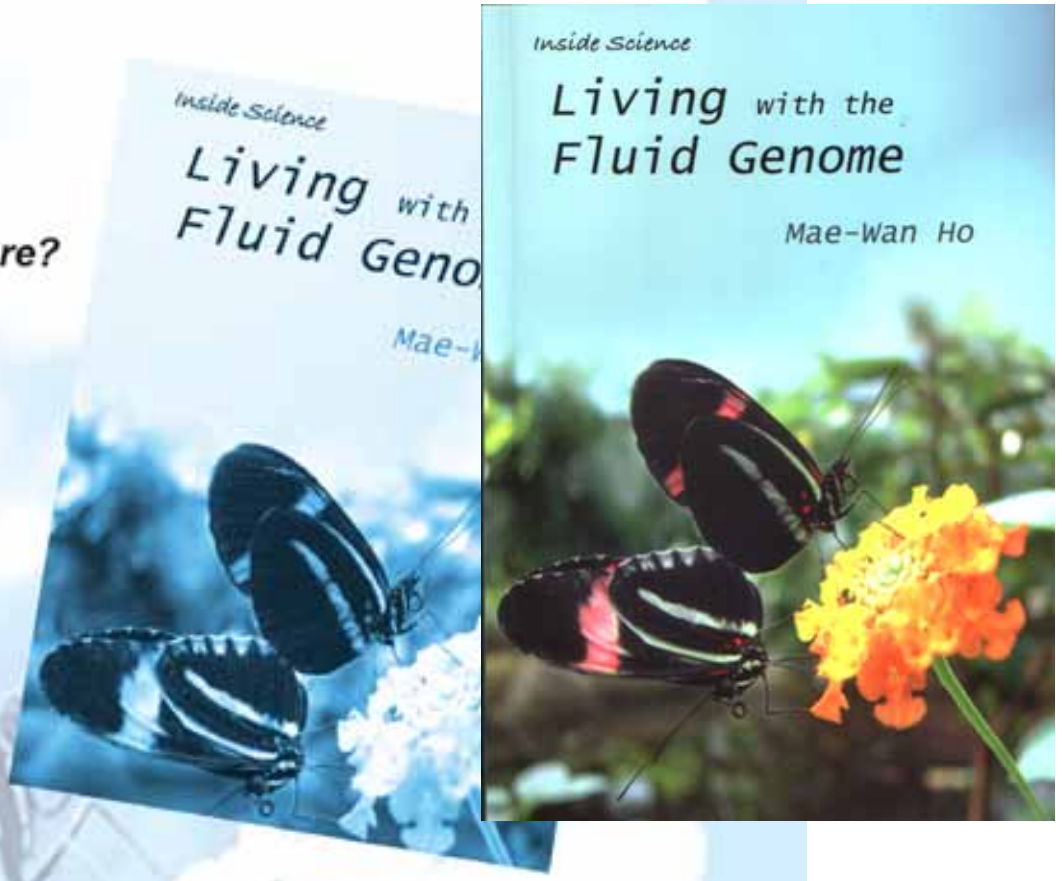
In the UK, the biotech meltdown continues apace. Earlier this year, it emerged that two biotech firms linked to science minister and donor to the Labour Party, Lord Sainsbury, are facing serious financial difficulties. Diatech Ltd, which holds several patents for techniques designed for use in GM foods, has gone into liquidation, while biotechnology investment firm Innotech is making huge losses.

At the end of June, the British GM science lobby despaired at news that Anglo-Swiss biotech giant Syngenta was withdrawing from the UK and transferring to North Carolina in the US. Syngenta was

Living with the Fluid Genome

By Mae-Wan Ho

Author of International best-seller,
Genetic Engineering Dream or Nightmare?



Readership
General public, suitable for all post-16 educational levels and as university course-book

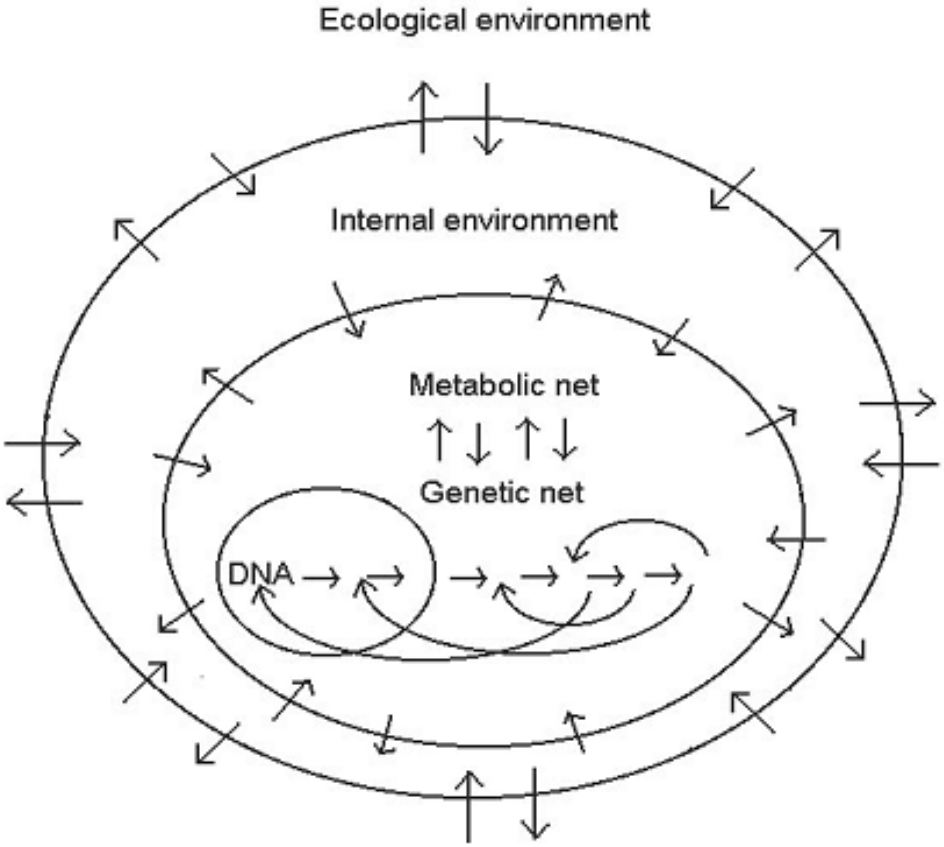
The biotech empire is showing all the signs of collapsing because it's got the science wrong.

Read this riveting inside-story of the fluid genome from a scientist who has been warning that genetic engineering is both dangerous and futile for over a decade.

Find out why the whole biotech enterprise, from GM crops to gene drugs and human

Central Dogma of Molecular Biology

The Fluid Genome



The Central Dogma

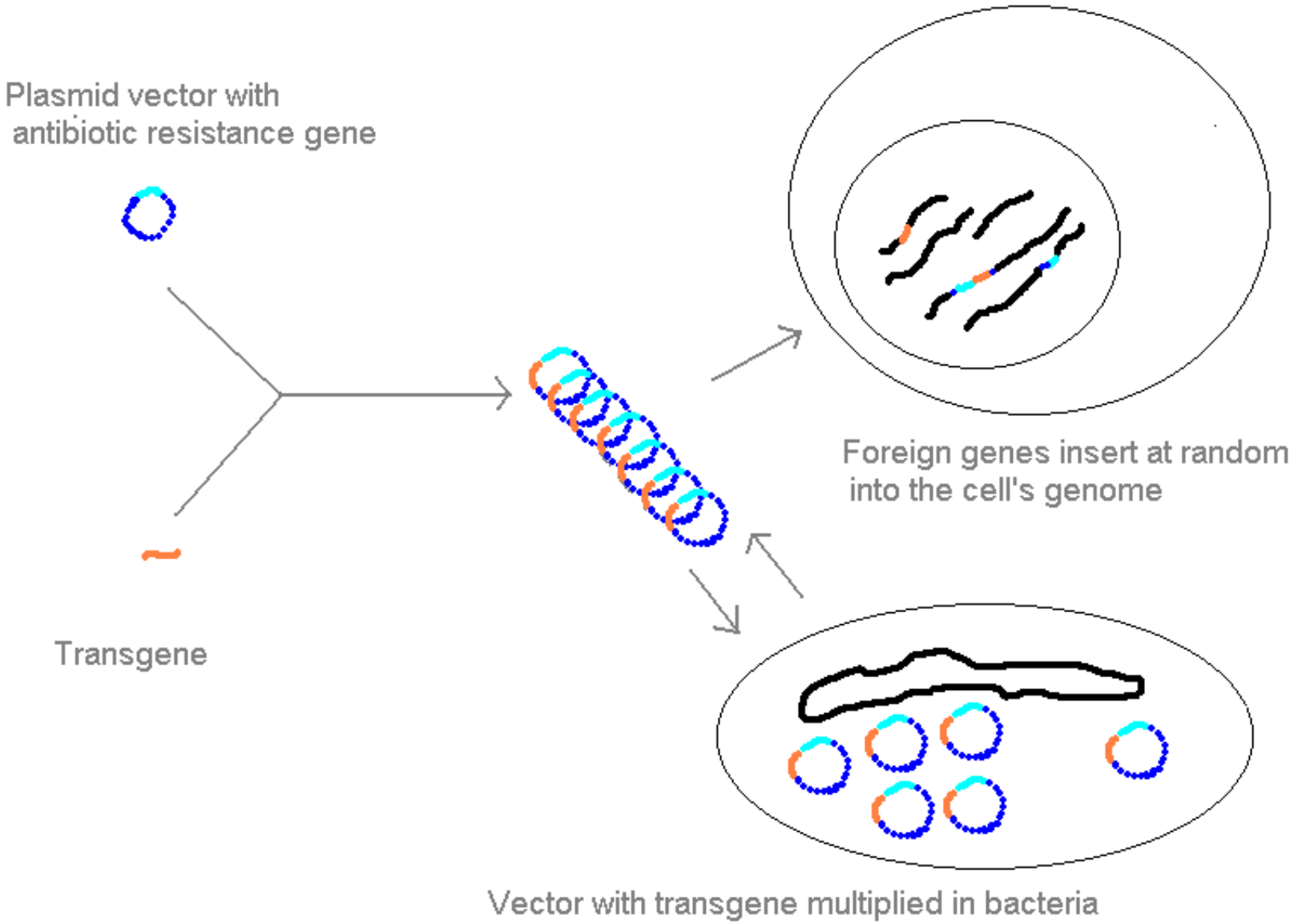
DNA ⟶ ⟶ ⟶

Natural Genetic Engineering

*Precisely regulated by the organism as a whole

Artificial Genetic Engineering

*Crude and Uncontrollable


Plasmid vector with
antibiotic resistance gene
Transgene
Foreign genes insert at random
into the cell's genome
Vector with transgene multiplied in bacteria

CHARACTERISATION OF COMMERCIAL GMO INSERTS: A SOURCE OF USEFUL MATERIAL TO STUDY GENOME FLUIDITY.

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Introduction

Labelling of food and feed containing more than a defined threshold of ingredients derived from authorized GMOs is mandatory in countries such as Europe, Japan, Australia and New Zealand. Reliable GMO identification and quantification methods are needed to comply with these regulations. Mostly based on PCR amplification (end point and quantitative real time PCR), GMO detection tests can be specific of recurrent regulatory sequences and genes (screening), construct-specific, or event-specific. Development of such tests requires **the sequencing and the detailed characterisation of the GMO inserts and their edge-fragments**. By contributing to the localization of the preferential integration sites, and by revealing unexpected rearrangements, duplications of genetic elements and/or inserts, these analyses show that commercial GMOs are a source of valuable material to study genome fluidity, especially DNA placement, recombination and repair mechanisms.

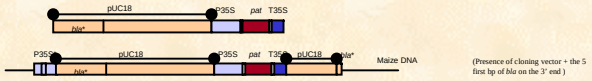
T25 maize - *Libertylink™* (Bayer)

Tolerance to herbicide glufosinate, Peg-mediated transformation

Construct content : truncated *bla* gene (*bla**), pUC cloning vector (pUC), synthetic *pat* gene (*pat*), CaMV 35S promotor and terminator (P35S, T35S).

Sequence expected (public data)

Sequence observed



DNA rearrangement: presence of a second truncated and rearranged P35S on the 5' end.

Insertion site: the 5' and 3' ends of the insert show homologies with Huck retrotransposons.

(Collonnier et al. (2003) Eur. Food Res. Tech. (submitted))

Why do DNA rearrangements occur ?

- In plants, exogenous DNA transfer elicites a wound response which activates nucleases and DNA repair enzymes. The transferred DNA is thus, either degraded or used as a substrate for DNA repair, resulting in its potential rearrangement and incorporation in the genomic DNA (Takano et al. (1997) Plant J 11: 353-361). Furthermore, specific transforming plasmid structure and construct properties can enhance recombination events all along the transformation process. Indeed, some genetic elements can act as **hotspots** and undergo recombination at high frequency. It is, for example, the case for **the 3' end of the CaMV 35S promotor** -an imperfect palindrome of 19 bp- when it is in conjunction with specific flanking sequences derived from transforming plasmid. Illegitimate recombination can also occur in **the borders of the Ti plasmid** of *Agrobacterium tumefaciens*, especially in the right border which contains an imperfect palindromic sequence of 11 bp. The 3' end of **the nos terminator** is also theoretically highly prone to recombination (Kohli et al. (1999) Plant J. 17(6): 591-601). Hot spots may lead to tandem transgene repeats with interspersed plant DNA sequences in a single genetic locus. Presence of several inserts may also result from multimerisation in the plasmid before transformation or from multiple insertions. - In addition to cellular mechanisms controlling the transgene integration, subsequent selection procedures of the GM material may introduce further genomic reorganisations (Hernandez et al. (2003) Transgenic Res. 12: 170-189).

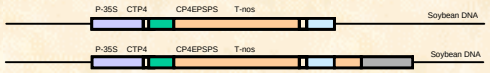
GTS 40-3-2 soybean (Monsanto)

Tolerance to herbicide glyphosate (Roundup Ready ™), Bombardment

Construct content : CaMV 35S promotor (P35S), N-terminal chloroplast transit peptide (CTP4), modified *epsps* gene (CP4EPSPS), nos terminator (T-nos).

Sequence expected (public data)

Sequence observed



DNA rearrangement: on the 3'end of the insert, presence of a 245bp sequence homologous to CP4 EPSPS and a 534 bp unknown sequence.
Insertion site: the two junction fragments share no homology: some DNA rearrangements or a large target site deletion on the 5' end of the insert.

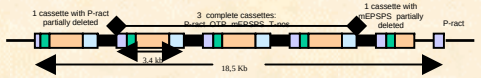
(Windels et al. (2001) Eur. Food Res. Technol. 213: 107-112)

GA21 maize (Monsanto)

Tolerance to herbicide glyphosate (Roundup Ready ™), Bombardment

Construct content : rice actin promotor (P-ract), N-terminal chloroplast transit peptide (CTP4), modified *epsps* gene (CP4EPSPS), nos terminator (T-nos).

Sequence expected (public data)



Results obtained : Confirmation of the presence of EPSPS and T-nos (unpublished data, MDO, INRA, Versailles, France). Similar junction between tandem repeats of EPSPS cassette (only one single PCR product (208 bp)) (unpublished data, IBMB, CSIC, Barcelona, Spain) .

DNA rearrangement: duplication of the EPSPS cassette, partial deletion of the P-ract and deletion of T-nos in two different cassettes.
Insertion site: the 3' end of the insert is flanked by sequences of the pol-polyprotein gene of a PREM2-retrotransposon (public data).

What are the DNA rearrangements observed in GMOs ?

The results presented here in the different frames show that various kind of rearrangements occur in GMOs: **deletion** (Mon810, GA21, Bt176), **recombinaison** (T25, GTS 40-3-2, Bt176), tandem or inverted **repeats** (T25, GA21, GTS 40-3-2, Bt176)... Moreover, in addition to insert recombinations, rearranged fragments of the insert can also be scattered in the genome (Mon810).

When do they occur ?

Rearrangements of transforming DNA have been reported both in direct and indirect transformation. Recombination may occur between plasmid molecules **before or during** the transformation, or between plasmid and genomic DNA **during or after** the transformation.

Mon810 maize- *YieldGard™* (Monsanto)

Resistance to lepidopteran insects, Bombardment

Construct content : CaMV 35S promotor (P35S), *CryIA(b)* toxin synthetic gene (*CryIA(b)*), nos terminator (T-nos).

Sequence expected (public data)

Sequence observed

DNA rearrangement: deletion of T-nos in the insert (but Tnos detected in the genome) and deletion of a part of *CryIA(b)*.
Insertion site: the 5' end of the insert shows homology with LTR sequences of the *Z. mays* alpha Zein gene cluster. No homology between LTR sequences and the 3' end: rearrangement of the integration site.

(Hernandez et al. (2003) Transgenic Res. 12: 179-189; Holck et al. (2002) Eur. Food Res. Tech. 214: 449-453)

How do they occur ?

In higher plants, most rearrangements involve **illegitimate recombination** during **DNA double-strand break repair (DSBR)** (Sargent et al. (1997) Mol. Cell Biol. 17: 267-277). Plasmid junctions are predominantly formed by **microhomology** dependent illegitimate recombination mainly based on single-strand annealing of complementary tails, followed by repair synthesis over the remaining gaps (Kohli et al., 1999). Several other mechanisms can also be involved in DNA rearrangement, such as non homologous end joining (rare), or polymerase slipping and template switching sometimes leading to deletion (Cf cruciform P35S - green frame).

A recombination hotspot in P35S

Two sequences of the 35S CaMV promotor are shown aligned in opposite orientations, representing a possible cruciform structure adopted by the 19bp palindromic sequences. The arrow indicates the position of a potential crossover – Kohli et al. (1999) Plant J. 17(6): 591-601.

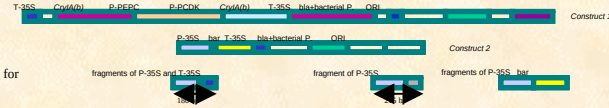
Bt176 maize (Syngenta)

Tolerance to herbicide glufosinate, male sterility, insect resistance – Bombardment.

Construct content : CryIA(b) toxin synthesis gene (*CryIA(b)*), bialaphos resistance gene (*bar*), ampicillin resistance gene (*bla*) + bacterial promoter, PEPC promotor (P-PEPC), PCDK promotor (P-PCDK), CaMV 35S promotor and terminator (P35S, T35S), plasmid replication origin (ORI).

Sequence expected (public data)

Sequences observed when looking for the *bar* cassette of Construct 2



DNA rearrangement: 3 rearranged fragments detected. The first of 118 bp is homologous to P35S and T35S. The second contains a fragment of P35S and an unknown sequence of 215 bp, the third contains P35S and the *bla* gene (deletion of T35S).
Insertion site: at least 3 integration sites for construct 2

(Unpublished data: Lab. MDO INRA, Versailles, France; TEPRAL, Strasbourg, France)

Where does the insert go ?

Transferred DNA preferential insertion sites include **mobile elements** such as **retrotransposons** (T25, Mon810, GA21), but also repeated sequences (Bt11 maize insert (Syngenta) is located in a tandem repeated sequence motif (Zimmermann et al. (2000) Lebensm-Wiss u-Technol 33: 210-216 ; Rønning et al. (2003) Eur. Food Res. Technol. 216: 347-354). Many retrotransposons containing long terminal repeats (LTRs) carry strong promotors. Insertions in these regions could then give rise to altered spatial and temporal expression patterns of genes in close proximity. Moreover, defective retrotransposons can transpose by the use of trans-acting factors, which could potentially affect the genetic stability of the recombinant DNA insert (Jank and Halsberger (2000) Tibtech 18: 326-327).

Conclusion

Studying GMOs structure is necessary to develop reliable quantification and detection tests complying with the different regulations, but it also leads to ask **fundamental questions about genome fluidity**. Many of the mechanisms involved in recombinant DNA integration are similar to those underlying **genome evolution**. Therefore, characterised **GMO inserts are a very good model to study the molecular systems involved in DNA rearrangements** in general. Furthermore, GMO progenies can be used to compare the evolution of an exogenous DNA insert to those of mobile or non mobile genetic elements already present in the plant genome. Lastly, characterising different GMO cultivars produced with the same initial construct should provide information on the effect of the genomic background on the DNA insert stability.

The European Commission is acknowledged for financial support through the Fifth (EC) Framework Programs: projects QPCRGMOFOOD (2000-2003) n° QLK-CT-1999-01301 and GMOCHIPS (2001-2004) n°G6RD-CT-2000-00419.

Two Latest Incidents in GM Safety

Monsanto's GM maize Mon863 containing a Bt biopesticide Cry3Bb1against the corn root worm was given a positive assessment by the European Food Safety Authority despite "very disturbing" health impacts including kidney malformations and increase in white blood cells in male rats and high blood sugar and reduced immature red blood cells in female rats.

Villagers in the south of the Philippines living near GM maize plots suffered from serious illnesses when the GM maize came into flower in last year, and again this year. Prof. Terje Traavik of the Norwegian Institute of Gene Ecology in Tromsø examined the blood of 39 villagers and found antibodies to Cry1Ab produced by the GM maize as biopesticide against the cornborer.


Gen-Futter –
Alles in Butter?
GREENPEACE
Gen-Futter –
Alles in Butter?
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Gen-Futter -
Alles in Butter?
GREENPEACE

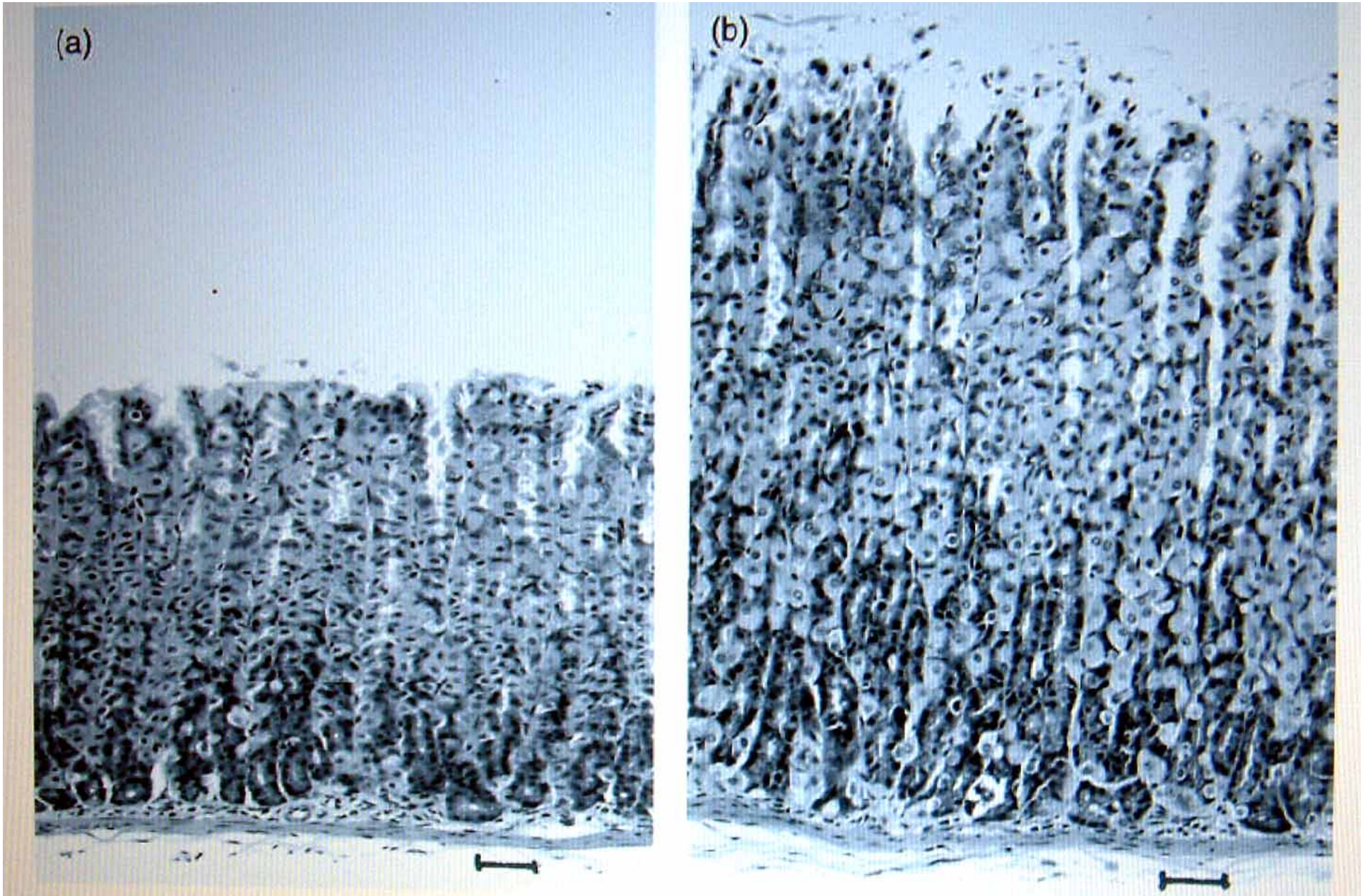
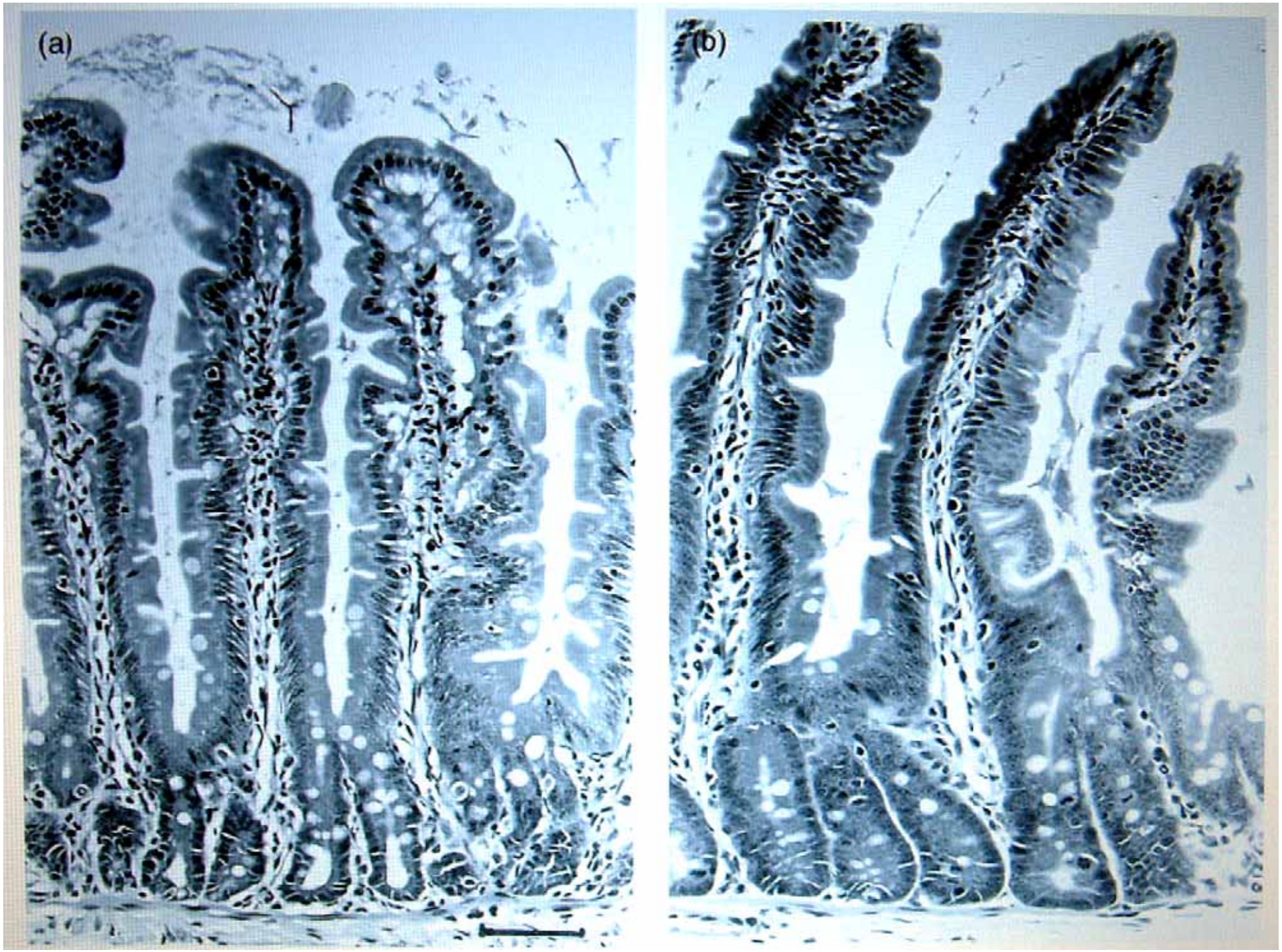


Fig. 16.1. Comparison of the stomach mucosa of rats fed with raw GM potato diet (b) shows marked thickening due to hypertrophy of mucosal cells in comparison with that of rats given the parental line (a) (bar = 100 µm).


(a)
(b)

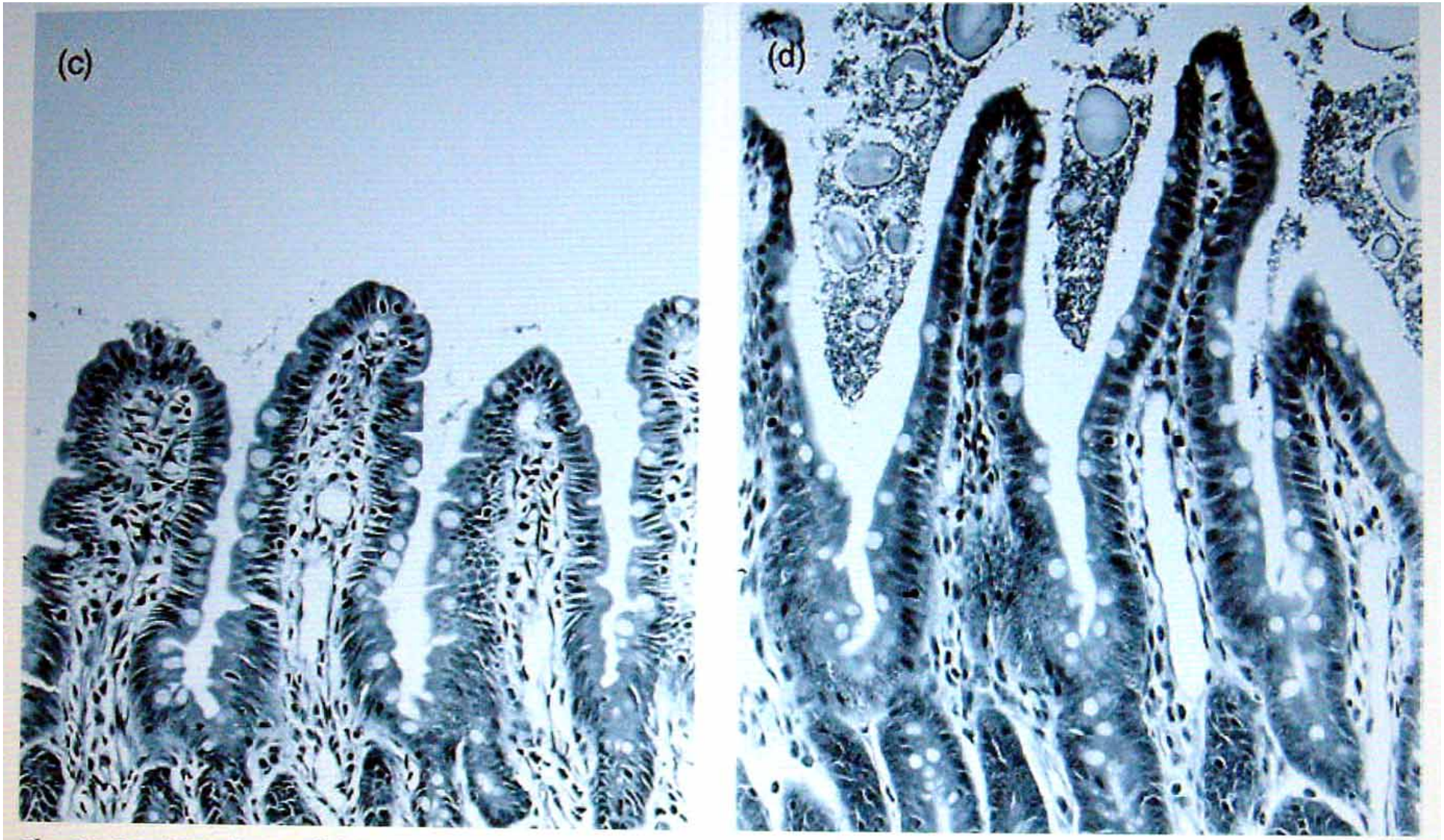


Fig. 16.2. Histology of the jejunum and ileum of rats fed raw GM or parent potato diets. Jejunal crypt length and cells exhibit marked enlargement after feeding rats GM potato diets for 10 days (b) in comparison with those of rats given parental line potato diets (a). The villus length is similar in both, but intraepithelial lymphocyte cell counts appear to be increased on the GM potato diet. In the ileum, both crypts and villi of rats on GM potato diets are elongated (d) in comparison with parent potato-fed rats (c) (bar = 100 μm).

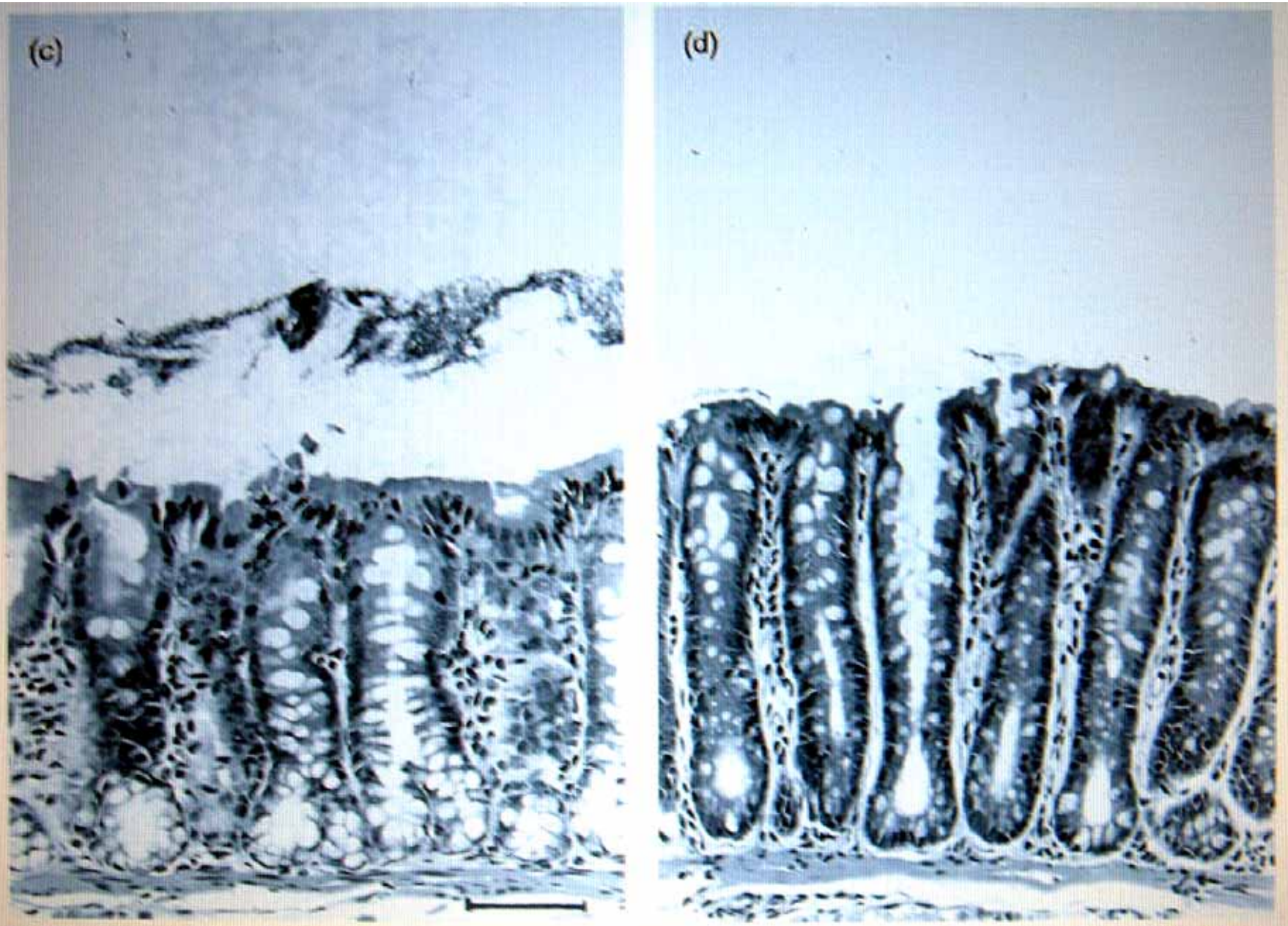


Fig. 16.3. The mucosa of the caecum demonstrates little change. Differences between GM-fed (b) and parent line potato-fed rats (a) are slight, while the colonic mucosa is moderately thickened in GM-fed rats (d) compared with that of rats given the parental line (c) (bar = 50 μm).

Spot the Common Factor *

Sick	rats	Monsanto	Bt maize Cry3Bb1
Sick	humans	Philippines	Bt maize Cry1Ab
Dead	cows	Hesse Germany	Bt maize Cry1Ac ?
Sick	rats	Pusztai et al	GNA-potato
Sick	mice	Fares & El-Sayed	Bt potato Cry1Ab
Sick	rats	US FDA	Antisense Tomato
Dead	Chickens	Aventis	Glufosinate-tolerant maize

* The GM process, GM construct or both

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Science *in* Society

One of the most significant discoveries over the past 50 years is that genes and genomes are dynamic and fluid.

Japanese stoneage venus - picture Mae-Wan Ho

Diet Trumping Genes

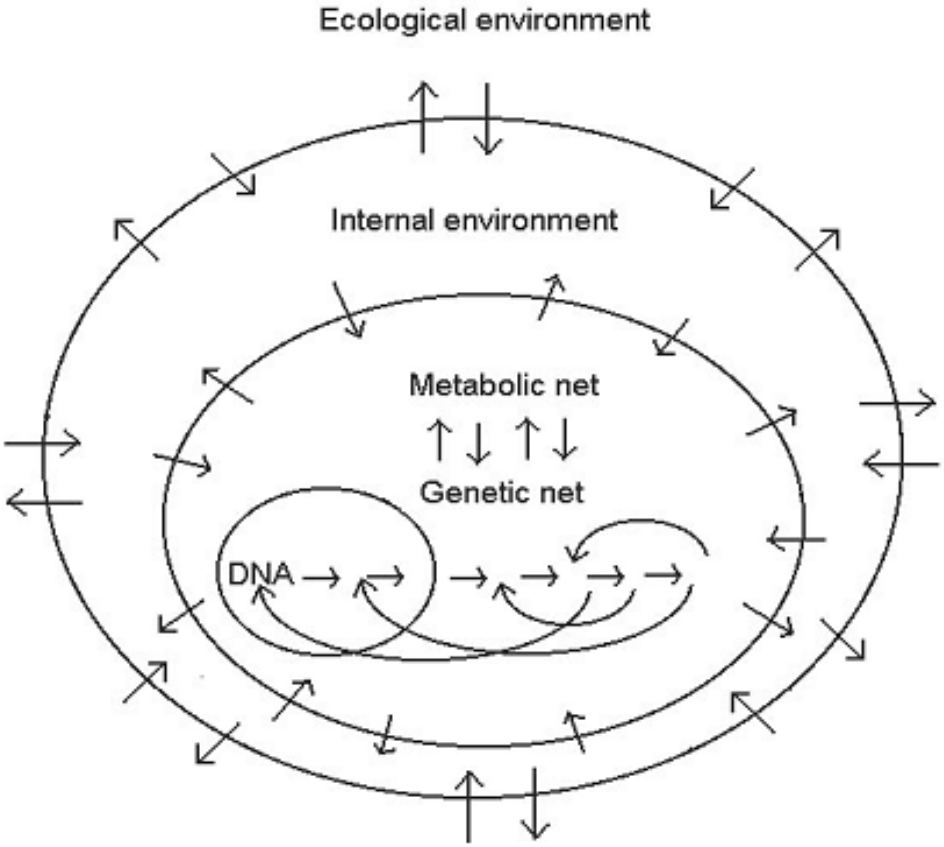
Most geneticists are still focussing on gene sequences to find out which gene variants go with which diseases. But that's a serious mistake, and for more reasons than one.

***Dr. Mae-Wan Ho** reports.*

genes downstream. The metabolic intermediate donating the methyl group to CpG is S-adenosylmethionine; and its availability will be influenced by dietary intake of methyl-donors and other co-factors necessary for its synthesis. That may be one way early nutrition can affect adult susceptibility to disease.

Patterns of DNA methylation are in part determined by transposable elements - mobile genetic units - scattered throughout the human genome, making up more than 35% of the genome. Most transposons are silenced by methylation, but a subset of them is metastable (not quite stable), and can change in methylation, thereby affect-

The Fluid Genome



The Central Dogma

DNA ⟶ ⟶ ⟶

The Rainbow and The Worm

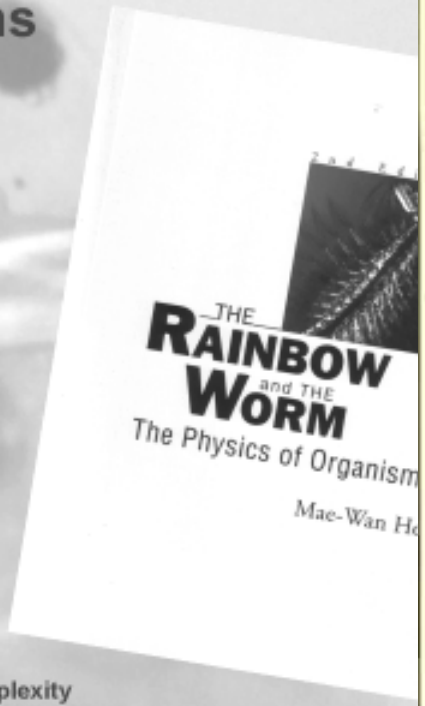
The Physics of Organisms

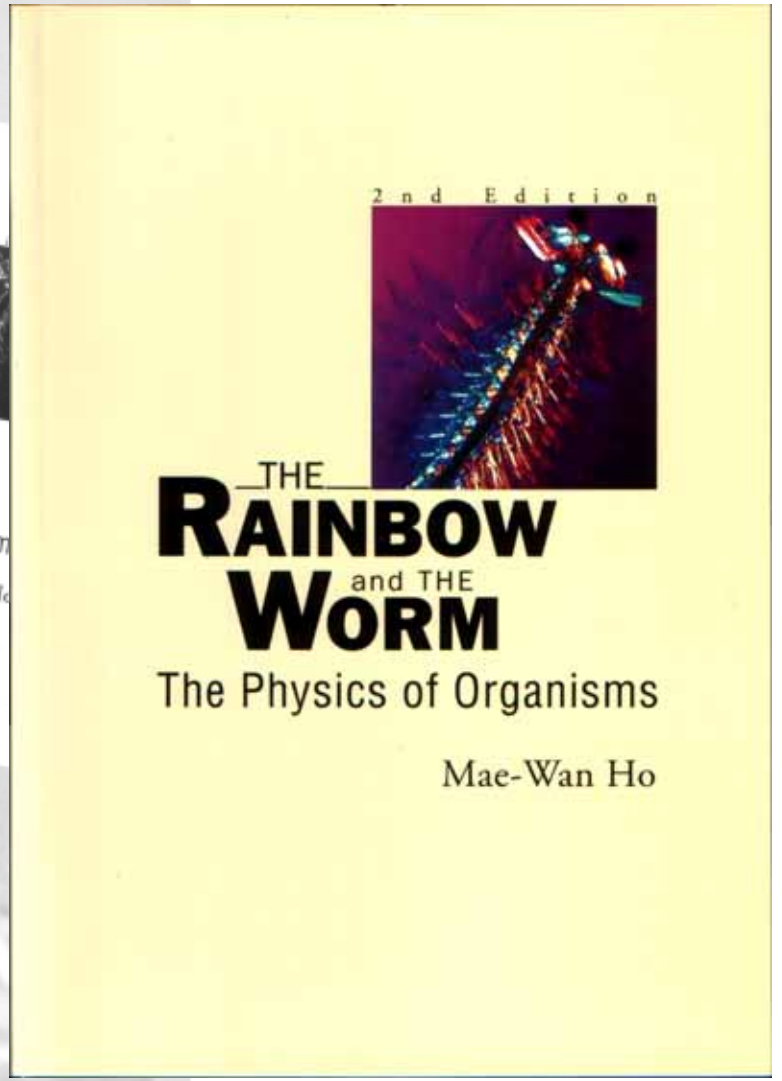
by **Mae-Wan Ho**
Institute of Science in Society

Readership: General

Contents

A serious, in-depth enquiry into Schrödinger's question, "What is Life?" and at the same time, a celebration of life itself



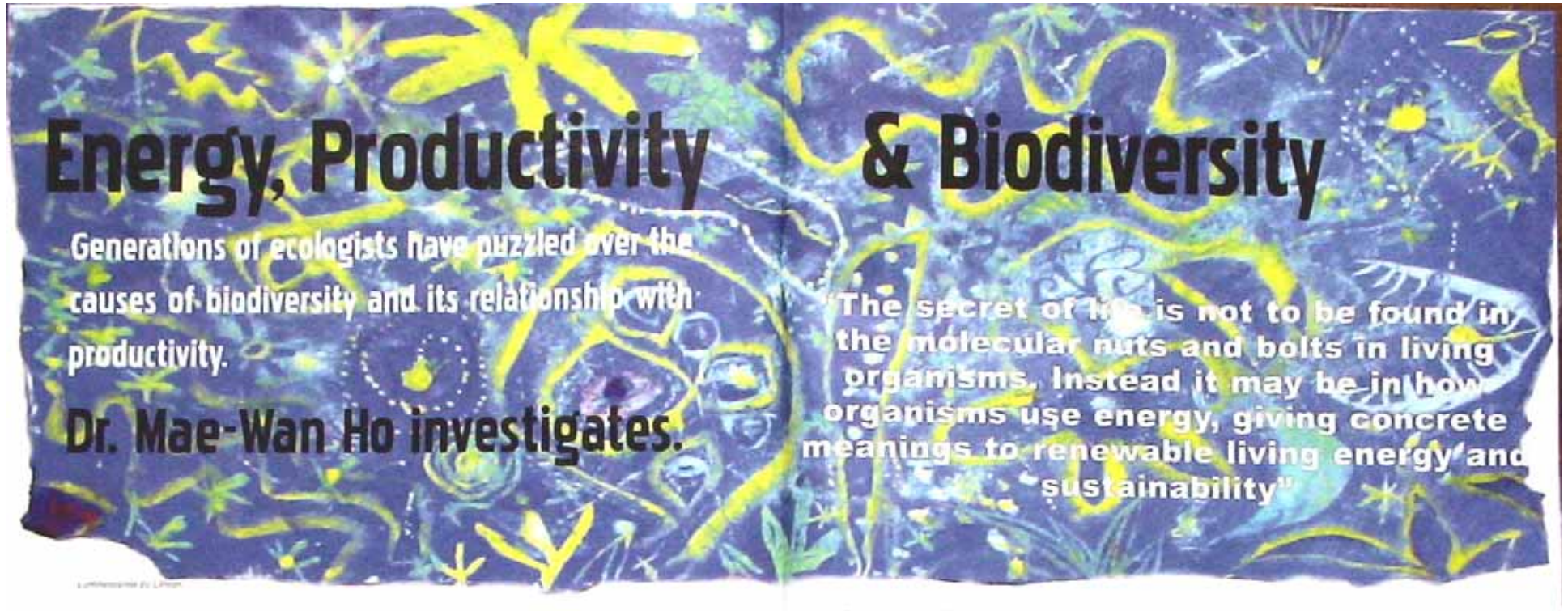


Energy, Productivity & Biodiversity

Generations of ecologists have puzzled over the causes of biodiversity and its relationship with productivity.

Dr. Mae-Wan Ho investigates.

"The secret of life is not to be found in the molecular nuts and bolts in living organisms. Instead it may be in how organisms use energy, giving concrete meanings to renewable living energy and sustainability"



Luminescence by Lange

"Why are there so many kinds of animals?"

This was the question asked by distinguished ecologist Evelyn Hutchinson in 1959, the centenary of Darwin's Origin of Species, a question that has remained as enigmatic today as it was then.

There are about a million described species of animals, three-quarters of them being insects, of which disproportionately large numbers belong to the order Coleoptera, or beetles. In contrast to plant animals, there are far fewer species in the sea.

Hutchinson considered a number of possible explanations. Could food chains or feeding relationships suffice? If one supposes an energy conversion efficiency of 20% at every link of the chain, and each predator being twice as big as its prey, the fifth animal link will have a population of one ten thousandth (10^{-4}) of the first, which is about as long as it would get. Food webs could hardly generate a great deal of biodiversity.

Natural selection can't going to help: an overly efficient predator will simply eat itself out of prey, thus trimming the tree and making itself extinct in the process. While lengthening the chain is difficult, shortening the chain is not, the most dramatic example is the whalebone whale, which can feed largely on plankton.

What about the diversity of terrestrial plants which provide a variety of different structures - bark, leaves, flowers and fruits - for different animals to feed on? A major source of biodiversity of land animals was indeed introduced by the evolution of almost 200,000 species of flowering plants, and the three-quarters of a million species of insects are a product of that diversity. But then, why are there so many different kinds of plants?

Part of the answer is that instead of linear food chains, nature is replete with food webs. Most predators eat more than one species of prey, which reduces the danger that it will die to prey and food extinct. So at least part of the answer to why there are so many kinds of animals and plants is that biodiverse communities are better able to persist than less diverse communities. And that was the origin of the view that complex ecosystems are more stable, which has been hotly debated to this day. While it may be intuitively obvious that the more flexible the links in the food web, the less likely they will break, mathematicians find it extraordinarily difficult to represent such flexibility and more so to agree on what constitutes stability let alone complexity.

Energy available?

Going back to Hutchinson, ecologists have long noticed that while a hectare of tropical rainforest contains an estimated 200 to 300 species of trees, the same area of temperate forest contains only 20-30 species. One hypothesis is that diversity is ultimately determined by the amount of energy available to an ecosystem. Support for this idea came from measures of productivity and biodiversity in different ecological communities. Productivity is the rate of production of biomass by an ecosystem, and is in general determined by the rate of energy supply.

High proportions of land and freshwater species on earth do occur in the tropics, which receive the highest amount of the sun's radiant energy. Average species richness increases from high to low latitudes and this has been documented for a wide spectrum of taxonomic groups, including protists (single-celled organisms), trees, birds, woodpeckers and primates, and for data across a range of spatial resolutions. Species richness also appears to increase with energy, measured as mean annual temperature, and evapotranspiration.

But that doesn't seem to be the whole story. The relationship between diversity and productivity also found to vary at different spatial scales. At large geographical scales, such as across continents or the same latitude, diversity generally increases with productivity. At smaller local scales (metres to kilometres), several different patterns emerge.

Early studies found biodiversity peaking at intermediate levels of productivity in a unimodal curve or curves with a single humped. More recent reviews came up with a variety of relationships, with diversity increasing, decreasing or remaining unchanged as productivity increases. Although some of these patterns suggest that energy is causally involved, other factors may also be important, such as environmental heterogeneity, spatial or temporal variation in the physical, chemical or biological features of the environment.

Complexity of the environment?

In a simple lab experiment, the bacterium *Pseudomonas fluorescens* was used to test the relationship between environmental heterogeneity and diversity. This bacterium is known to rapidly differentiate into distinct 'morphs' in different microhabitats in unmixed culture vessels. One major morph flourishes at the interface between air and the liquid growth medium, another does best in the centre of the culture vessel and a third occupies the bottom of the vessel. The researchers found that even one further variation within each major morph, so that a total of ten types can be distinguished. Shaking the vessel eliminates environmental heterogeneity and, with it, diversity. With a gradient of productivity, a unimodal diversity curve was obtained. In other words, diversity increased with energy available up to a peak, and then decreased as available energy increased further.

Ecosystems typically consist of plants and animal species of vastly different sizes, from big mammals to birds, insects and microbes in the soil, which would use resource that matches their size. Thus, the more finely the species can divide up space and resources, the more species can coexist in the same habitat. But how best to represent this environmental heterogeneity?

Mark Ritchie from the University of Utah Logan in the United States, and Han Olff in Wageningen Agricultural University in the Netherlands reasoned that the distributions of habitat, food and resources often appear to be statistically self-similar over three to four orders of magnitude. If so, their volume or area can be described with fractal geometry.

A fractal is a structure that has dimensions in between the usual 1, 2 or 3, and 'self-similar' refers to the property that the structure appears the same over many scales. Typical examples are fern leaves, branching blood vessels and the coastline.

In a fractal environment, birds can determine the abundance of food and resources that a species perceives, and it sets limits to the similarity in body size between any two species. Ritchie and Olff derived a body size ratio between species of adjacent sizes that declines with increasing organism size. That in turn predicts how diverse the community can be.

Thus, energy, productivity and environmental heterogeneity all appear to play a role in creating biodiversity.

In the next article ("Why are organisms so complex?" this series), I shall show how biodiversity and productivity are intimately linked through energy capture and storage in a sustainable system.


Bantul, Yogyakarta, Centre for Conservation Insect Studies

Loss of Biodiversity in Food Plants from Monocultures of the Green Revolution

Species consumed by people	7 000
Species in 90% world food crops	103
Species providing 60% calories & 56% protein	3 (rice, wheat, maize)

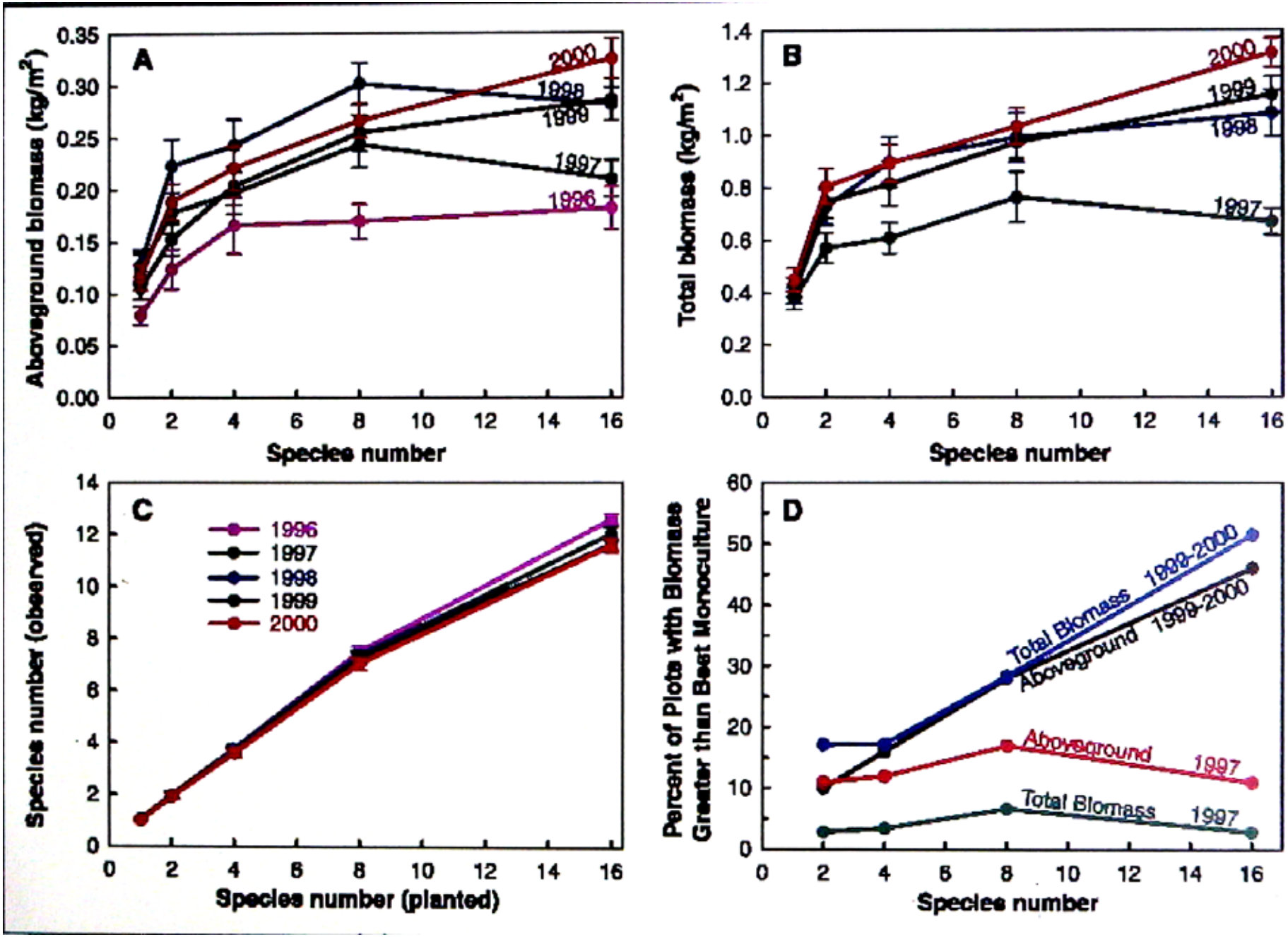
(Lori Ann Thrupp, World Resources Institute, Washington DC, 1998)


Rice terraces & forest gardens in Gunung Haliman National Park, Sukabumi, West Java, by Damajanti

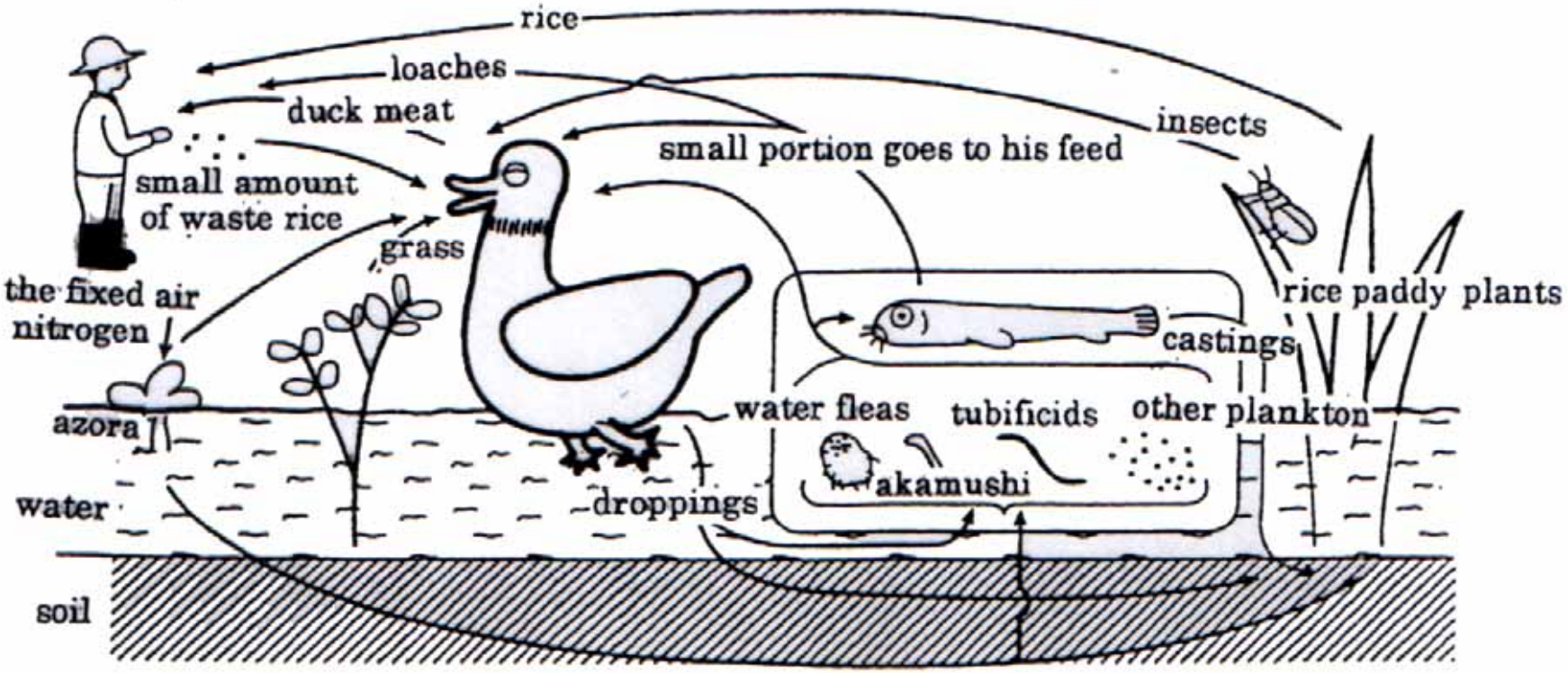
Diversity and Productivity in a Long-Term Grassland Experiment

David Tilman,[1]* Peter B. Reich,[2] Johannes Knops,[3] David Wedin,[4] Troy Mielke,[1] Clarence Lehman[1]

Plant diversity and niche complementarity had progressively stronger effects on ecosystem functioning during a 7-year experiment, with 16-species plots attaining 2.7 times greater biomass than monocultures. Diversity effects were neither transients nor explained solely by a few productive or unviable species. Rather, many higher-diversity plots outperformed the best monoculture. These results help resolve debate over biodiversity and ecosystem functioning, show effects at higher than expected diversity levels, and demonstrate, for these ecosystems, that even the best-chosen monocultures cannot achieve greater productivity or carbon stores than higher-diversity sites.


A
Aboveground biomass (kg/m²)
Species number
2000
1998
1999
1997
1996
B
Total biomass (kg/m²)
Species number
2000
1999
1998
1997
C
Species number (observed)
Species number (planted)
1996
1997
1998
1999
2000
D
Percent of Plots with Biomass Greater than Best Monoculture
Species number
Total Biomass 1998-2000
Aboveground 1998-2000
Aboveground 1997
Total Biomass 1997

One Duck Ten Thousand Treasures



Takao Furuno

Kyushu International Centre

DESERT HARVEST

With only a few sheep and a shovelful of dung, local farmers are reclaiming their land from the Sahara. Fred Pearce reports

IT MUST be true. We've been told it so many times. The over-farmed and overgrazed soils of Africa, especially on the fringes of the Sahara, are losing their fertility and eroding away. As the population grows, poor farmers are mining the last goodness from their soils. Their animals graze the grasslands away to nothing and the desert sands move in. Environmentalists say it; development economists say it; politicians say it; soil scientists say it.

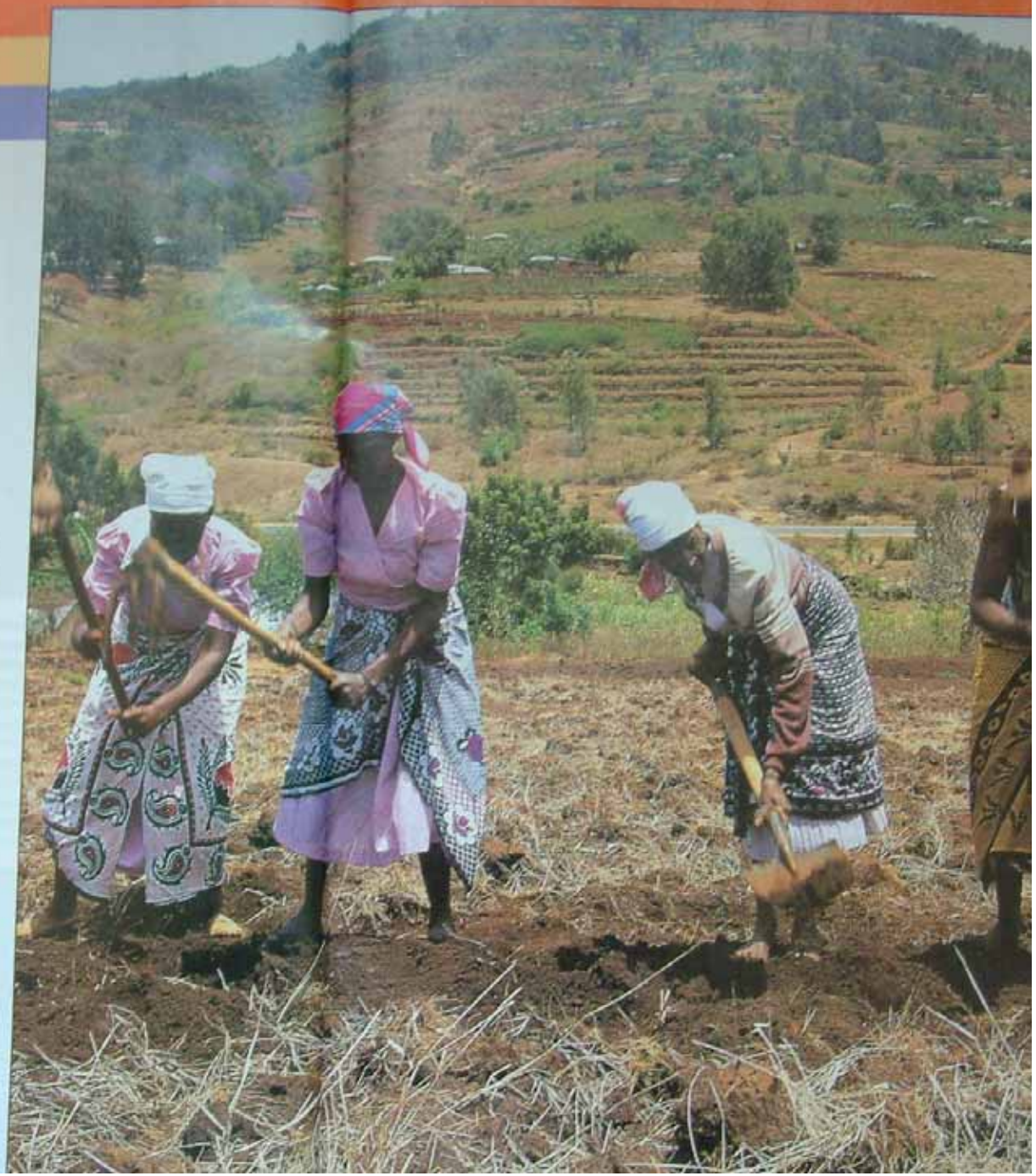
"An area the size of Somalia has become desert over the past 50 years. The same fate now threatens more than one-third of the African continent," says the UN Food and Agriculture Organization, adding that "the main cause is mismanagement of the land." Its sister body the UN Environment Programme claims that 900 million Africans face starvation as their soils crumble away. UNEP masterminded a UN Desertification Convention in 1996 in an effort to reverse the trend.

But out in the shimmering heat of arid Africa, where tens of millions of farmers scratch a living from the soil, new research suggests that this apocalyptic vision is little more than a mirage. Farmers are finding ways to intensify their farming methods without destroying their soils. Farm yields are often up, not down. Soils are often getting better, not worse. Fast-growing populations continue to be fed. In places the desert sands are even retreating. Indeed, for most places at most times, the whole notion of desertification increasingly looks like a myth.

Consider the dusty desert margins of northern Nigeria around the ancient caravan city of Kano, for example. Here, population density has soared to levels similar to Belgium, and some 70 per cent of the land is now cultivated. Rainfall is declining, the availability of chemical fertiliser has fallen by 80 per cent, and only the richest farmers can afford high-yielding grain varieties or irrigation. The poor make do with small scraps of sandy soils. Surely these fields should be turning to desert dust as yields plummet, hunger spreads and refugees head for the cities?

But that's not what I saw when agricultural scientist BB Singh, who heads the Kano office of the International Institute of Tropical Agriculture, drove me through the area this summer. The dusty roadsides between the closely spaced villages were busy with fruit and vegetable stalls and behind them the fields were already green with bushes laden with the first cowpeas.

Under the burning sun, we visited Ado, a farmer who tends a 2-hectare plot on the outskirts of Gadume village, 50 kilometres northwest of Kano. Ado was exultant. The previous year, he had harvested just two bags of cowpeas from his plot. This year, he got seven bags for the same plot. He took me behind the high mud walls of his compound to an inner sanctum where the reasons for his success were bleating. He used to let his sheep roam free. Now he had half a dozen of the animals tethered in his backyard, munching away at straw left over from his harvest and creating a large pile of manure for his fields.



The case for

A GM-Free Sustainable World

Independent Science Panel

* Ban GM crops

* Adopt Sustainable Agriculture

Independent Science Panel

www.indsp.org

The Independent Science Panel (ISP) is a panel of scientists from many disciplines, committed to the **Promotion of Science for the Public Good.** Read our statement here

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Some members of the Independent Science Panel at the launch conference, 10 May 2003, in London. more

- The Independent Science Panel was launched with a one-day conference entitled 'GM Crops: Do We Need Them? Are They Safe?' (read more about the conference)
- A Report was simultaneously released 'The Case for a GM-free Sustainable World' (read more about the report)

The Case for a GM-free Sustainable World

136 page report compiled by the Independent Science Panel
Read the summary
Download the report

Add your signature to show your endorsement of this report here

Did You Miss the Launch?

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