A New Agricultural Revolution

another look at how plants protect themselves against pests and diseases.

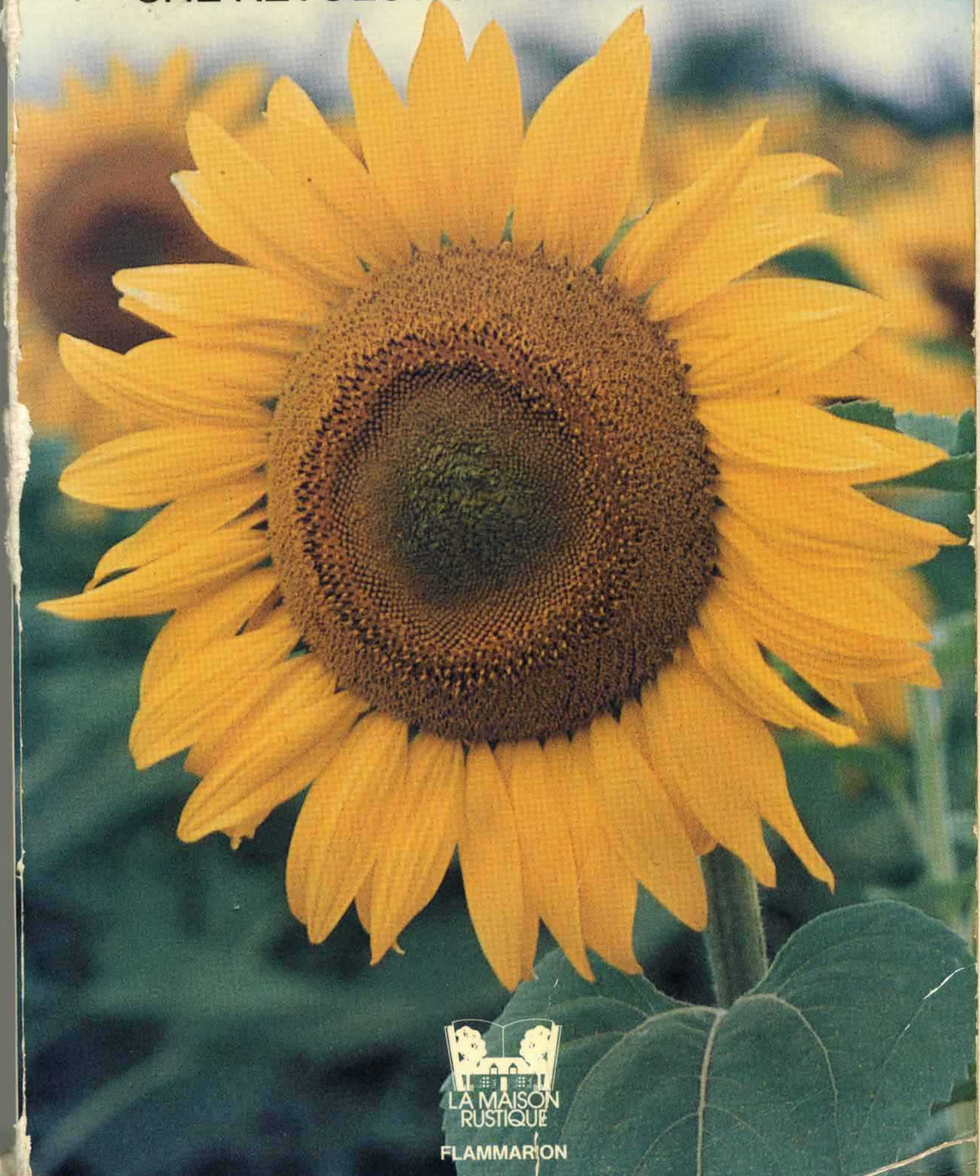
Dr Ulrich Loening, emeritus Director, Centre for Human Ecology, Edinburgh

March/April 2006

FRANCIS CHABOUSSOU

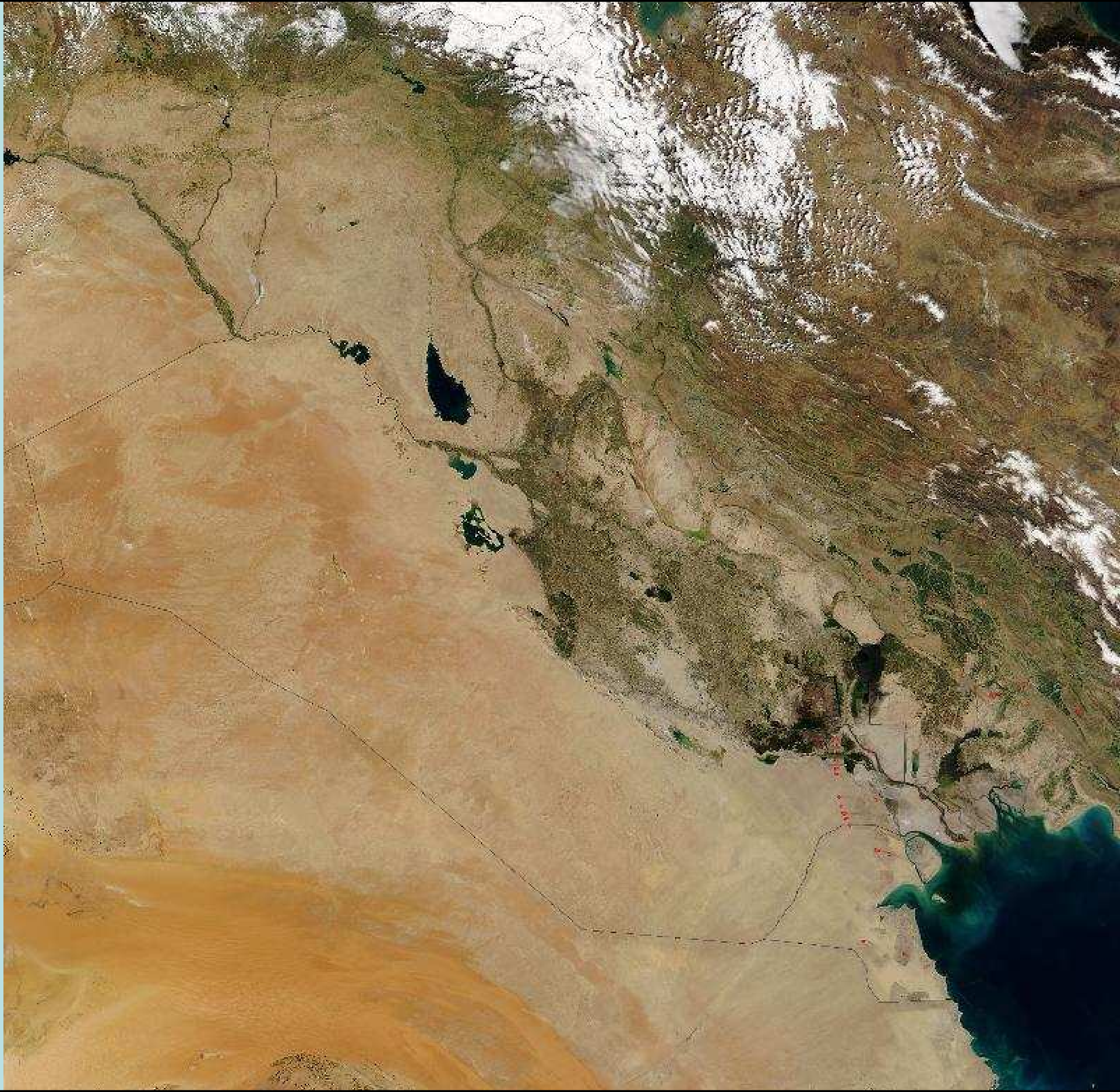
santé des cultures

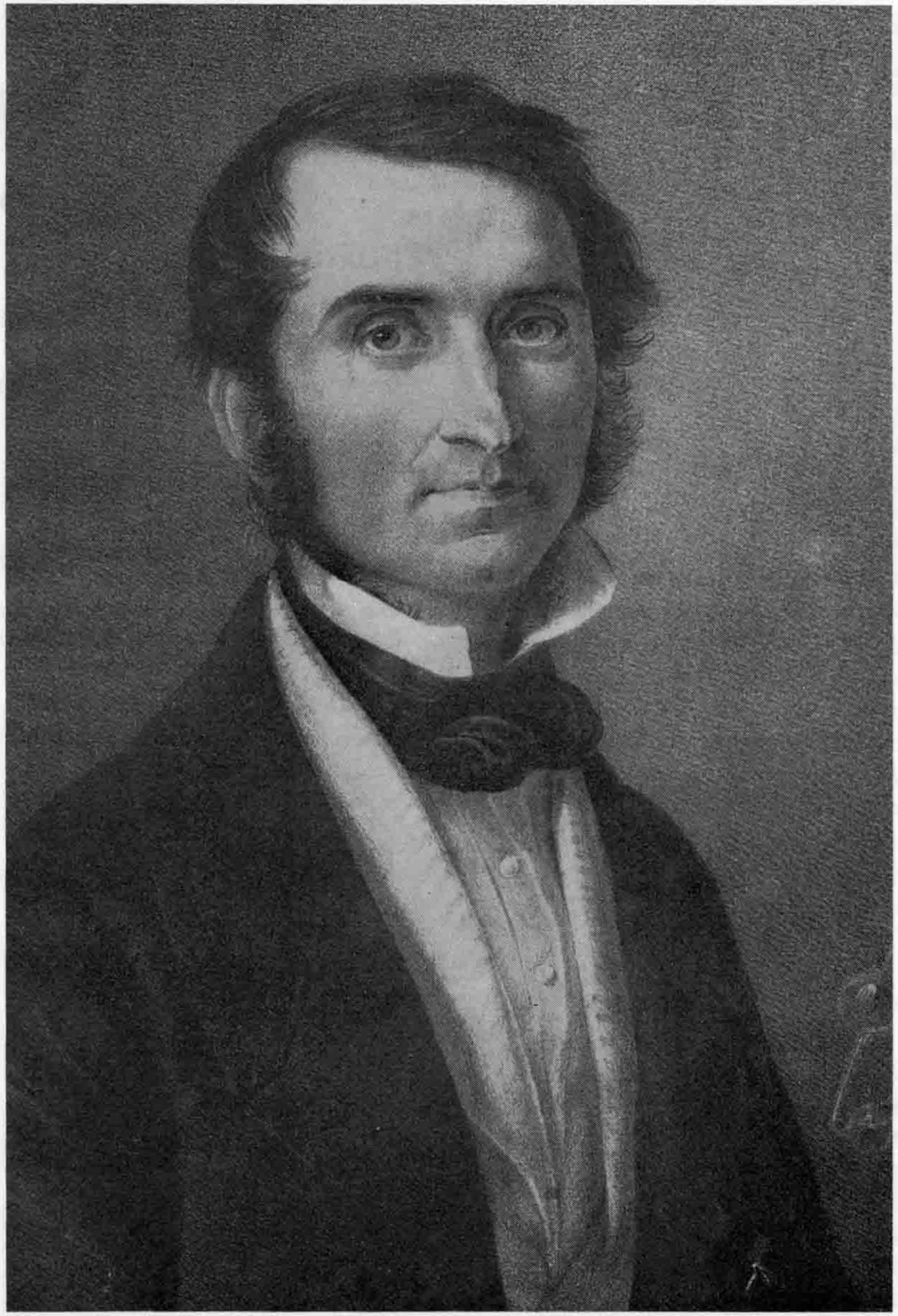
UNE RÉVOLUTION AGRONOMIQUE



LA MAISON RUSTIQUE

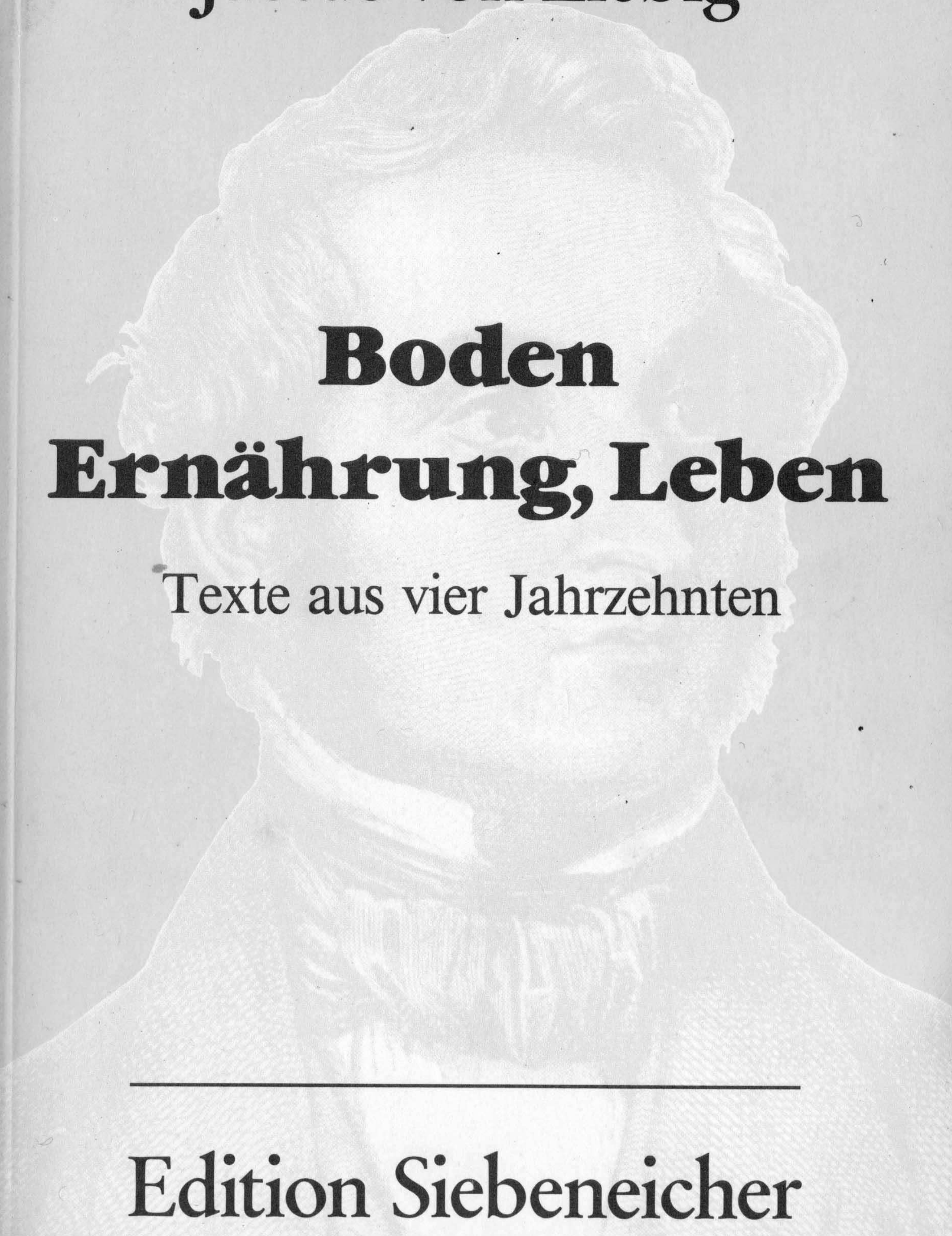
FLAMMARION





Liebig mit 36 Jahren (1839). In diesem Jahr entstand auch sein Analytisches Labor und der Entwurf zu seiner „Agrikulturchemie“.

Justus von Liebig



Boden Ernährung, Leben

Texte aus vier Jahrzehnten

Edition Siebeneicher


Büste Lise Meitner
Bust of Lise Meitner

news feature
894 NATURE|VOL 425 | 30 OCTOBER 2003 |www.nature.com/nature

Fertilized to death

Vast quantities of nitrogen being poured onto farmers' fields are wreaking havoc with our forests. Nicola Nosengo investigates.

Dotted throughout forests around the world, yellowed leaves and thinning crowns suggest that some trees are dying an early death. But the culprit may come as something of a surprise. It isn't just pollution spewed from car fumes, or damage from insects proliferating thanks to global warming. Our forests are facing a quieter villain. They're being plagued by the very stuff that has provided people with food for the past hundred years — fertilizer.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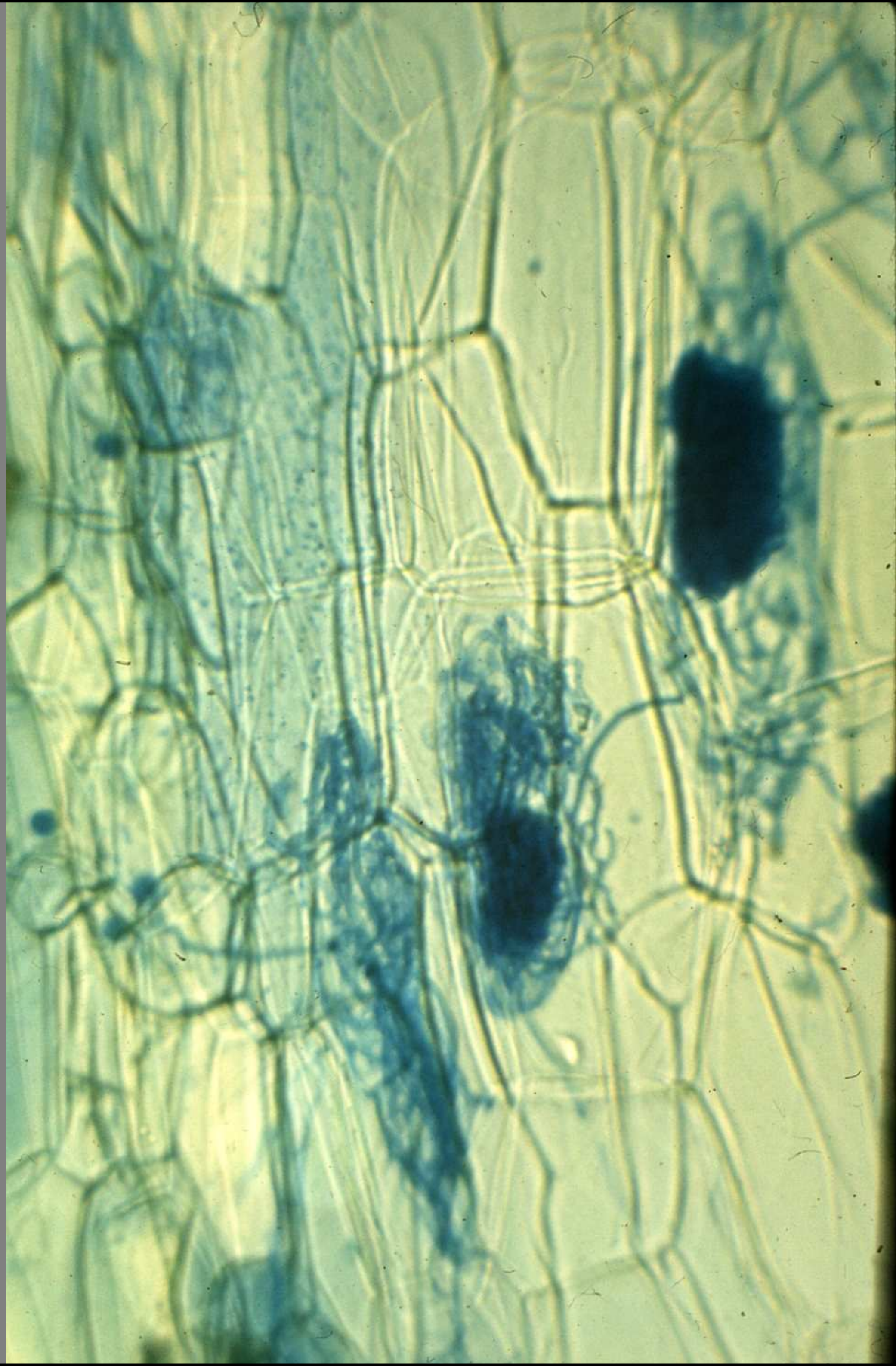

AN AGRICULTURAL TESTAMENT

BY

SIR ALBERT HOWARD, C.I.E., M.A.

Formerly Director of the Institute of Plant Industry
Indore, and Agricultural Adviser to States
in Central India and Rajputana

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MICROBIOLOGY

Conspirators in blight

Ian R. Sanders

A fungus and a bacterium have been found in a symbiotic alliance that attacks rice plants. Rice feeds more people than any other crop, but the significance of this finding extends beyond its potential agricultural use.

Rice suffers from a serious disease called seedling blight. The cause was thought to be a toxin released by some species of the fungal group *Rhizopus*. The toxin kills root cells, after which the fungus digests the remains of the dead root. But as Partida-Martinez and Hertweck report on page 884 of this issue[1], that is not the case — they find that the toxin is produced not by the fungus, but by bacteria that live in symbiosis inside it.

This finding may help in controlling seedling blight, no minor consideration given that rice feeds more people in the world than any other crop plant (Fig. 1). Moreover, the toxin — rhizoxin — stops cell division in some lines of human cancer cells. It is under investigation as a potential antitumour agent, so identification of the genes involved in rhizoxin production could also provide lessons for cancer researchers.

An enzyme, a polyketide synthase (PKS), has been implicated in the biosynthesis of rhizoxin, which is associated with only some species, or strains, of *Rhizopus*. But when Partida-Martinez and Hertweck looked for fungal PKS genes in the genome of *Rhizopus* strains known to release the toxin, they could not find them. However, the authors did detect PKS genes in the fungus that were similar to a known class of bacterial PKS genes.

The next and obvious question was whether these genes really exist in bacteria living inside the fungus. Partida-Martinez and Hertweck first amplified and sequenced a particular set of genes — 16S ribosomal genes, unique to bacteria — from DNA extracted from the fungus (which would include DNA of any bacteria living inside it). They found that the 16S sequences belong to bacteria of the genus *Burkholderia*, a group that occupies a remarkably wide range of ecological niches[2]. *Burkholderia* 16S genes were not found in strains of *Rhizopus* that do not release the toxin.

Using laser microscopy, the authors were

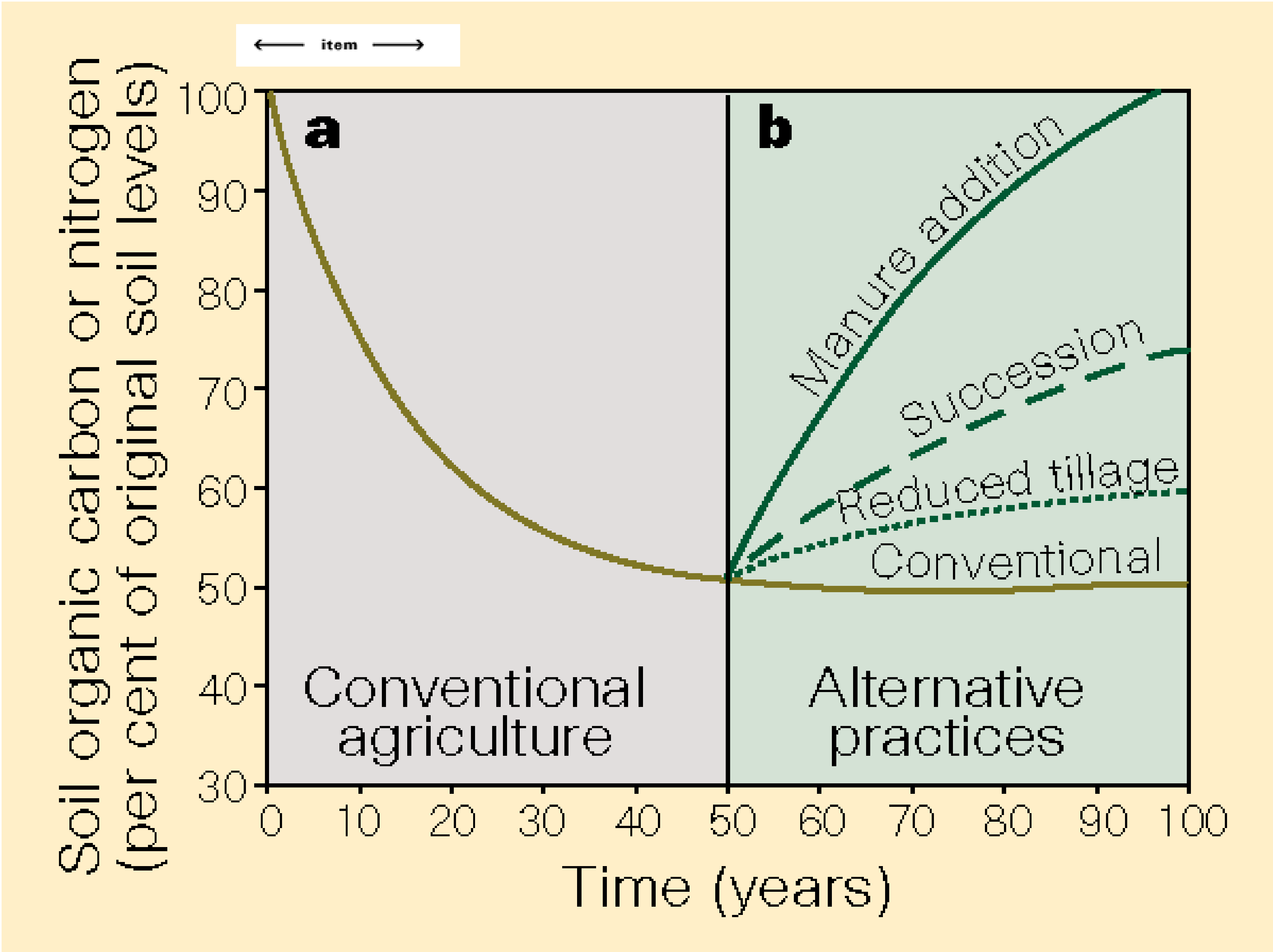
P. BRONSTEIN/GETTY

Figure 1 | Rice under cultivation in Vietnam. World production in 2004 exceeded 600 million tonnes[7], but rice plants are prey to many diseases, including seedling blight.

teria were reintroduced into a bacterium-free fungus, the fungus again produced significant amounts of rhizoxin. Although the toxin stops cell division in human cells, for example, it clearly doesn't harm the fungus.

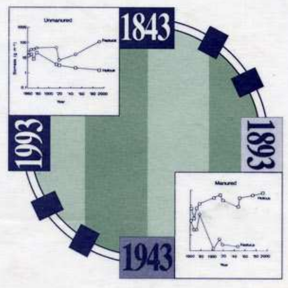
The exciting aspects of this research[1] go beyond the prospects for controlling seedling blight in rice and using rhizoxin to treat cancer: the existence and evolution of such a symbiosis between the fungus and bacterium are in themselves intriguing. Close relatives of *Burkholderia* are well known as symbionts that commonly live inside other fungi, called arbuscular mycorrhizal fungi, which in turn live symbiotically in the roots of most plant species[4,5]. The role of these bacteria in mycorrhizal fungi has remained elusive because of the difficulty of culturing them. So the new work also tells us more about a *Burkholderia*–fungus association.

Finally, Partida-Martinez and Hertweck found that although bacterial production of



item
Soil organic carbon or nitrogen
(per cent of original soil levels)
100
90
80
70
60
50
40
30
a
b
Manure addition
Succession
Reduced tillage
Conventional
Conventional
agriculture
Alternative
practices
0
10
20
30
40
50
60
70
80
90
100
Time (years)

Long-term Experiments in Agricultural and Ecological Sciences



Edited by
R.A. Leigh and A.E. Johnston

CAB INTERNATIONAL

Healthy Crops

A New Agricultural Revolution

FRANCIS CHABOUSSOU

PROTEIN

↕

↑ **protein synthesis**↑ ↓**degradation**↓

↕

AMINO ACIDS

↑

AMMONIUM SALTS

↑

NITRATE in Plant Cell

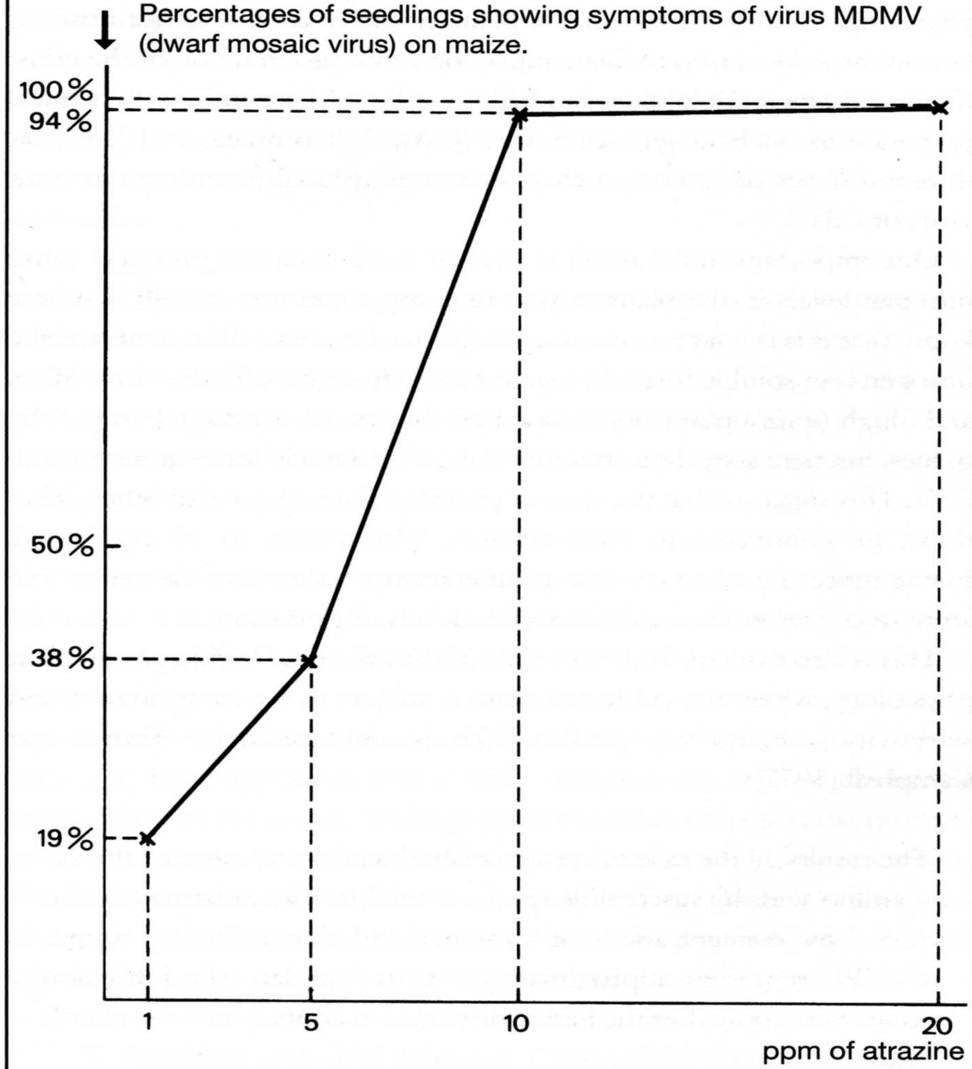
↑

↑

NITRATE in Soil

Table 11. – Ratios between various elements in rice, according to their state of resistance to *Piricularia*.

Ratios	Values in healthy rice	Values in diseased rice
K/Ca	7.6	2.0
Ca/Mg	1.5	4.0
Ca/Na	2.1	2.2
K/Na	19.1	6.4
P/S	6.4	2.2
N/Cu	35.0	54.7
P/Mn	35.6	118.4
Base/Acid	3.6	2.3
Macro-elements/Mn	231.0	656.0



• Abscissa: ppm of atrazine mixed with the soil (laboratory trials)
• Cf. McKenzie,Cole H., and Ercégovitch, C.D.: *Phytopathology* (1968), p. 1058.
• N.B. 20 ppm is the standard dose of the herbicide (cf. Oka and Pimentel).

Fig. 5. Repercussions of atrazine, according to soil levels, on the level of symptoms of MDVM (dwarf mosaic virus) on corn.

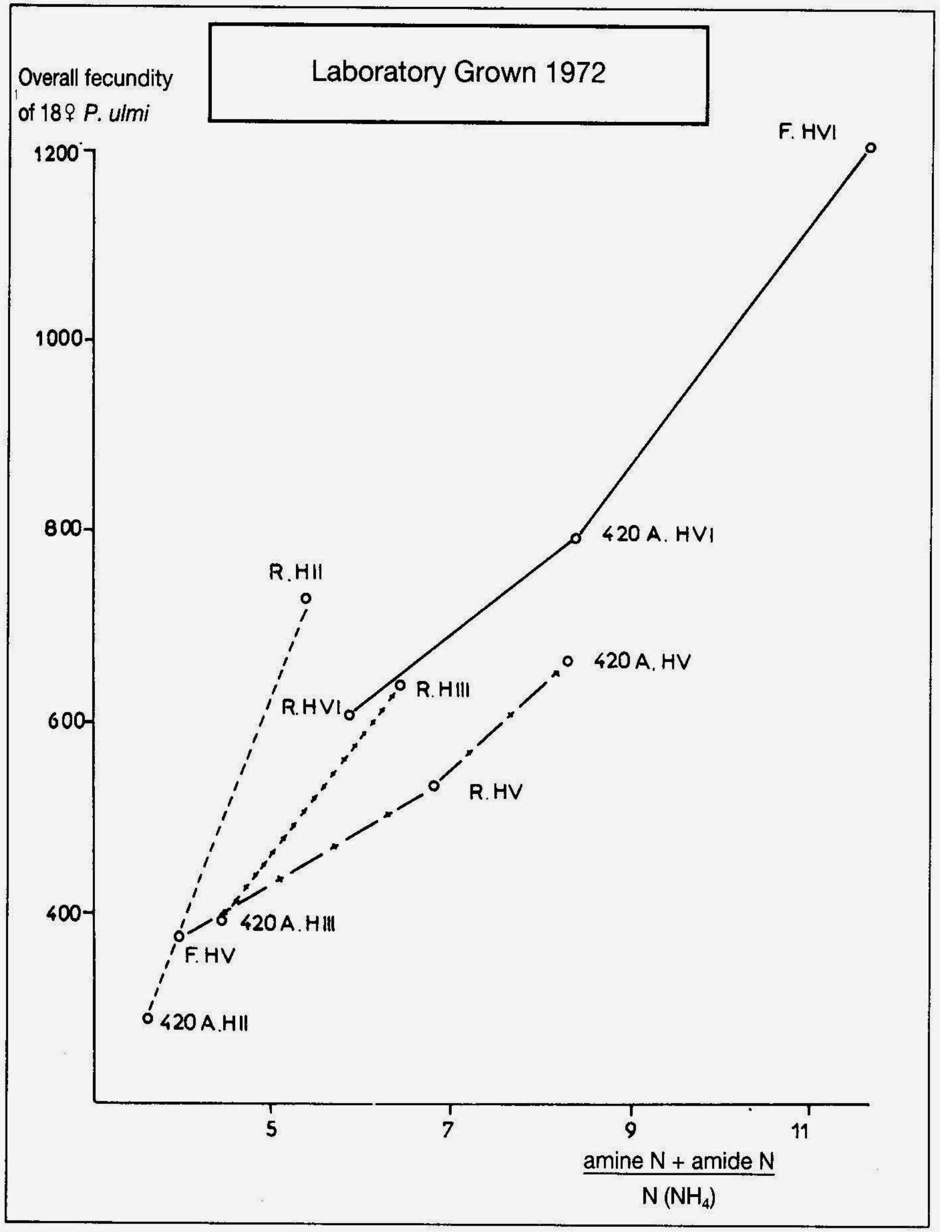
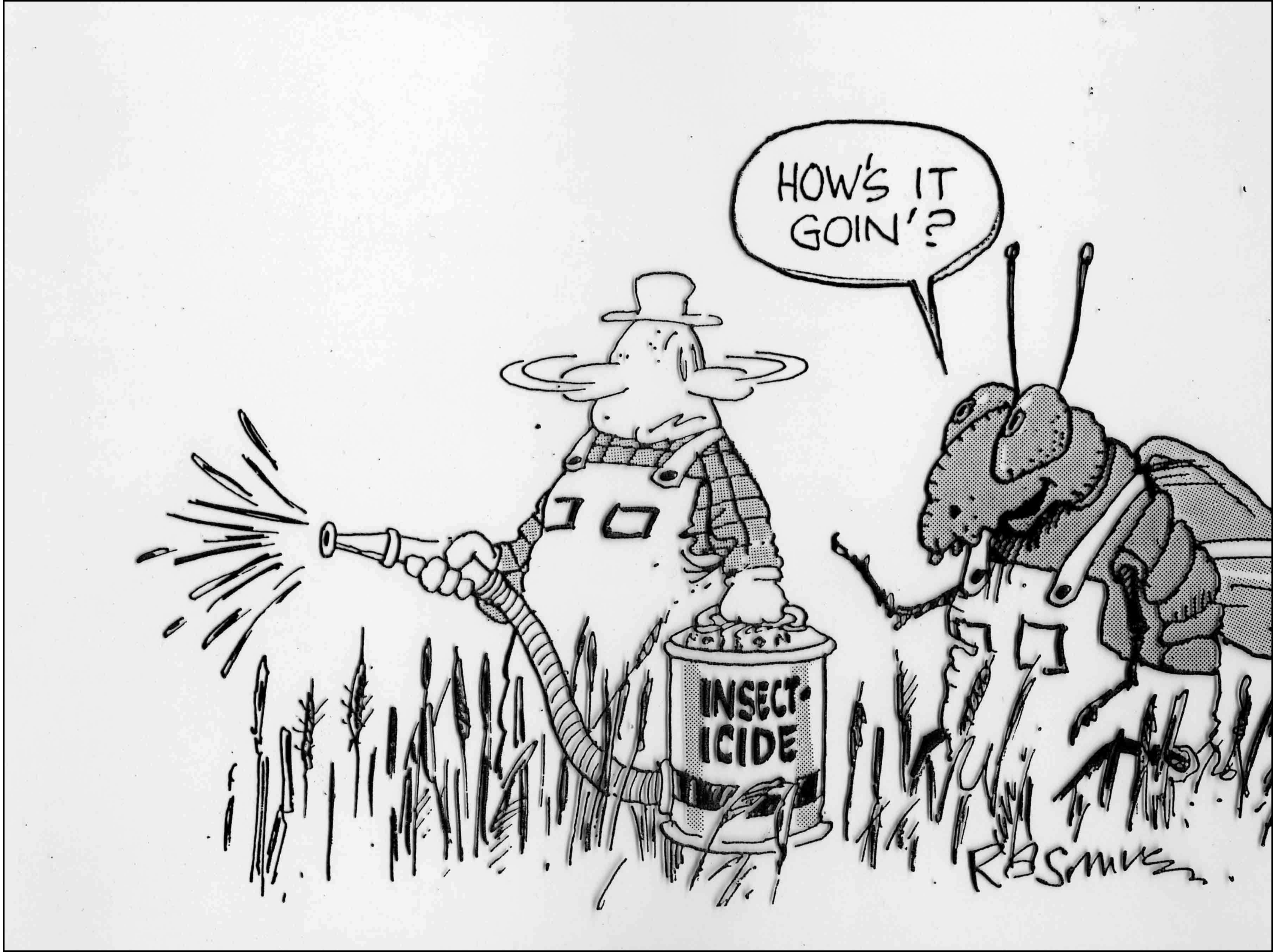


Fig. 8 C. Fecundity of *Panonychus ulmi* in relation to the ratio: amine N and amide N / N (NH4), in grapevine leaves for the aphid populations II, III, IV, and VI.


HOW'S IT GOIN'?
INSECT-ICIDE
RBSMITH

Phil. Trans. R. Soc. Lond. B **318**, 109–376 (1988) [109]
Printed in Great Britain

BIOLOGICAL CONTROL OF PESTS, PATHOGENS AND WEEDS: DEVELOPMENTS AND PROSPECTS

A Discussion organized and edited by
R. K. S. Wood, F.R.S., and M. J. Way

(*Discussion held* 18 *and* 19 *February* 1987 – *Typescripts received* 18 *May* 1987)

CONTENTS


LEITOS DE SECAGEM
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From here on, other materials

Figure 1. Higher productivity technologies. The CIMMYT maize (left) used in Africa can yield 30–80% more grain under drought conditions than conventional commercial varieties (right).

Molecular biology comes of age

MOLECULAR STRUCTURE OF NUCLEIC ACIDS

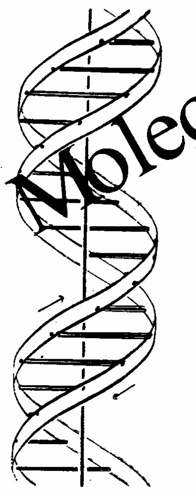
A Structure for Deoxyribose Nucleic Acid

WE wish to suggest a structure for the salt of deoxyribose nucleic acid (D.N.A.). This structure has novel features which are of considerable biological interest.

A structure for nucleic acid has already been proposed by Pauling and Corey[1]. They kindly made their manuscript available to us in advance of publication. Their model consists of three intertwined chains, with the phosphates near the fibre axis, and the bases on the outside. In our opinion, this structure is unsatisfactory for two reasons: (1) We believe that the material which gives the X-ray diagrams is the salt, not the free acid. Without the acidic hydrogen atoms it is not clear what forces would hold the structure together, especially as the negatively charged phosphates near the axis will repel each other. (2) Some of the van der Waals distances appear to be too small.

Another three-chain structure has also been suggested by Fraser (in the press). In his model the phosphates are on the outside and the bases on the inside, linked together by hydrogen bonds. This structure as described is rather ill-defined, and for this reason we shall not comment on it.

We wish to put forward a radically different structure for the salt of deoxyribose nucleic acid. This structure has two helical chains each coiled round the same axis (see diagram). We have made the usual chemical assumptions, namely, that each chain consists of phosphate diester groups joining β-D-deoxyribofuranose residues with 3′,5′ linkages. The two chains (but not their bases) are related by a dyad perpendicular to the fibre axis. Both chains follow right-handed helices, but owing to the dyad the sequences of the atoms in the two chains run in opposite directions. Each chain loosely resembles Furberg's[2] model No. 1; that is, the bases are on the inside of the helix and the phosphates on the outside. The configuration of the sugar and the atoms near it is close to Furberg's 'standard configuration', the sugar being roughly perpendicular to the attached base. There is a residue on each chain every 3·4 A. in the z-direction. We have assumed an angle of 36° between adjacent residues in the same chain, so that the structure repeats after 10 residues on each chain, that is, after 34 A. The distance of a phosphorus atom from the fibre axis is 10 A. As the phosphates are on the outside, cations have easy access to them.



This figure is purely diagrammatic. The two ribbons symbolize the two phosphate—sugar chains, and the horizontal rods the pairs of bases holding the chains together. The vertical line marks the fibre axis

The structure is an open one, and its water content is rather high. At lower water contents we would expect the bases to tilt so that the structure could become more compact.

The novel feature of the structure is the manner in which the two chains are held together by the purine and pyrimidine bases. The planes of the bases are perpendicular to the fibre axis. They are joined together in pairs, a single base from one chain being hydrogen-bonded to a single base from the other chain, so that the two lie side by side with identical z-co-ordinates. One of the pair must be a purine and the other a pyrimidine for bonding to occur. The hydrogen bonds are made as follows: purine position 1 to pyrimidine position 1; purine position 6 to pyrimidine position 6.

If it is assumed that the bases only occur in the structure in the most plausible tautomeric forms (that is, with the keto rather than the enol configurations) it is found that only specific pairs of bases can bond together. These pairs are: adenine (purine) with thymine (pyrimidine), and guanine (purine) with cytosine (pyrimidine).

In other words, if an adenine forms one member of a pair, on either chain, then on these assumptions the other member must be thymine; similarly for guanine and cytosine. The sequence of bases on a single chain does not appear to be restricted in any way. However, if only specific pairs of bases can be formed, it follows that if the sequence of bases on one chain is given, then the sequence on the other chain is automatically determined.

It has been found experimentally[3,4] that the ratio of the amounts of adenine to thymine, and the ratio of guanine to cytosine, are always very close to unity for deoxyribose nucleic acid.

It is probably impossible to build this structure with a ribose sugar in place of the deoxyribose, as the extra oxygen atom would make too close a van der Waals contact.

The previously published X-ray data[5,6] on deoxyribose nucleic acid are insufficient for a rigorous test of our structure. So far as we can tell, it is roughly compatible with the experimental data, but it must be regarded as unproved until it has been checked against more exact results. Some of these are given in the following communications. We were not aware of the details of the results presented there when we devised our structure, which rests mainly though not entirely on published experimental data and stereochemical arguments.

It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material.

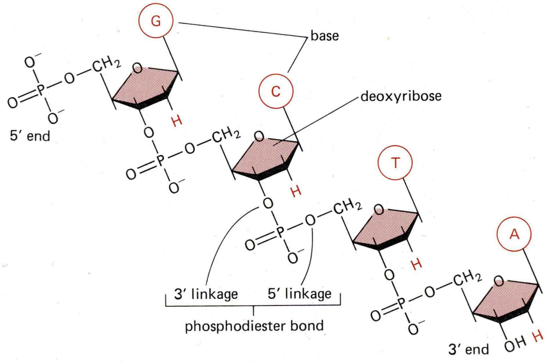
Full details of the structure, including the conditions assumed in building it, together with a set of co-ordinates for the atoms, will be published elsewhere.

We are much indebted to Dr. Jerry Donohue for constant advice and criticism, especially on interatomic distances. We have also been stimulated by a knowledge of the general nature of the unpublished experimental results and ideas of Dr. M. H. F. Wilkins, Dr. R. E. Franklin and their co-workers at King's College, London. One of us (J. D. W.) has been aided by a fellowship from the National Foundation for Infantile Paralysis.

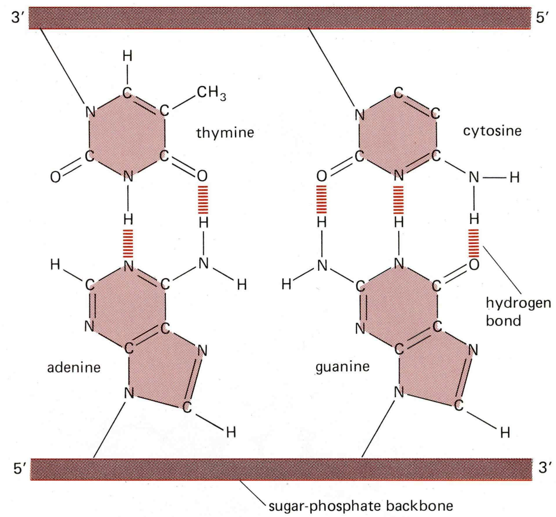
J. D. WATSON
F. H. C. CRICK

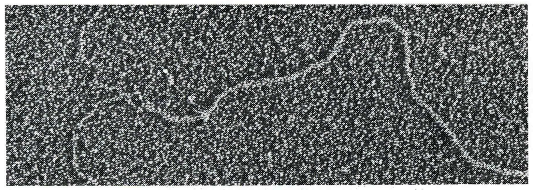
Medical Research Council Unit for the Study of the Molecular Structure of Biological Systems,
Cavendish Laboratory, Cambridge.
April 2.

SUGAR-PHOSPHATE BACKBONE OF DNA



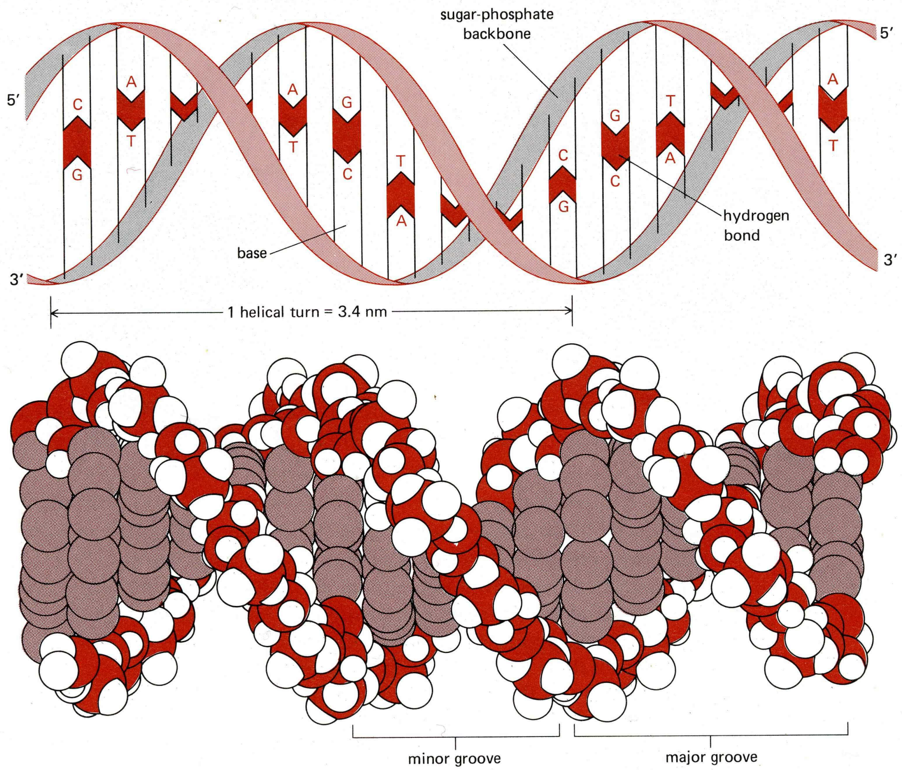
FOUR BASES AS BASE PAIRS OF DNA

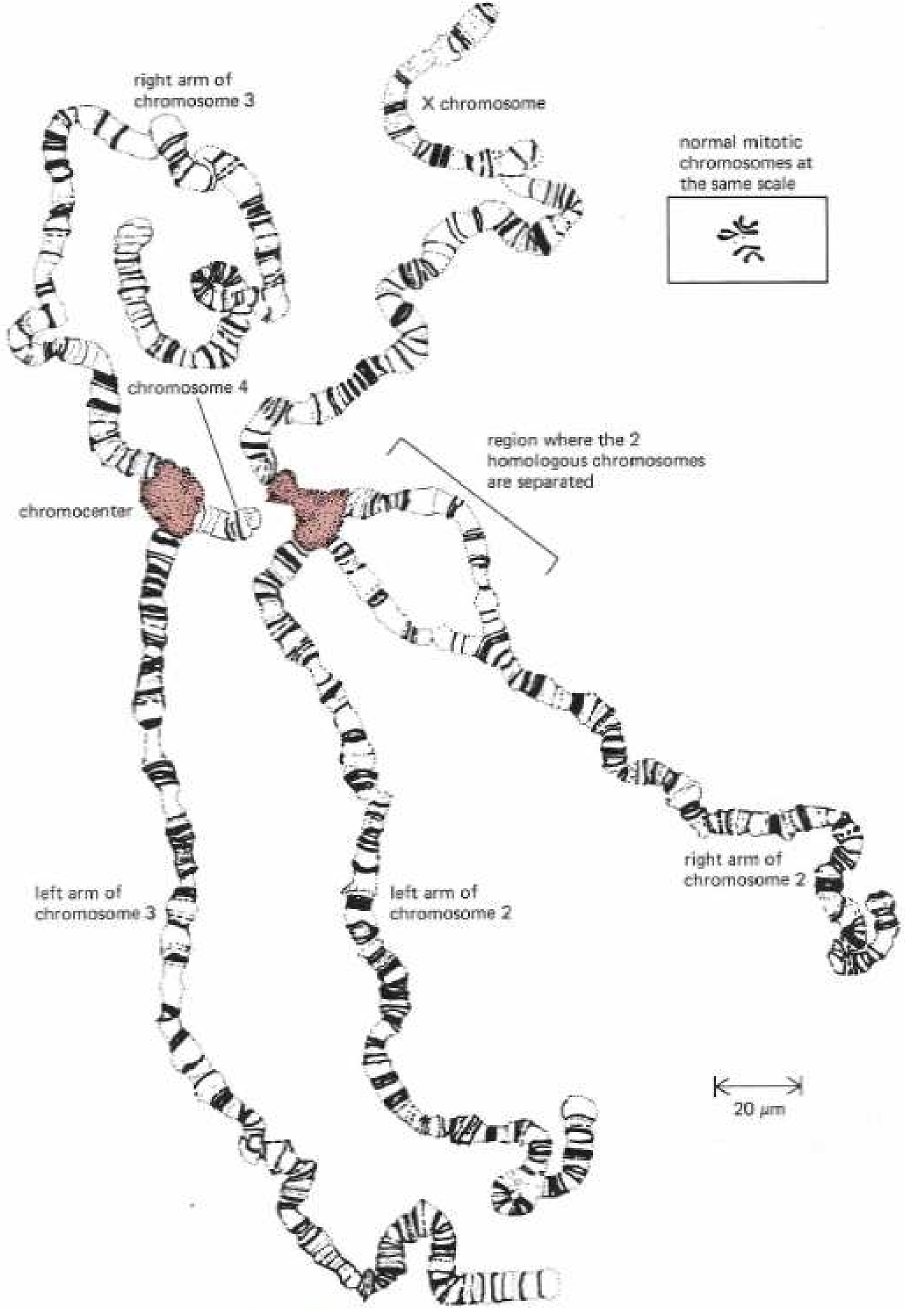




ELECTRON MICROGRAPH OF DNA

DNA DOUBLE HELIX





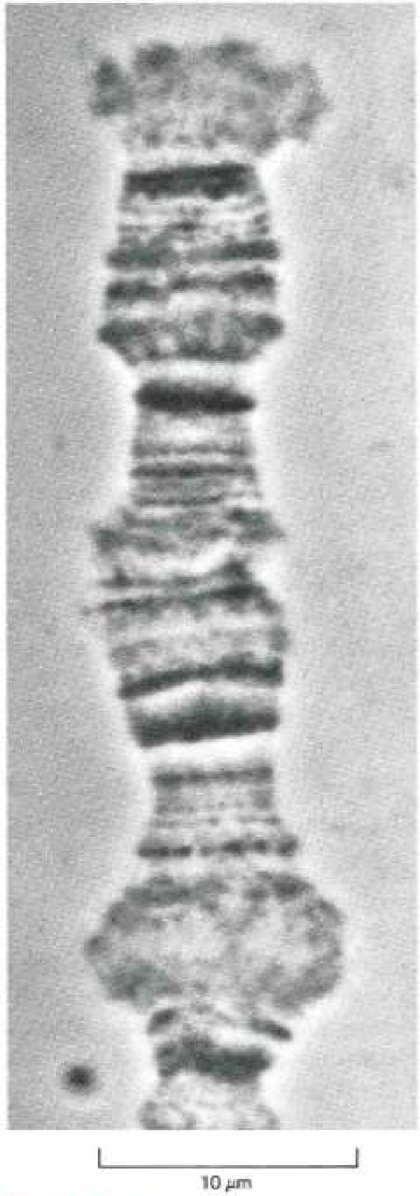


Figure 8–29 A detailed sketch of the entire set of polytene chromosomes in one *Drosophila* salivary cell. These chromosomes have been spread out for viewing by squashing them against a microscope slide. Note that there are four different chromosome pairs present. Each chromosome is tightly paired with its homolog, and the four chromosome

Figure 8–30 Light micrograph of a portion of a polytene chromosome from *Drosophila* salivary glands showing the distinct patterns recognizable in different chromosome bands. These bands occur in