

THE WORLD'S VANISHING BEES

GM crops: the unmentionable threat

Reg Morrison

The wholesale disappearance of bees, sometimes called the Vanishing Bee Syndrome or Colony Collapse Disorder, has resulted in the loss of a quarter of all managed honey-bee colonies in the US since 1990. And a growing number of European and Asian nations, have reported similar declines.

Despite intensive research, the collapse of US bee populations remains largely unexplained. Two species of mite have been implicated in some of this carnage, but about a quarter of the current decline seems unrelated to any specific cause.

A variety of agencies have been suggested, but the multiplicity of potential villains suggests that it may, in fact, be due to a degradation of the bees' immune system.

Such a massive extinction of bees in the US, home of Genetically Modified crops, should be cause for extreme alarm here in Australia, given the current deterioration in agricultural environments, the acceleration of global warming, and the imminent acceptance of GM crops.

Widespread ignorance of genetics and the evolutionary process is a common impediment to grasping the nature and size of this problem. For example, there is a general belief that there are specific 'genes for' this or that structure or behaviour—even some academics have been seduced by this comforting myth. In fact of course, genes code for protein. Nothing more. Structure and behaviour are emergent by-products that inevitably arise from the administration of that protein.



DNA methylation

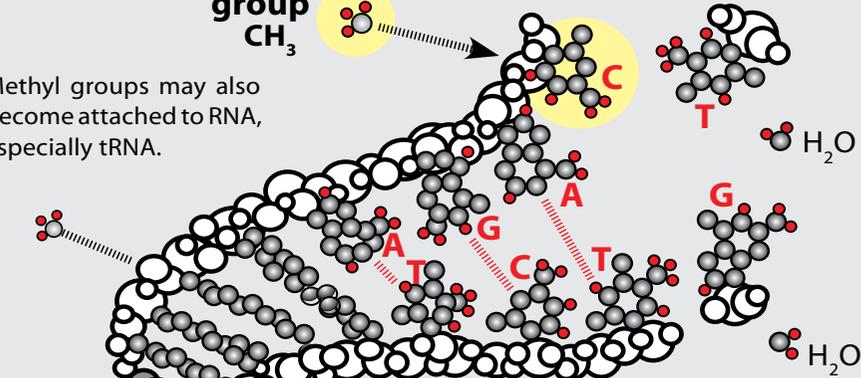
Methyl groups are commonly attached to cytosine, but occasionally to adenine and other sites, including the histone 'bollards' around which the chromatin is wrapped.

Methyl groups may also become attached to RNA, especially tRNA.

THE MOLECULAR 'CODE' OF DNA

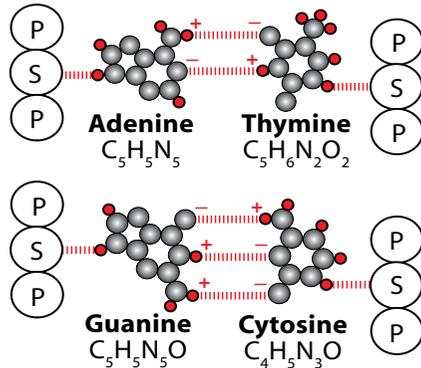
Adenine **A** **T** Thymine
 Guanine **G** **C** Cytosine
 (**H** weak hydrogen bonds)

methyl group
 CH_3



The side rails of DNA coil into a flexible double helix that consists of alternate phosphate (P) and sugar (S) molecules.

THE NUCLEOTIDE BONDS



The bases are attached to sugar molecules in the side rails and held together by weak hydrogen bonds.

chromosomes

By restricting DNA's ability to achieve tight folds, epigenetic carbon tags determine which genes can be fully transcribed. DNA's epigenetic code thereby constitutes a highly flexible management system—a system so fragile that it is available to adjustment by environmental factors such as stress and particular kinds of nutrient.

EPIGENETICS and METHYLATION

Few people are aware that all DNA is subject to a second, overriding molecular code known as epigenetics. It consists of a pattern of external hydrocarbon switches, or methyl groups, that are attached at various points to the side rails of DNA and determine whether or not particular genes or groups of genes are available for transcription.

Methylation is crucial to all DNA and even helps to determine gender in all sexually-reproducing species. The attachment or detachment of methyl groups is also known to be implicated in a number of genetic ailments in humans. Some dysfunctions (such as Fragile X Syndrome) are caused by inappropriate methylation and are clearly heritable.

If all of the DNA present in each of our cells was stretched out in a line, it would be almost 3 meters (10 feet) long, so DNA must be folded up and compressed to fit inside the cell nucleus. Exactly how this is done plays a crucial role in determining which genes can be read and expressed. In general, genes in tightly compressed DNA are not well expressed, while genes in more loosely packed DNA are more available to the machinery involved in transcribing the gene into its intermediate expression, messenger RNA (mRNA), and ultimately into protein. Methyl tags help to determine the pattern of folding and thereby, the degree of compression. Appropriate DNA methylation is therefore essential for the normal development and functioning of all organisms. Mice that have been genetically engineered so that they can't make the enzymes that attach methyl tags to DNA invariably die before birth.

The epigenetic mastercode is extraordinarily flexible because each methyl tag is attached to the side-rails of DNA only by a single carbon bond. This enables environmental factors to occasionally attach or detach methyl tags to an organism's DNA, thereby modifying it in response to the changing environment. So while genes determine the basic structure of an organism it is the epigenetic code of methylation that determines the details of its contemporary form. It 'fleshes out' the skeleton prescribed by the genes.

The crucial importance of this overriding genetic code is most spectacularly expressed in the European honey bee, *Apis mellifera* ...

Lamarck v Darwin

Despite their physical fragility, genes are astonishingly durable. Individual genes can out-last the rise and fall of mountains and the drift of continents from pole to pole. And yet species occasionally alter their structure and behaviour within relatively short periods of time with no change to their genetic code.

That old biological enigma now appears to have an answer: epigenetics. It seems that the French biologist Jean Baptiste de Lamarck was right after all: the environment DOES directly interact with the biota—although not in the simplistic fashion that he proposed.

Indeed, the environment is able to modify both the structure and behaviour of organisms, often in heritable fashion, via the attachment or detachment of tiny methyl tags to the organism's DNA.

Honey bees best illustrate the extraordinary power that is inherent in this subtle switching mechanism.



A sterile worker bee, *Apis mellifera*, on a bottlebrush flower.

According to new Australian research the bees' rigid, three-tiered society, consisting of queen, female workers and male drones, rests entirely on their pattern of epigenetic attachments, and this, in turn, is entirely determined by the food they feed their larvae.

The queen and her army of workers have identical genes, and yet the queen is a giant egg factory and the workers are small and sterile. The sole determining factor seems to be the exclusive diet of Royal Jelly that is fed to prospective queens when they are in larval form.

New Australian research

In the words of Ryszard Maleszka, Senior fellow at the ANU School of Biological Sciences, *"Genes and environments cannot be separated. For billions of years these two entities co-evolved to generate living forms. Any disturbance in an organism's environment must be sensed by its genome,"* he said, *"and epigenetic mechanisms are responsible for maintaining the [organism's] proper responses."*¹

Maleszka maintains that this ancient feedback mechanism comes into clearest focus in the rigidly structured society of the European honeybee. In an article published last year Dr Maleszka described the research undertaken by he and his team into the making of a honey-bee queen:

"Royal jelly is a thick, creamy, and highly concentrated source of proteins, essential amino acids, unusual fats, vitamins and other nutrients, and is produced by worker-bee head-glands."

¹ Ryszard Maleszka (pers. comm. 8/2008).

A huge amount of royal jelly, in which a developing larva virtually swims, sets her on her journey to become a very lucky creature. ... Her lifespan will be at least 20 times longer than that of a regular worker bee. ... In return for all these privileges and rewards she will lay up to 2000 eggs per day, equal to almost three times her bodyweight, for the next 2–3 years. ... The queen larva has exactly the same genetic composition as a regular worker larva, but these two virtually different organisms follow two very different developmental paths."

*"Genetically identical female larvae develop into queens or workers on the basis of larval nutrition. Developmental switches render workers almost entirely sterile while queens develop into one of the most fecund animals known."*²

² Ryszard Maleszka, "A Queen is Made, not Born", (*Australasian Science*, April 2007).

This new Australian research has provided a key to unlock some of the complexity that has enshrouded the co-evolutionary interactions between genes and the environment.

The recent mapping of the honey-bee genome has meanwhile shown that the genes involved in the production of royal jelly are bacterial in origin and exist only in bacteria and a few insects. They are known as the 'yellow genes'.

When bacterial B.t. genes are artificially embedded in a plant's genome they, like all genes, no longer act in isolation but in concert with other genes in the genome. Meanwhile, any interaction between the bacterial genes inserted into B.t. crops and the 'yellow' bacterial genes that produce royal jelly in head-glands of worker bees is entirely beyond our ability to assess. So the insertion of B.t. genes into crop plants to make them toxic to particular insect pests has the potential to play Russian roulette with genetic relationships that have taken millions of years to develop between plants and their insect pollinators.

Canadian Research

According to a 2004 paper by Dr. Moshe Szyf and Dr. Michael Meaney, researchers at McGill University in Montreal, if a rat is not licked, groomed and nursed enough by its mother, chemical tags known as methyl groups are added to the DNA of a particular gene. The affected gene codes for the glucocorticoid receptor, expressed in the hippocampus of the brain. The gene helps to mediate the animal's response to stress, and in poorly-raised rats, the methylation damped down the gene's activity. Such pups produced higher levels of stress hormones and were less confident exploring new environments. ¹

Subsequent research by the same team at McGill University in Montreal showed that a common amino acid and food supplement, L-methionine, has a similar effect on well-reared rats. When it was injected into their brains the amino acid methylated the glucocorticoid gene, and the animal's behaviour pattern changed.

¹ (*Nature Neuroscience* vol.7 p.847, 2004)

"They were almost exactly like the poorly-raised group," Dr Szyf said.

This highlights the crucial question that faces us with GM crops: if a common amino acid and food supplement can alter the methylation pattern of rat DNA, then genetically modified pollen might well alter the methylation pattern and gene expression of bees when the modified pollen is fed to their larvae.

Indeed, a 1990 study found that very high concentrations of B.t. (var. *tenerionis*) "*reduced longevity of honey bee adults.*" ² This variety is widely used against insect pests such as the Colorado potato beetle.

NB: Unlike most other insects, bees not only display a strong pattern of methylation, they also exhibit a very well defined aging process. ³

² (Vandenberg, J. D. "Safety of four entomopathogens for caged adult honeybees" *Econ. Entomol.* 83(3): 756-59, 1990.10-152.)

³ (<http://www.sciam.com/article.cfm?id=social-honeybee-shares-ge&print=true>)

CONCLUSION:

This evidence suggests that B.t. genes or their toxins, acting on bee larvae via pollen, could have at least four disastrous outcomes. They could:

1. disturb methylation patterns within the bees' immune-system, thereby increasing their vulnerability to disease.
2. alter the methylation patterns within those genes that are responsible for the manufacture of royal jelly, the critical ingredient in making queen bees and shaping bee society.
3. disturb the methylation or interact with one or more genes involved in regulating worker-bee behaviour, thereby making them incompetent or dysfunctional during foraging.
4. increase the natural rate of apoptosis (cell death), leading to accelerated ageing and an abbreviated life-span in the adult bees.



The fractal tides of rainbow colour that swirl across the surface of a soap film perfectly illustrate the chaotic dispersal of energy that characterises all aspects of the cosmos we inhabit. The colours are produced by wave interference between light reflected from the front and back surfaces of the film and they precisely express the thinning of the soap film as it loses energy via evaporation.

CHAOTIC ENTROPY

Our species is currently racing towards a population precipice and a very painful collapse that should, according to UN data, begin within the next 20 years (see graph on p.14). If however, a genetically modified crop should manage to add a methyl tag or two to the DNA of its human consumers, thereby shortening their lifespan slightly, that may well be the best possible outcome for our species. A general reduction in the average human lifespan would at least postpone and flatten out the peak of the plague pulse that our population graph so eloquently describes, and it would thereby reduce the angle—and pain—of our species' imminent decline.

By contrast, if genetically modified pollen should contribute directly or indirectly to the collapse of the world's primary pollinator, the European honeybee, precisely the reverse would occur. Tides of starvation would swiftly sweep most of our species from the planet, greatly steepening the angle of our graph's descent and immeasurably increasing the pain of our collapse.

All technology comes with an ultimate energy cost that is somewhat greater than the energy advantage gained. The laws of thermodynamics and cosmic entropy demand it. The downside may be too delayed or too dispersed for us to immediately perceive it, but it cannot be avoided. 'Gene modification' is no exception to this iron-clad cosmic rule. Just as the much-feted Green Revolution locked our species into petroleum slavery and disastrous population growth, so genetic modification will carry with it an evolutionary cost of even greater consequence ... somehow, somewhere, sometime.

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VANISHING BEES: quotes from the media

Latest reports (April 2009) from Apimondia, the international beekeeping body, state that more than 70 percent of the bees that used to pollinate crops along the east coast of the United States have disappeared since late last year while the west coast has lost up to 60 percent of its bees. And the news from Europe is no better. About 30 percent of Europe's 13.6 million hives died last year, with losses that reached 80 percent in south-west Germany and 50 percent in Slovenia. Severe losses have also been reported from Canada, Britain, France and Italy.

Scientific American, May 15, 2007

Searching For What's Behind the Bee Decline

"Of the 2.4 million honeybee colonies in the US, about one million died off this past winter. Big declines have also been seen in Europe and Asia. The dieoff has been dubbed Colony Collapse Disorder and the Vanishing Bee Syndrome.

A couple of species of mites that attack bees were responsible for similar dieoffs in the winters of '95-'96 and 2000-2001. And the mites may be partly to blame for the most recent honeybee loss. But a quarter of the current carnage seems unrelated to mites or any other pests. Other suggested causes of the bee decline include genetically modified foods, parasites, pesticides, and cell-phone radiation. But bee expert Nicholas Calderone of Cornell University said last week that a definitive cause remains elusive."

The Chronicle, Washington Bureau, July 6, 2007

"U.S. populations of pollinating honeybees are mysteriously collapsing, and that could cause irreparable damage to crops worth billions of dollars a year across the nation. That in turn could mean higher food prices, and because all kinds of wildlife depend on pollinated plants for food, the decline of pollinators could spell trouble for other animals.

The cause of the decline—estimated to be as much as 25 percent of the honeybee population—is a matter of scientific debate. But it is mirrored by rapid population loss among such native pollinators as butterflies, bats, birds and bumblebees."

"... Scientists say the first sign of Colony Collapse Disorder is dramatic and final. A beekeeper will put out boxes containing colonies, leave the bees alone to do their work, and upon returning discover that almost all the worker bees have vanished. They leave behind their queen and brood, the young bees. The missing bees never return."

Global Pesticide Campaigner, San Francisco, CA. December 1996.

"The number of commercial bee colonies plummeted from 5.9 million in the late 1940s to 4.3 million in 1985, and 2.7 million in 1995. The loss of one quarter of all managed honey bee colonies since 1990 signals one of the most severe declines U.S. agriculture has ever experienced in such a short period. There are fewer bee hives in the U.S. today than at any time in the last 50 years."

Cause of Colony Collapse Disorder Eludes Investigators

http://vegetablegardens.suite101.com/article.cfm/the_honey_bee_crisis_of_2007

"Although the honey bee crisis of 2005 was attributed to the varoa mite, the 2006-2007 malady is of unknown origin. Researchers have been unable to isolate a common cause. While they have found numerous disease organisms present in dying bee populations, along with a few common management issues, the common link affecting all the populations continues to elude investigators."

BBC News, Florida USA, 11 March 2007

Vanishing bees threaten US crops

"Bees are driven around Florida to help pollinate early crops All over America, beekeepers are opening up their hives in preparation for the spring pollination season, only to find that their bees are dead or have disappeared. Nobody, so far, knows why. The sad mystery surrounding the humble honeybee—which is a vital component in \$14bn-worth of US agriculture—is beginning to worry even the highest strata of the political class.

GM CROPS: A GLOBAL THREAT

In 2006 US farmers sowed some 281,500 km² with genetically modified corn and cotton (165,600 km² of B.t. corn and 115900 km² of B.t. cotton). This was equivalent to 11.1% and 33.6% respectively of the global plantings of corn and cotton in that year. US crops were pollinated by bees from about 2.4 million managed bee colonies. But during that winter almost one million of those bee colonies vanished, largely without trace. Similar declines have occurred in Europe and Asia where there was a coincidental expansion of GM cropping.

Our incomplete understanding of genetics explains why so many unexpected effects have occurred in GM feeding studies. For example, a peer-reviewed study, published in 2007 found evidence of liver and kidney toxicity when rats were fed an approved GE maize variety (MON863). Similar effects were observed when Monsanto fed its GT73 Roundup-Ready canola variety to rats. The rats showed a 12-16% increase in liver weight. And in 2005 CSIRO abandoned a decade-long project to develop GM peas after tests showed that the



peas caused allergic lung damage in mice. The allergic reaction is believed to have been triggered by unexpected changes to the protein expressed in the pea (see Greenpeace submission [NSW] on p.7).

The possibility that GM crops might somehow affect human health may indeed be relatively minor and worth the risk in order to preserve Monsanto's massive profits, but to risk the

integrity of Australian bee genomes and Australia's food production in this casual fashion—merely for the sake of an economic advantage that is both suspect and small—is surely tantamount to criminal insanity.

There is no direct evidence to link GM crops to bee declines, but to fully assess the possibility that such link *might* exist, we must seek answers to three crucial questions:

1. Has the B.t. toxin ever been known to disrupt any aspect of the expression of insect genes—the way some viruses, commercial products and industrial pollutants are able to interfere with the expression of human genes?
2. Have B.t. genes ever been known to add or detach a methyl tag to an insects' DNA, mRNA or tRNA?
3. Since there is every reason to believe that B.t genes inserted into the plant's DNA are heritable via its sperm, this will allow B.t. genes to be fed to bee larvae. Might not B.t. genes then embed themselves in bee genomes and disrupt normal genetic expression in future generations of bees?

In short, given the extreme motility of bacterial genes, our general ignorance in the field of genetics, and the monumental scale of the stakes involved, we should immediately invoke the Precautionary Principle and halt all further trials of genetically modified crops. To do otherwise is to play dice with our species' survival.

Greenpeace Submission to the NSW Review of the Gene Technology (GM-Crop Moratorium)

27 August 2007

"In June this year, new research published in the leading scientific journal *Nature* revealed serious flaws in the science behind genetic engineering. The research calls into question the assumption that each DNA sequence can be isolated and has its own function. Instead, genes operate in a complex network where they react, interact and overlap with each other in ways that are still far from being understood. This new research shows that genes cannot be considered isolated units - nor can they be controlled. The research raises serious questions about the safety of GE crops.

This incomplete understanding of genetics explains why so many unexpected effects have occurred in GE feeding studies. For example, the attached peer reviewed study, published this year, found evidence of liver and kidney toxicity when rats were fed an approved GE maize variety (MON863).[60] Similar effects were observed when Monsanto fed its GT73 Roundup Ready canola variety to rats. The rats showed a 12-16% increase in liver weight, yet Food Standards Australia New Zealand (FSANZ) still rubber stamped the canola as safe for human consumption.

In 2005 CSIRO abandoned a decade-long project to develop GE peas after tests showed they caused allergic lung damage in mice.[62] The allergic reaction is believed to have been caused by unexpected changes to the protein when it was expressed in the pea. FSANZ typically uses proteins expressed by bacteria in its toxicity studies, rather than proteins isolated from the plants in which they are expressed.[63] This allergenic pea would therefore have been approved for human consumption had it gone through FSANZ's normal testing regime."

On GM Crop Segregation

"GM crop agriculture is incompatible with other forms of farming-non-GM and organic ... because GM crops contaminate and because segregation is impossible." Canadian National Farmers Union (2005)

"... A Western Australian Parliamentary inquiry into genetic engineering formed the view that 'contamination of non-GM crops by GM crops is inevitable, segregation is not practical and that identity preservation (IP) can be achieved, but at a significant cost.'[66] The WA inquiry found that 'extra costs will arise with an identity preservation system due to the additional work involved throughout the supply chain, including in growing, handling, storage, transport, processing, cleaning and administration. Certification and/or testing of the GM status of bulk commodities in the marketing chain and labelling will also contribute to the additional costs.'[67]

Europe currently has a 0.9% threshold for GE contamination. However this is for 'adventitious or technically unavoidable presence', not a legislated tolerance threshold. A 'zero tolerance' segregation system would therefore be required to serve EU markets. The Australian Bureau of Agricultural and Resource Economics (ABARE) has noted that, 'zero tolerance in an importing country for contamination with GM canola would make it very difficult, if not impossible, for a country producing a mix of GM and non-GM canola to address that market.'[68]

Segregation advocates point to organic growers who successfully segregate their crops from the rest of the food supply. However such comparisons fail to appreciate how segregation systems work. Keeping the general pool of

product from contaminating a small subset is a very different task to trying to keep grains separate within the commercial system, with its huge bulk-handling facilities, intermixing, port blending, sketchy paperwork, and numerous delivery points - to say nothing of pollen drift and seed contamination.[69]

...Initial attempts to segregate non-GE canola in Canada failed and it is now nearly impossible to grow non-GE canola in most of Canada. The proliferation of GE canola, uncertainty over seed supply purity, and the risk of contamination from windblown pollen mean that non-GE farmers have little certainty that their canola will be free of GE seeds. If these farmers try to grow non-GE canola, they face huge risks that their products may be rejected by buyers, possibly when those products reach overseas ports.[70]

Based on the North American experience, it is virtually guaranteed that a GE/non-GE segregation system will fail. Canadian researchers tested 33 samples of certified non-GM canola seed and found that 32 samples were contaminated with GE varieties-and three of those samples had contamination had levels above 2%.[71] Another study in the US found that virtually all samples of non-GE corn, soybeans, and canola seed were contaminated by GE varieties.[72] Widespread contamination is not surprising.

A recent UK study found that GE canola cross-pollinated with non-GE canola more than 26 km away.[73]"

Greenpeace Submission Reference Notes:

- 60 Séralini, G-E, Cellier, D. & Spiroux de Vendomois, J. (2007) New analysis of a rat feeding study with a genetically modified maize reveals signs of hepatorenal toxicity. Archives of Environmental Contamination and Toxicology DOI: 10.1007/s00244-006-0149-5. (Hepatorenal = of or pertaining to the liver and kidneys).
- 62 Young, E. (2005) GM pea causes allergic damage in mice, New Scientist, <http://www.newscientist.com/article.ns?id=dn8347>.
- 63 Various FSANZ safety assessments can be viewed at: <http://www.foodstandards.gov.au/newsroom/technicalreportserie1338.cfm>.
- 66 Western Australia Standing Committee on Environment and Public Affairs (2001) Inquiry into the Gene Technology Bills: Executive Summary, para. 18.
- 67 Western Australia Standing Committee on Environment and Public Affairs (2001) section 9.52. 68 Foster, M. et al (2003) Market Access Issues for GM Products: Implications for Australia, ABARE Research Report 03.13, p. 9. Available at: <http://abareonlineshop.com/product.asp?prodid=12559>.
- 68 Foster, M. et al (2003) Market Access Issues for GM Products: Implications for Australia, ABARE Research Report 03.13, p. 9. Available at: <http://abareonlineshop.com/product.asp?prodid=12559>.
- 69 Ibid.
- 70 Ibid.
- 71 Friesen, L., Nelson, A. & Van Acker, R. (2003) Evidence of Contamination of Pedigreed Canola (*Brassica napus*) Seedlots in Western Canada with Genetically Engineered Herbicide Resistance Traits," *Agronomy Journal* 95, 2003, pp. 1342-1347, cited in NFU (2005b).
- 72 Mellon, M & Rissler, J. (2004) Gone to Seed: Transgenic Contaminants in the Traditional Seed Supply, Union of Concerned Scientists, cited in NFU (2005b).
- 73 Ramsay, G., Thompson, C. & Squire, G. (2004) Quantifying landscape-scale gene flow in oilseed rape, Scottish Crop Research Institute and the UK Department for Environment, Food, and Rural Affairs (DEFRA), October 2004, p. 4. www.defra.gov.uk/environment/gm/research/pdf/epg_rg0216.pdf.

IMPRINTING VIA METHYLATION

Sexual imprinting was first discovered in corn. Its kernels are dark purple if a 'Red' gene is inherited from the egg (female), but they are blotchy lavender if the same gene is transmitted via sperm. This observation was first made in 1910. Today we know that in corn pollen, which contains the plant's sperm cells, the Red gene is methylated. During kernel development the methyl tags are successively removed, thereby permitting full genetic expression to gradually appear as it matures.

RIGHT & BELOW: Some strains of corn still display this process of de-methylation in all of its colour-variant stages.



B.t. genes

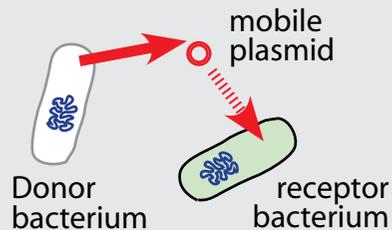
The bacterium known as *Bacillus thuringiensis* is widely used as a Lepidopteron-specific bio-insecticide. During sporulation, the bacterium produces a toxin crystal otherwise known as the parasporal body. Once ingested by the tomato hornworm or other susceptible leaf-eating caterpillars, these toxin units form hexagonal-shaped pores within the plasma membrane of the caterpillar midgut leading to loss of osmotic balance and finally, the death of the caterpillar. The *Bacillus thuringiensis* toxin gene has been incorporated into corn, canola and other crops in order to confer the toxin's protective effects against caterpillar attack.

BACTERIAL PROMISCUITY

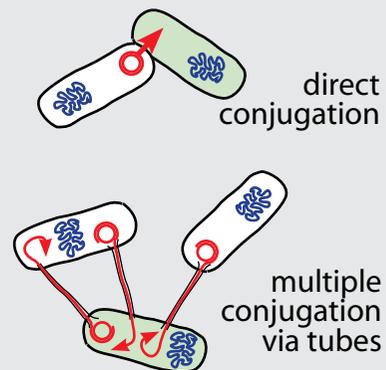
Bacteria share their genetic material very freely—by inserting segments of it directly into neighbouring bacteria in many cases, but also by indiscriminately shedding loops of it into the surrounding medium. This means that bacterial genes (unlike eukaryote genes) tend to be itinerant and do not necessarily stay put when they are inserted into other organisms.

BACTERIAL 'SEX'

Indirect transfer of genetic material



Direct transfer (conjugation)



The promiscuous dissemination of genetic material by bacteria enables just a few drug-resistant individuals to quickly spread their resistance within the population—in some cases to very different strains of bacteria. This is the reason that most pesticides and herbicides become ineffective against crop pathogens within just a few years, and it is the reason anti-bacterial drugs eventually become ineffective in preventing the spread of disease in human populations.

THREE LAYERS OF GENETIC CONTROL

In order to properly understand the threat that alien bacterial genes pose when they are inserted into crop plants we need to keep in mind the complex nature of the eukaryote cell and to be aware of the three layers of checks and balances that are built into such a symbiosis:

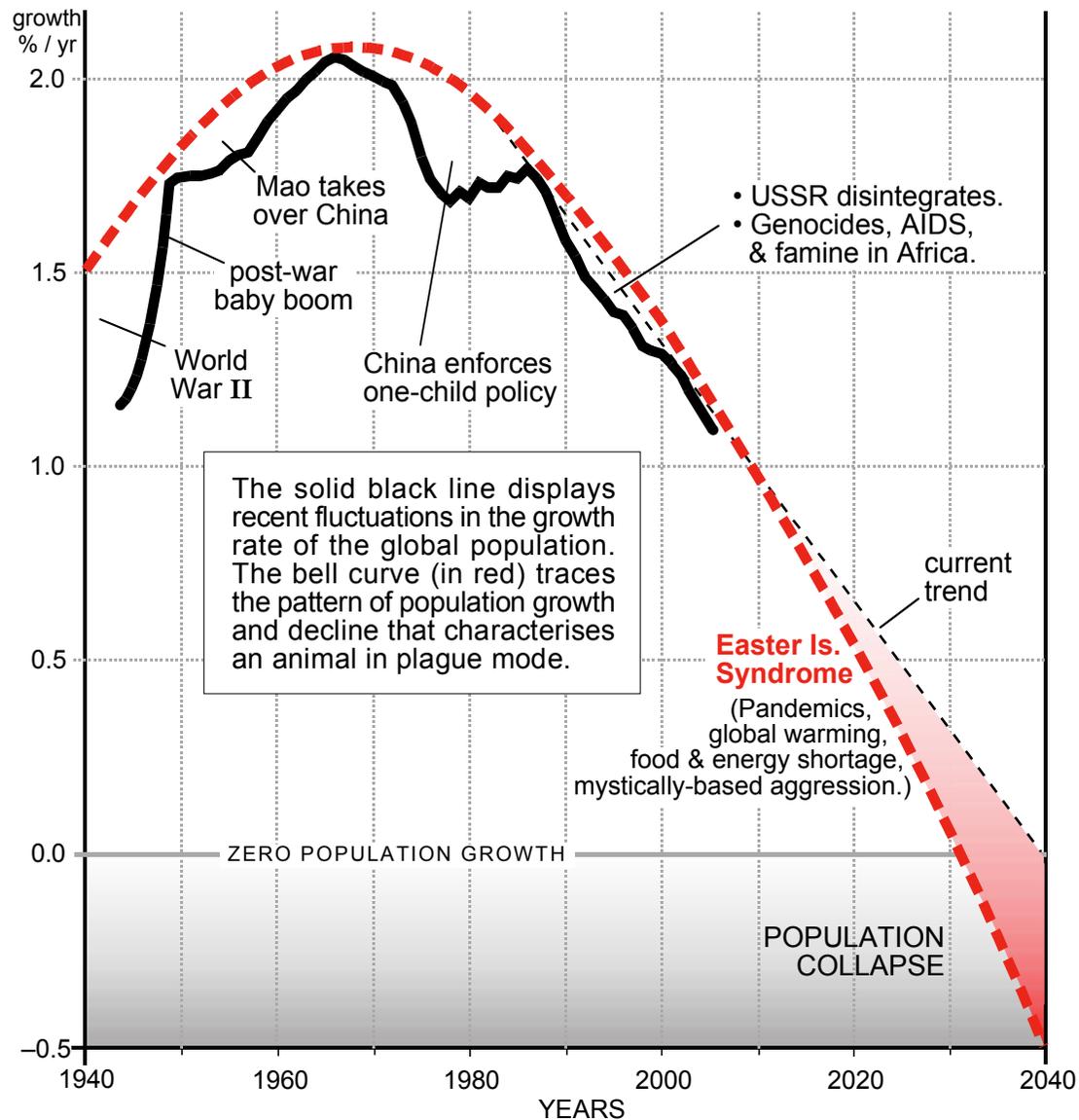
- Plant and animal genes prescribe 20 standard amino acids. Nothing else. The structures and behaviours that characterise particular organisms are emergent characteristics that result from the complex synthesis and interplay of the particular proteins that are assembled from those amino acids when they reach the cell's ribosomes. (The common belief that particular genes 'code for' this or that structure or behaviour is a dangerous myth propagated largely by ill-informed journalists and politicians.)
- There is an overriding sequence of external methyl switches that determines which genes are 'on' and which are 'off' at any particular time. They do this by altering the pattern of folding of the chromatin strands within the chromosome. Science has only recently become aware of this cryptic external code, consisting as it does of nothing more than a sequence of minute methyl tags attached along each side of DNA's double helix.
- It is essential that the messenger RNA (mRNA) used by nucleic DNA to convey its torrent of instructions through pores in the nucleic membrane to the cell's organelles is fully readable to them. The translation of mRNA to protein is performed in ribosomes by transfer RNA (tRNA). This too can become methylated.

All of this means that the 'normal' operation of a cell demands an astonishing level of cooperation between the nucleic DNA, its overriding master switches, and the eubacterial relicts that 'live' on as organelles within the body of the cell. As relicts of ancient bacterial invasions these organelles take instruction from the nucleus but still reproduce independently and run their own operations according to the dictates of their own eubacterial DNA.

In short, each plant or animal cell is like a finely tuned orchestra of virtuosos playing a Beethoven symphony in perfect unison—with no conductor on the podium. Synchronicity is paramount, with no room for error. We play dice with this at our peril.

POPULATION GROWTH

Expressed in percent per year



Based on UN data, 2004

The data plotted in this graph were extracted from annual growth-rate figures published by the United Nations between 2001 and 2003. The UN subsequently converted to five-yearly estimates and subsequent estimates appear to have been adjusted to conform to the prevailing belief that the global population is headed for a minimum of 9 billion by 2045. These five-year estimates now form what is known as the Medium Variant.

This graph, which is based on the earlier, annual figures, tallies with the UN's current Low Variant projection.

It reflects my personal opinion that the so-called 'unaccountable' fecundity decline that began in the early 1970s has generated such worldwide demographic uncertainty that UN demographers decided to publish vague five-year estimates only. Meanwhile, the traumatic cultural upheavals (civil wars and genocides) that have racked many nations in Africa and the Middle East during the past two decades have made accurate census-taking virtually impossible in those populous regions. In conjunction with the global spread of HIV-Aids and drug resistant TB and Malaria in those and other heavily populated areas, the UN's current Medium Variant is therefore a monument to human optimism and imagination.

Vanishing Bees

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