

- (1996).
10. D'Onofrio, G., Mouchiroud, D., Aissani, B., Gautier, C. & Bernardi, G. Correlations between the compositional properties of human genes, codon usage, and amino acid composition of proteins. *J. Mol. Evol.* **32**, 504–510 (1991).
 11. Filipinski, J. Correlation between molecular clock ticking, codon usage, fidelity of DNA repair, chromosome banding and chromatin compactness in germline cells. *FEBS Lett.* **217**, 184–186 (1987).
 12. Sueoka, N. Directional mutation pressure and neutral molecular evolution. *Proc. Natl Acad. Sci. USA* **85**, 2653–2657 (1988).
 13. Wolfe, K. H., Sharp, P. M. & Li, W.-H. Mutation rates differ among regions of the mammalian genome. *Nature* **337**, 283–285 (1989).
 14. Bernardi, G. & Bernardi, G. Compositional constraints and genome evolution. *J. Mol. Evol.* **24**, 1–11 (1986).
 15. Eyre-Walker, A. Evidence of selection on silent site base composition in mammals: potential implications for the evolution of isochores and junk DNA. *Genetics* **152**, 675–683 (1999).
 16. Hughes, A. L. & Yeager, M. Comparative evolutionary rates of introns and exons in murine rodents. *J. Mol. Evol.* **45**, 125–130 (1997).
 17. Holmquist, G. P. Chromosome bands, their chromatin flavors and their functional features. *Am. J. Hum. Genet.* **51**, 17–37 (1992).
 18. Eyre-Walker, A. Recombination and mammalian genome evolution. *Proc. R. Soc. Lond. B* **252**, 237–243 (1993).
 19. Nagylaki, T. Evolution of a finite population under gene conversion. *Proc. Natl Acad. Sci. USA* **80**, 6278–6281 (1983).
 20. Meuth, M. The molecular basis of mutations induced by deoxyribonucleoside triphosphate imbalances in human cells. *Exp. Cell Res.* **181**, 305–316 (1989).
 21. Phear, G. & Meuth, M. A novel pathway for the transversion mutation induced by dCTP misincorporation in a mutator strain CHO cells. *Mol. Cell. Biol.* **9**, 1810–1812 (1989).
 22. Phear, G. & Meuth, M. The genetic consequences of DNA precursor pool imbalance: sequence analysis of mutations induced by excess thymidine at the hamster apt locus. *Mutat. Res.* **214**, 201–206 (1989).
 23. Leeds, J. M., Slabaugh, M. B. & Matthews, C. K. DNA precursor pools and ribonucleotide reductase activity: distribution between the nucleus and the cytoplasm of mammalian cells. *Mol. Cell. Biol.* **5**, 3443–3450 (1985).
 24. McCormick, P. J., Danhauser, L. L., Rustim, Y. M. & Bertram, J. S. Changes in ribo- and deoxyribonucleoside triphosphate pools within the cell cycle of a synchronised mouse fibroblast cell line. *Biochim. Biophys. Acta* **755**, 36–40 (1983).
 25. Holmquist, G. P. Evolution of chromosome bands: molecular ecology of noncoding DNA. *J. Mol. Evol.* **28**, 469–486 (1989).
 26. Federico, C., Saccone, S. & Bernardi, G. The gene-richest bands of human chromosomes replicate at the onset of the S-phase. *Cytogenet. Cell Genet.* **80**, 83–88 (1998).
 27. Consortium, M. S. Complete sequence and gene map of a human major histocompatibility complex. *Nature* **401**, 921–923 (1999).
 28. Eyre-Walker, A. Evidence that both G+C-rich and G+C-poor isochores replicate early and late in the cell cycle. *Nucleic Acids Res.* **20**, 1497–1501 (1992).
 29. Boulikas, T. Evolutionary consequences of nonrandom damage and repair of chromatin domains. *J. Mol. Evol.* **35**, 156–180 (1992).
 30. Brown, T. C. & Jiricny, J. Different base/base mispairs are corrected with different efficiencies and specificities in monkey kidney cells. *Cell* **54**, 705–711 (1988).
 31. Eyre-Walker, A. DNA mismatch repair and synonymous codon evolution in mammals. *Mol. Biol. Evol.* **11**, 88–98 (1994).
 32. Fryxell, K. & Zuckerkandl, E. Cytosine deamination plays a primary role in the evolution of mammalian isochores. *Mol. Biol. Evol.* **17**, 1371–1383 (2000).
 33. Galtier, N. & Mouchiroud, D. Isochore evolution in mammals: a human-like ancestral structure. *Genetics* **150**, 1577–1584 (1998).
 34. Macaya, G., Thiery, J. P. & Bernardi, G. An approach to the organization of eukaryotic genomes at a macromolecular level. *J. Mol. Biol.* **108**, 237–254 (1976).
 35. Thiery, J. P., Macaya, G. & Bernardi, G. An analysis of eukaryotic genomes by density gradient centrifugation. *J. Mol. Biol.* **108**, 219–235 (1976).
 36. Bernardi, G. & Bernardi, G. Compositional patterns in the nuclear genomes of cold-blooded vertebrates. *J. Mol. Evol.* **31**, 265–281 (1990).
 37. Hughes, S., Zelus, D. & Mouchiroud, D. Warm-blooded isochore structure in Nile crocodile and turtle. *Mol. Biol. Evol.* **16**, 1521–1527 (1999).
 38. Galtier, N. & Lobry, J. Relationships between genomic G+C content, RNA secondary structures and optimal growth temperature in prokaryotes. *J. Mol. Evol.* **44**, 632–636 (1997).
 39. Hurst, L. D. & Merchant, A. R. High guanine–cytosine content is not an adaptation to high temperature: a comparative analysis amongst prokaryotes. *Proc. R. Soc. Lond. B* **268**, 493–497 (2001).
 40. D'Onofrio, G., Jabbari, K., Musto, H. & Bernardi, G. The correlation of protein hydrophathy with the composition of codin sequences. *Gene* **238**, 3–14 (1999).
 41. Ikemura, T. & Wada, K.-N. Evident diversity of codon usage patterns of human genes with respect to chromosome banding patterns and chromosome numbers: relation between nucleotide sequence data and cytogenetic data. *Nucleic Acids Res.* **16**, 4333–4339 (1991).
 42. Fullerton, S. M., Bernardo Carvalho, A. & Clark, A. G. Local rates of recombination are positively correlated with GC content in the human genome. *Mol. Biol. Evol.* **18**, 1139–1142.
 43. Mouchiroud, D., Gautier, C. & Bernardi, G. The compositional distribution of coding sequences and DNA molecules in humans and murids. *J. Mol. Evol.* **27**, 311–320 (1988).
 44. Filipinski, J. Chromosome localization-dependent compositional bias of point mutations in *Alu* repetitive sequences. *J. Mol. Biol.* **206**, 563–566 (1989).
 45. Casane, D., Boissinot, S., Chang, B. H. J., Shimmin, L. C. & Li, W.-H. Mutation pattern variation among regions of the primate genome. *J. Mol. Evol.* **45**, 216–226 (1997).
 46. Francino, P. & Ochman, H. Isochores result from mutation not selection. *Nature* **400**, 30–31 (1999).
 47. Smith, N. G. C. & Eyre-Walker, A. Synonymous codon bias is not caused by mutation bias in G+C-rich genes in humans. *Mol. Biol. Evol.* **18**, 982–986.
 48. Eyre-Walker, A. Differentiating selection and mutation bias. *Genetics* **147**, 1983–1987 (1997).
 49. Smith, N. G. C. & Hurst, L. D. The effect of tandem substitutions on the correlation between synonymous and nonsynonymous rates in rodents. *Genetics* **153**, 1395–1402 (1999).
 50. Bielawski, J. P., Dunn, K. A. & Yang, Z. Rates of nucleotide substitution and mammalian nuclear gene evolution: approximate and maximum-likelihood methods lead to different conclusions. *Genetics* **156**, 1299–1308 (2000).
 51. Hurst, L. D. & Williams, E. J. B. GC content and the silent site substitution rate do covary in rodents: implications for methodology and for the evolution of isochores. *Gene* **261**, 107–114 (2001).
 52. Eyre-Walker, A. The effect of constraint on the rate of evolution in neutral models with biased mutation. *Genetics* **131**, 233–234 (1992).
 53. Eyre-Walker, A. The role of DNA replication and isochores in generating mutation and silent substitution rate variance in mammals. *Genet. Res.* **60**, 61–67 (1992).
 54. Gu, X. & Li, W.-H. A model for the correlation of mutation rate with GC content and the origin of GC-rich isochores. *J. Mol. Evol.* **38**, 468–475 (1994).
 55. Wolfe, K. Mammalian DNA replication: mutation biases and the mutation rate. *Theor. Biol.* **149**, 441–451 (1991).
 56. Duret, L. & Hurst, L. D. The elevated G and C content at exonic third sites is not evidence against neutralist models of isochore evolution. *Mol. Biol. Evol.* **18**, 757–762.
 57. Smit, A. Interspersed repeats and the other mementos of transposable elements in the mammalian genomes. *Curr. Opin. Genet. Dev.* **9**, 657–663 (1999).
 58. Feng, Q., Moran, J. V., Kazazian, H. H. & Boeke, J. D. Human L1 retrotransposon encodes a conserved endonuclease required for retrotransposition. *Cell* **87**, 905–916 (1996).
 59. Jurka, J. Sequence patterns indicate an enzymatic involvement in integration of mammalian retroposons. *Proc. Natl Acad. Sci. USA* **94**, 1872–1877 (1997).
 60. Toda, Y., Saito, R. & Tomita, M. Characteristic sequence pattern in the 5- to 20-bp upstream region of primate *Alu* elements. *J. Mol. Evol.* **50**, 232–237 (2000).
 61. Gu, Z., Wang, H., Nekrutenko, A. & Li, W.-H. Densities, length proportions, and other distributional features of repetitive sequences in the human genome estimated from 430 megabases of genomic sequence. *Gene* **259**, 81–88 (2000).
 62. Eyre-Walker, A. & Keightley, P. D. High genomic deleterious mutation rates in hominids. *Nature* **397**, 344–347 (1999).
 63. Keightley, P. D. & Eyre-Walker, A. Deleterious mutations and the evolution of sex. *Science* **290**, 331–333 (2000).

Acknowledgements

Many thanks to M. Lercher, N. Smith, E. and A. Urrutia. Both A.E.-W. and L.D.H. are supported by the Royal Society, to whom they are grateful.

SCIENCE AND SOCIETY

Molecular metaphors: the gene in popular discourse

Dorothy Nelkin

Geneticists deploy a striking range of metaphors to communicate their science, to promote its value and to suggest its social meaning to the public. So too, critics of science and special interest groups use metaphorical constructs to express their concerns about the implications of the 'genetic revolution'. Through metaphors, genetics can seem a source of salvation or a means of exploitation, a boon to health or a source of risk. This paper is a critical review of the metaphors used to communicate genetic information to the public.

"There's a metaphor contest going on"¹

Harold Varmus, former Director of the National Institutes of Health

The human genome is "like the torn pages of a giant novel, written in an unknown language, blowing about helter skelter in an air-conditioned, enclosed space such as Houston's Astrodome"². The scientists involved in mapping and sequencing the genome, so this extended metaphor implies, will capture all these pages, put them in proper order and analyse the meaning of the resulting text.

Metaphors are a prevalent and important vehicle of public communication, and they are especially important in conveying scientific information. Explaining and popularizing unfamiliar and frequently technical material can be done most effectively through images that are chosen for their richness of reference, their familiar meanings and their graphic appeal. By connecting different orders of reality, metaphors enable the translation of very complex scientific information in culturally meaningful ways.

But metaphors are more than an aid to explanation: repeated metaphors affect the ways we perceive, think and act, for they shape our understanding of events. They also structure our attitudes about public — and scientific — issues. By their choice of metaphors, scientists, their public relations strategists, and science writers, convey certain beliefs about the nature and importance of science and technology, and their limits, impacts and implications. Although people interpret scientific information and ascribe meaning to metaphors according to their personal experience and previous knowledge³, metaphors are powerfully persuasive tools.

Geneticists deploy a striking range of metaphors to promote their science, suggest its meanings and persuade the public of its value to health care and social policy. So too, critics use metaphorical constructs to express concerns about the problematic implications of the genetic revolution. And special interest groups mobilize images in their debates. Anthropologist Jose van Dijk describes genetics today as a “spectacle”, a “theatre of representation”, as various

“Media stories extend the essentialist images conveyed by scientists by endowing the genes with social attributes: there are obesity genes, gay genes, risk genes, violence genes, genes for saving, genes for directional ability, and even genes for sinning.”

interests interact to produce images and metaphors⁴. These groups, including scientists, have become increasingly skilled at pre-packaging images for the media⁵. Journalists then amplify their messages in ways that are likely to have popular resonance. Through metaphors, genetics can seem to be a source of salvation or a means of exploitation and control. Are people simply the sum of their genes or are they a product of history? Is genetic engineering a ‘boon’ to health, or a way to ‘tamper’ with genes? Is the effort to understand the genome a quest for the ‘holy grail’ or are scientists ‘playing God’?

Metaphors of the eugenics movement During the eugenics movement of the 1920s and 1930s, scientists applied the principles of genetics and animal breeding towards improving the human race. Eugenists

defined the germplasm, then believed to be the hereditary material, as the essence of the person, determining personality and character traits — “The blood will tell”. At that time, essentialist metaphors prevailed. The germplasm, carried from one generation to the next, was “the master key to history”, the “very soul” of the individual, and the source of social and moral order.

The animal breeding business also became a source of imagery: eugenicists emphasized the importance of “good stock” and worried about the products of “cross-breeding” and the “pollution of the gene pool”. During the 1920s, the American Eugenics Society, placing moral value on eugenic fitness, sponsored a series of “better baby” and “fitter family” contests at state fairs (FIG. 1). Families with diseases or deformities, that is “bad blood”, were defined as dangerous (“born criminal”), and their “breeding” had to be controlled⁶.

Eugenic metaphors reflected the political anxieties of that time — concerns about the social and economic threat of immigration and fears about the growing ethnic diversity of the population. But the eugenics movement declined in influence after 1935, its social agenda called into question by the unfolding events in Germany and the eugenic-inspired policies of the Nazis. As a result, there was a general cultural shift away from biological determinism as an explanation of health and behaviour.

When molecular genetics first began to emerge in the early 1970s, the new recombinant DNA research evoked fearful images of risk. Scientists called a brief moratorium on the research until risks could be ascertained and contained, and they convened the 1975 Asilomar Conference to examine the issues raised by this emerging research area. But their caution also raised public alarm. Reporters referred to a “biological holocaust” and wrote of Frankenstein monsters and Andromeda-like strains. *Time*, in 1977, ran a cover story called “The DNA Furor: Tinkering with Life”. *The New York Times Magazine* wondered about “New Strains of Life or Death?” The message in the metaphors was that runaway science needs to be controlled⁷.

Only three years later, reflecting the optimism of the early Reagan years in the United States, the metaphors of risk turned to those of revolution. The media welcomed DNA research as “a new miracle”, and “a race towards better human health”. The runaway science became a technological frontier; geneticists were the pioneers, “unlocking the basic laws of nature” and discovering “the secrets of life”⁸.



Figure 1 | **Fitter family contests.** This photo, taken in 1920, shows the ‘Fitter Families’ exhibit and examination building, Kansas State Free Fair, Topeka. (Courtesy of the American Philosophical Society, Philadelphia, Pennsylvania, USA.)

Today, in their public communication, scientists and the media have resurrected some of the old metaphors of the eugenics movement that suggest how genetics can be used to understand personal identity, immortality and fate. Genetic metaphors, collected from contemporary sources, cluster around four repeated and related themes: first, essentialist metaphors: genes are the essence of personal identity; second, religious metaphors: the gene is a sacred entity; third, fatalistic metaphors: genes are destiny; and last, commercial metaphors: genes are commodities.

Genes — essence of personal identity
When, in 1953, **Francis Crick and James Watson** discovered the double helical structure of DNA, they described the sequence of the bases as a “master molecule” — a “code” that carries the genetic information. The computer sciences and information theory have since provided a wealth of images to describe the new genetics. The body is less a conscious being than a set of ‘instructions’, a ‘programme’, or a ‘master code’ transmitted from one generation to the next⁸. People are ‘readouts’ of their genes.

This ‘molecular vision of life’⁹ sees genes as the essence of the person; they are ‘what makes us human’. DNA, proclaims James Watson, is the “stuff” of life. A related set of metaphors compares the gene to a text or a script, played out in phenotypic characteristics and behaviour¹⁰. The person, according to science writer Matt Ridley, is but “the victim, plaything, battleground, and vehicle for the genes”¹¹.

Media stories extend the essentialist images conveyed by scientists by endowing the genes with social attributes: there are obesity genes, gay genes, risk genes, violence genes, genes for saving, genes for directional ability, and even genes for sinning¹². Behaviour reflects and reveals our latent, but innate, predispositions. And, metaphorically, genes are moral molecules: there are ‘good’ and ‘bad’ genes. References to good and bad genes have become a way to explain individual differences. Good genes (for example, ‘the genes of genius’) help to explain special talents, the success of celebrities and, in advertisements, even the qualities of inanimate objects and consumer products, such as cars or perfume. As one manufacturer claimed: “A BMW has a genetic advantage”. Bad genes (for example, ‘criminal chromosomes’, ‘alcohol genes’) help to explain social problems. Some people are simply ‘born criminal’¹³. Or, as a *New York Times* reporter claimed: “Evil is embedded in the coils of chromosomes that our parents pass on to us at conception”¹⁴.

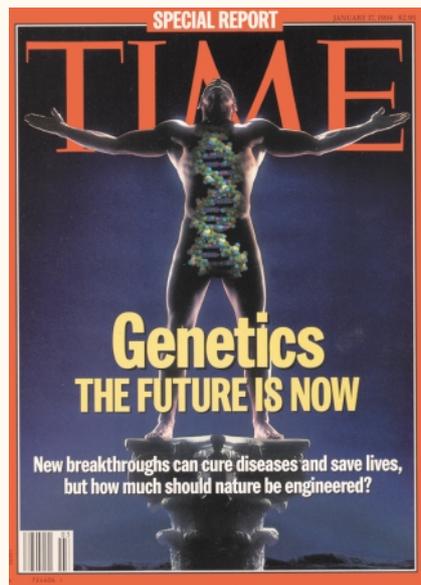


Figure 2 | Cover of *Time* magazine, Jan 17, 1994.

Geneticist Walter Gilbert introduces his public lectures on gene sequencing by pulling a compact disk from his pocket and announcing “this is you”¹⁵. When celebrating the completion of the genome sequencing effort in June 2000, scientists described the genome as “a portrait of who we are”, and a “blueprint for a human being”¹. Such metaphors imply that if scientists can decipher and decode the text, classify the markers on the map and read the instructions, they will be able to reconstruct the essence of human beings and reveal the ‘secrets’ of human nature. Nicholas Wade, a *New York Times* science reporter, amplified this message, enthusiastically predicting that “over the next few years we should get to read [the] behavioural instructions. Whatever they are — instincts to slaughter or show mercy, the contexts for love and hatred, the taste for obedience or rebellion — they are the determinants of human nature.”¹⁶. But such metaphors also inspired bioethicist George Annas to call the gene a “future diary”, suggesting that concerns about privacy must protect such secret and personal information¹⁷.

Genes as a sacred entity

Geneticists, while popularizing and promoting their work, refer to the genome as the Bible, the Holy Grail and the Book of Man, conveying an image of this molecular structure, not only as a biological entity, but also as a sacred text¹². “Is DNA God?” asks Gregory Henderson, a writer in a medical journal, *The Pharos*. “Given its essential roles in the origin, evolution and maintenance of life, it is tempt-

ing to wonder if this twisted sugar string of purine and pyrimidine base beads is, in fact, God”¹⁸. When Francis Collins announced the first draft of the sequence of the human genome in June 2000, he proclaimed “We have caught our first glimpse of our own instruction book previously known only to God”¹⁹. And in a popular book called *The Genetic Gods*, biologist John Avise describes how “genetic gods” figure in our emotional disposition, personality and ethical leanings²⁰.

In its metaphorical construction, DNA shares striking qualities with the Christian soul. It seems relatively independent of the body, giving the body life, power and true identity. DNA, like the soul, bears the marks of good and evil. A man might look fine to the outside world, but despite external appearances, if he is evil or ill, it will be marked in his soul — or in his genes. And DNA, an invisible entity, seems to be immortal, containing in it everything needed to bring the body back.

This is, of course, the theme of popular stories and films, such as *Jurassic Park*, in which the DNA is a powerful molecule with magical powers that can resurrect the dead. But scientists have also encouraged such images. They have proposed to resurrect the characteristics of past presidents and other celebrities by extracting DNA from their remains²¹. Nobelist **Kary Mullis** started a company, StarGene, using PCR techniques to create molecular relics that will make a revered person ‘present’ for admirers²². **The Human Genome Diversity Project**, an international plan to collect DNA from indigenous peoples, was built around a concept of DNA as an ‘immortal’ text that can reveal the history of ancient civilizations and ‘immortalize’ vanishing populations.

By taking on the social and cultural functions of the soul, the DNA — a molecular structure — gains mystical power and iconic importance as a way to explore the most fundamental questions about human life, to explain the essence of human existence, to imagine immortality and to anticipate human fate. And endowing the gene with spiritual importance also empowers science and provides a foundation for its cosmic claims.

Genes predict future fate

In a media interview at an early stage of gene-sequencing research, biochemist Robert Sinsheimer called the genome “the complete set of instructions for making a human being”²³. Similarly, a decade later, scientists celebrating the completion of the sequencing effort called the genome the “book of life”, an “atlas”, and a “master parts list”.

When promoting the practical usefulness of their research in public speeches and media interviews, geneticists frequently refer to the genome as a dictionary, a map, a library or a recipe book; that is, a comprehensive and orderly reference work that needs only to be deciphered and read to predict a person's future health or behavioural predispositions. Their metaphors emphasize prediction. The genome is a "Delphic Oracle", a "time machine", a "trip into the future", or a "medical crystal ball". James Watson has announced in frequent interviews that "our fate is in our genes"²³.

The fatalistic metaphors of genetic destiny are not only a way to talk about health and disease, but also about blame, moral responsibility and appropriate social order. To locate human fate in the genes indicates a certain inevitability in the structure of existing social categories. They seem 'natural' and therefore 'right'. The great and famous, the successful and celebrated, are what they are because of their genes. Human life is what it has to be: it is 'mapped' and pre-ordained.

These metaphors of destiny have policy implications, implying that there are natural limits that constrain the possibilities of both individuals and social groups. Human beings are not perfectible if flaws and failings are inscribed in a 'blueprint of destiny', a map, or an unchangeable text. Such metaphors pervade science communication, implying that even under the most ideal conditions, DNA will determine fate. We are programmed by nature to succeed or to fail.

Debates among geneticists reveal, in fact, serious doubts about the meaning of the genome and the possibility of reading a person's destiny from this very complex text. Yet scientists, keen on promoting the diagnostic value of their work, continue to deploy futuristic metaphors. And these are amplified by the media, who are attracted to the tantalizing possibility of prediction and its implication for control (FIG. 2).

Genes as a commodity

The expectations of controlling disease have, of course, attracted considerable commercial interest in genes and cell lines, both as a source of information for the development of diagnostic and therapeutic techniques, and as the raw material for commercial products. There is a rush to patent genes. The growth of the biotechnology business and associated patent practices have evoked a new set of metaphors that portray DNA as a commodity — a valuable and marketable

"Given its essential roles in the origin, evolution and maintenance of life, it is tempting to wonder if this twisted sugar string of purine and pyrimidine base beads is, in fact, God."

G. Henderson, 1998.

entity. The gene is not just the essence of a person, it has also become a kind of property, an item to be bought and sold, a part of our system of exchange. Describing the value of genes, scientists are using a commercial language of supply and demand, contracts, investment, exchange and compensation²⁴. In the quest for valuable genes, body tissue is extracted like a mineral, mined like a resource, procured like land or goods and banked like money.

A physician who patented his patient's cell line referred to his patient's body as a "gold mine"²⁵. Pathologists seeking access to archived human tissue in government or hospital repositories have called these human tissue banks "national resources" or "treasure troves"²⁶. And, describing the collection of population-based genetic databases in Iceland, the director of the **deCODE Genetics** project, Kari Stefansson, compares gene databases to a cash-dispensing system. Credit cards allow us to withdraw currency because the world is a network of centralized databases of personal information on finance. Similarly, gene banks are centralized repositories of personal information on health, and, like a cash dispenser (ATM), they enable the withdrawal of useful and valuable currency²⁷.

Ironically, images that reduce the body to an object, a commodity with monetary value, conflict with the essentialist and religious metaphors that are commonly used to describe genetic material. Indeed, the commercial thrust of genetics these days is placing the human body in an ambiguous space. Are genes the essence of the person, or a valued material or commercial product? How can we believe that the human body is sacred if it is also for sale? If genetic material is both the essence of the person and valuable property, what legal claims would a person have over his or her genes? Who in fact owns our DNA?

Counter-metaphors and critiques

Critics of the genome programme have constructed their own set of metaphors, and many build upon Frankenstein myths²⁸. To some critics, DNA is "forbidden territory" to be transgressed at very high cost. They see scientists as "tinkering" or "tampering" with life, or as "playing God". They see the sanctity of life and the sovereignty of God at stake²⁹.

Indigenous peoples, the subjects of genetic research on certain disease genes, use metaphors such as "bio-colonialism" or "gene prospecting" to describe the scientific efforts to obtain information from their genes. Their language indicates that science is just another means of exploitation. The patenting of genes has also evoked pejorative images as "the biggest race for property since the great land rush of 1889"³⁰. Geneticists are "striking gold" and "staking claims". Where, ask critics, are the limits of science?

In my view, the metaphors used to promote the Human Genome Project — the maps, codes and dictionaries — are often less illuminating than misleading to the public³¹. The apparent precision of such reference works tends to obscure the interests and priorities that, in fact, have shaped them. As forms of knowledge, all reference works are products of cultural choices, reflecting social perspectives on the world at the time of their making. Geographical maps, for example, are socio-political artefacts that serve particular political and economic interests³². They select certain features of the complex world, transforming them to create a coherent landscape. And maps are instruments of persuasion. As a geographer put it, "a good map tells a multitude of little white lies. It suppresses truth to help the user see what needs to be seen"³³. The mapping metaphors that are used to describe the genome indicate that once a gene is located, its interpretation will be objective and independent of context. But although a mapped gene might seem to be a straightforward detail that can be extracted without reference to social context, it must be contextualized if its meaning is to be properly understood.

Metaphors of dictionaries or libraries also fail to shed much light. To develop meaning from a dictionary requires integrating data as well as extracting information. Similarly, the meaning of genes for human development and even for complex diseases requires an understanding of their social and developmental context. This crucial point is often lost as scientists use simple metaphors to promote their work, and it virtually disappears in popular representations.

The gene continues to be described as a “master molecule” or “blueprint”, in both scientific and media communication. But such metaphors are also fundamentally flawed, for they are based on impoverished ideas of causation. As Evelyn Fox Keller observes, “The secrets of life have proven to be vastly more complex and more confusing than they had seemed in the 1960s and 70s”³⁴.

Scientists must use metaphors to explain their complex and esoteric subject, to attract popular interest in their technical fields and to win public funds. But their metaphorical constructions, endowing genes with a kind of autonomous power, are neither neutral nor benign. To geneticist Richard Lewontin: “The transfer of causal power from social relations into inanimate agents that then seem to have power and life of their own is one of the major mystifications of science and its ideologies”³⁵.

DNA, after all, is a biological entity, a text without context, data without dimension. To explain human beings in biological terms, to jump from the molecular level of genetic systems to expression in behaviour or complex clinical disorders, requires a profound leap of faith. But this is a leap conveyed to the public through molecular metaphors, deployed by scientists to promote their research and by the media to explain the science of genetics.

Dorothy Nelkin is at the New York University School of Law, Vanderbilt Hall, 40 Washington Square South, Room 510, New York, New York 10012-1066, USA. e-mail: dorothy.nelkin@nyu.edu



FURTHER INFORMATION **Francis Crick and James Watson | Kary Mullis | The Human Genome Diversity Project | deCODE Genetics | Image archive on the American Eugenics Movement**

1. Angier, N. A pearl and a hodgepodge: human DNA. *New York Times* A21 (June 27, 2000).
2. Wallace, B. in *The Search for the Gene* 199 (Cornell Univ. Press, Ithaca, New York, 1992).
3. Condit, C. *The Meaning of the Gene: Public Debates about Human Heredity* (Wisconsin Univ. Press, Madison, 1999).
4. Van Dijk, J. *Imagination: Popular Images of Genetics* (New York Univ. Press, New York, 1998).
5. Nelkin, D. *Selling Science: How the Press Covers Science and Technology* 2nd edn (W. H. Freeman, New York, 1994).
6. Kevles, D. *In the Name of Eugenics* (Knopf, New York, 1985).
7. Altmore, M. The social construction of a scientific controversy. *Sci. Technol. Human Values* 7, 24–31 (1982).
8. Hedgecoe, A. Transforming genes: metaphors of information in modern genetics. *Science as Culture* 8, 209–228 (1999).
9. Kay, L. *The Molecular Vision of Life* (Oxford Univ. Press, London, 1995).
10. Lewis, J. The performance of a lifetime: a metaphor for the phenotype. *Perspect. Biol. Med.* 43, 112–127 (1999).
11. Ridley, M. *Genome* (Fourth Estate, London, 2000).
12. Nelkin, D. & Lindee, M. S. *The DNA Mystique: The Gene as Cultural Icon* (W. H. Freeman, New York, 1995).
13. Rafter, N. H. *Creating Born Criminals* (Illinois Univ. Press, Chicago, 1997).
14. Franklin, D. What a child is given. *New York Times Magazine* 36 (September 3, 1969).
15. Gilbert, W. Current state of the HGI. *Harvard Univ. Dibern Center Lecture* (June 15, 1990).
16. Wade, N. The four letter alphabet that spells life. *New York Times* 4 (July 2, 2000).
17. Annas, G. Protecting future diaries. *J. Am. Med. Assoc.* 270, 234 (1993).
18. Henderson, G. Is DNA God? *The Pharos* 2–6 (Winter, 1988).
19. Collins, F. White House remarks on decoding of genome. *New York Times* F8 (June 27, 2000).
20. Avise, J. *The Genetic Gods* (Harvard Univ. Press, Cambridge, Massachusetts, 1998).
21. Leary, W. Scientists seek Lincoln DNA to clone for a medical study. *New York Times* 1 (February 10, 1991).
22. Kary Mullis interview. *Omni* 69–92 (April, 1992).
23. Jaroff, L. The gene hunt. *Time* 62–67 (March 20, 1989).
24. Andrews, L. & Nelkin, D. *Body Bazaar: The Market for Human Tissue in the Biotechnology Age* (Crown Publishers, New York, 2001).
25. Moore, J. Testimony to the Committee on Human Genome Diversity of the National Academy of Sciences, September 16, 1996.
26. Steinberg, K. (Centers for Disease Control) Comments at National Institutes of Health meeting on “Genetics Research on Human Tissue” January 19, 1996.
27. Stefansson, K. Interview. *Technol. Rev.* 55 (April, 2001).
28. Turney, J. *Frankenstein’s Footsteps: Science, Genetics, and Popular Culture* (Yale Univ. Press, New Haven, Connecticut, 1998).
29. Stone, R. Religious leaders oppose patenting of genes. *Science* 268, 1126 (1995).
30. Sloan, P. in *Controlling our Destinies* 176 (Notre Dame Univ. Press, Notre Dame, 2001).
31. Myers, G. The double helix as icon. *Science as Culture* 9, 49–72 (1990).
32. Harley, J. B. *The New Nature of Maps* (Johns Hopkins Press, Baltimore, Maryland, 2001).
33. Monmonier, M. in *How to Lie with Maps* 199 (Chicago Univ. Press, Illinois, 1991).
34. Keller, E. F. in *The Century of the Gene* 54–55 (Harvard Univ. Press, Cambridge, Massachusetts, 2000).
35. Lewontin, R. in *Biology as Ideology* 48 (Harper Perennial, New York, 1992).

We welcome correspondence

Has something in the journal caught your attention?

If so, please write to us about it by sending an email to: naturereviews@nature.com and flag it for the attention of the *Nature Reviews Genetics* editors.

Correspondence to the journal will be selected by the editors for publication on the *Nature Reviews Genetics* website at <http://www.nature.com/reviews/genetics/> where it will be linked to the relevant article.