

Future Global Warming Scenarios

IN A STUDY COMMISSIONED BY THE PENTAGON, Peter Schwartz and Doug Randall (*1*) present a very alarming scenario regarding the short-term consequences of global warming. This scenario, which predicts a shutdown of the Atlantic Ocean's conveyor circulation in the next 10 to 15 years, is based on analogies to two large and abrupt climate changes, which occurred 12,700 and 8200 years ago. Both are thought to have been triggered by catastrophic releases of meltwater stored in lakes that formed along the southern margin of the retreating Canadian ice sheet. These floods appear to have squelched deep water formation in the North Atlantic and, by as yet unknown mechanisms, caused Earth's climate to plunge back toward its glacial condition. Clearly, if global warming were to cause a repeat of such an abrupt change, the consequences would be akin to those alluded to in the warning to the Pentagon, namely, a large cooling of northern Europe. But there is no reason to believe that the impacts could occur in a mere decade, nor would they be so awesome.

“ Exaggerated scenarios serve only to intensify the existing polarization over global warming. What is needed is not more words but rather a means to shut down CO₂ emissions to the atmosphere.”

—BROECKER

As the one who first pointed out the link between the Atlantic's conveyor circulation and abrupt climate changes, I take serious issue with both the timing and the severity of changes proposed in the Pentagon scenario. Computer simulations do suggest that a greenhouse-induced warming would increase the delivery of precipitation and river runoff to the North Atlantic and, further, that given a large enough warming, this excess fresh water could cause the conveyor to sag and, in the extreme, shut down. However, the time required for this to happen is more likely a century, not a decade. Further, no full-fledged global model has yet reproduced the immense impacts coincident with the two meltwater floods. We suspect that the required amplifier involves sea ice formation in the North

Atlantic. If indeed this is the case, then as the globe warms, amplification by this mechanism becomes ever less likely.

Exaggerated scenarios serve only to intensify the existing polarization over global warming. What is needed is not more words but rather a means to shut down CO₂ emissions to the atmosphere. Although we are powerless to accomplish this by 2015, we certainly have the wherewithal to do it by 2075.

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Reference

1. P. Schwartz, D. Randall, "Abrupt climate change," report prepared by Global Business Network (GBN) for the Department of Defense, available at www.gbn.org/ArticleDisplayServlet.srv?aid=26231.

Human Being Redux

TWO YEARS AGO, AS ONE OF THE MEMBERS OF the President's Council on Bioethics, I and others on the Council outlined a logic for letting therapeutic cloning go forward. Then, as now, few favor reproductive cloning—cloning for baby-making. But cloning for biomedical research, a process that only involves cells in a petri dish and may well ultimately relieve human suffering, is another matter.

Now South Korean scientists have made a major advance in biomedical cloning ("Evidence of a pluripotent human embryonic stem cell line derived from a cloned blastocyst," W. S. Hwang *et al.*, *Reports*, 12 March, p. 1669; published online 12 Feb., 10.1126/science.1094515). They have shown the world that therapeutic cloning that allows for the production of stem cells, which may lead to remedies for human diseases, is possible. The hopes raised by this advance belie the fear, raised 2 years ago by those against letting the American biomedical community into this scientific hunt, that biomedical cloning would undermine the dignity of the human race. Indeed, the one million Americans who suffer from Parkinson's disease would undoubtedly feel more affronted if these advances had not taken place.

How did we get to the point where the United States, one of the world's great scientific powers, is sitting on the sidelines while this work is being done? At the center of the discussion is the belief on the part of some that a blastocyst, the entity in the petri dish, is morally equivalent to a living postnatal

Letters to the Editor

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human being. The human embryo, the entity created by the union of an egg and sperm, carries all the genetic information of a member of the human species. Thus, those opposed to therapeutic cloning consider the embryo a human being. Of course, to develop into a human being, the embryo must be implanted into the uterus of a woman and be allowed to develop. This potential to become a human being is what sticks in the minds of the supporters of the moral equivalence argument and persuades them that manipulation of embryos for anything but normal reproduction is not acceptable.

Looking at a miniscule ball of cells in a petri dish, so small that it could rest on the head of a pin, one may be hard pressed to think of it as a human being. After all, it has no brain or capacity to think and feel. Merely possessing the genetic material for a future human being does not make a ball of cells a human being. The developing embryo that becomes a fetus that becomes a baby is the product of a dynamic interaction with its *vivo* environment, its postnatal experiences, and a host of other factors. A pure genetic description of the human species does not describe a human being. A human being represents a more complex level of organization, as distinct from a simple embryo as an embryo is distinct from an egg and sperm. It is the dynamics between genes and environment that make a human being.

The South Korean scientists seem to understand these distinctions. They are not in the baby-making business. They have constructed a fence around developing embryos through a cloning process unfolding in a petri dish. Their embryos are allowed to develop for only a few days, at which time the all-important stem cells are harvested for possible therapeutic use, and simultaneously the rest of the cell mass dies. There is no slippery slope here; there is no beginning of the much-feared world of cloned humans. The South Korean scientists have found a way to let biomedical cloning go forward with all of its spectacular promise for restoring human dignity to the seriously diseased and infirm patients of the world, while avoiding the creation of a social atmosphere that might use such advances for baby making. What could be better?

The United States can solve its dilemma quickly and easily. Congress could vote to outlaw reproductive cloning. At the same time, they could allow therapeutic cloning to go forward, inspired by the example of the South Koreans. Therapeutic cloning, si; reproductive cloning, no!

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The Science Behind Forensic Science

DONALD KENNEDY'S EDITORIAL "FORENSIC science: oxymoron?" (5 Dec., p. 1625) raises a number of troubling questions about forensic science. They are especially troubling for those of us who work in crime laboratories, law enforcement agencies, medical examiner's offices, and other parts of the criminal justice system that deal with evidence and scientific analysis.

Forensic science professionals heartily support research into the scientific underpinnings of forensic science. Daubert and subse-

quent cases have changed the way courts review knowledge-based evidence. It is therefore not unreasonable for courts to demand that nonacademic-based procedures be shown to be reliable by scientists independent of law enforcement laboratories. The challenge is to ensure that the methods and techniques that protect the innocent and incriminate the guilty are reliable and actually work.

The Consortium of Forensic Science Organizations (CFSO) represents over 11,000 individuals who work in forensic science worldwide. These organizations and their members endorse the notion that their work must be grounded in scientific principles. The CFSO endorses research into the underpinnings of forensic science techniques. However, money is needed to fund that research. Congress must provide the National Institute of Justice (NIJ) with adequate resources and a mandate to undertake the research needed to demonstrate the validity and reliability of these techniques. Other funding agencies that have not traditionally funded forensic research, such as the National Science Foundation, should also be engaged. Research conducted by impartial scientists working in research institutes, coupled with input from the forensics community, is needed.

Will research quiet the naysayers to forensic science? Probably not, but carefully directed research aimed at some of the key problems will promote fairness in our justice system and lead to ever more powerful and reliable technology. Now for the hard part: How can the scientific/academic community, in cooperation with the forensics community, put these issues on the radar screen of those who can provide appropriate funding?

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Testing Genome Complexity

IN THEIR REPORT "THE ORIGINS OF GENOME complexity" (21 Nov., p. 1401), M. Lynch and J. S. Conery argue that many modifications that determine eukaryotic genome complexity (such as retention of duplicate genes and transposable elements) emerged by random genetic drift (nonadaptively) in response to the long-term population-size

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reductions that accompanied increases in organism size. This is an important proposal because so-called “progressive evolution” (increase of complexity) is not explained by modern evolutionary theory. For example, bacteria are as adapted as mammals. The proposed solution is intriguing and paradoxical and may have profound philosophical implications: Progressive evolution is due to relaxation of selection [the general idea can be traced to S. Ohno's *Evolution by Gene Duplication* (1)]. The authors express a hope that “[i]n the very near future, we will experience an enormous proliferation of phylogenetically well-distributed genomic data” (p. 1404), which will allow testing of this model. They propose one general prediction that follows from this model: “carnivores should exhibit the genomic hallmarks of population-size reduction compared with related herbivores” (p. 1404) (because population size decreases with the elevation of trophic level and with the increase of body size).

However, this test is already available. The important genomic hallmark of population-size reduction, according to this model, is the enlargement of the genome caused by propagation of transposable elements and duplication of genomic segments. Therefore, carnivores and, generally, larger animals should have the larger genomes. However, comparison of genome sizes in four well-studied mammalian orders, differing in trophic level and body size (carnivores, artiodactyls, insectivores, and rodents) shows quite the opposite picture (2). Thus, rodents (low trophic level, small body size) have larger genomes than carnivores (high trophic level, moderate/large body size): 0.539 ± 0.007 versus 0.478 ± 0.025 , respectively (Mann-Whitney, $P < 10^{-3}$). Insectivores (high trophic level, small body size) also have larger genomes than carnivores: 0.553 ± 0.013 versus 0.478 ± 0.025 , respectively ($P < 10^{-6}$). Artiodactyls (low trophic level, large body size) have smaller genomes than rodents: 0.508 ± 0.026 versus 0.539 ± 0.009 , respectively ($P < 0.1$). Thus, both the effect of trophic level and body size argue against Lynch and Conery's model. By reverse inference, this test supports the adaptive interpretation of genome enlargement.

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References

1. S. Ohno, *Evolution by Gene Duplication* (Springer-Verlag, Heidelberg, Germany, 1970).
2. The raw data are taken from the Animal Genome Size Database (www.genomesize.com/) and are presented in log-transformed picograms.

Response

WE THANK VINOGRADOV FOR HIS COMMENTS

on our Report, in which we called attention to the population-genetic mechanisms that may have been responsible for the dramatic genomic reorganization that occurred in the stem eukaryote and the subsequent modifications experienced in lineages of multicellular species.

As a possible means to test the theory further, we somewhat cavalierly suggested comparisons of related carnivore and herbivore species, invoking ecological reasoning that suggests that the former should generally have reduced effective population sizes. Although Vinogradov argues that our theory is not supported in mammalian species, there are several concerns with his analysis.

First, the Animal Genome Size Database (AGSD) contains multiple entries for several species and numerous genera are represented by more than one species. Moreover, given the close relationships of the members of individual lineages relative to the time scale of genomic evolutionary events, the data employed cannot be regarded as phylogenetically independent. Because the true lineage-specific means may be substantially different than the estimates presented, and the standard errors will certainly be much larger, no conclusions on the importance of selection can be derived from the data as presented.

Second, a more thorough test would ideally consider issues such as intron number and size and mobile-element abundance, rather than focus on the less illuminating measure of total genome size. We certainly do not rule out adaptive evolution as a mechanism in genome evolution, and it is conceivable that the evolution of carnivory promotes the expansion of genome size through the proliferation of various gene families that facilitate this way of living.

Third, the theory that we present is meant to explain broad patterns. Because evolution and population dynamics are stochastic processes, we expect to find significant scatter around the general expectations, and ample evidence of this can be found in our Report. Thus, the above caveats aside, work of this sort should be based on multiple independent contrasts between herbivores and carnivores, large- and small-body-sized species, and so forth.

Finally, there is a real need to formally evaluate, with molecular marker data, whether carnivores do in fact have reduced effective population sizes. This is a potentially significant issue in mammals, where groups with different dietary habits can also have rather different mating systems and population dynamics.

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CORRECTIONS AND CLARIFICATIONS

News of the Week: “Japan ponders starting a global journal” by D. Normile (12 March, p. 1599). Shin Ichi Murahashi was incorrectly identified in the story. He is a professor of chemistry at Okayama University of Science and professor emeritus at Osaka University.

News of the Week: “In sex reversal, protein deterred by nuclear barrier” by A. Sreenivasan (19 Dec., p. 2050). The article described work by David Jans and colleagues demonstrating for the first time that specific mutations in the SRY protein prevent it from binding to importin β or calmodulin, and that this, in turn, impairs the import of SRY into the nucleus. These and other mutations in SRY had previously been linked to a rare syndrome in which babies are born with a male set of chromosomes and female sexual organs. The article stated that the Jans group's work is the “first demonstration that a clinical syndrome can be caused by a molecule's inability to get into the nucleus.” However, Michael Weiss and colleagues reported in 2001 that a specific SRY mutation impairs the molecule's ability to enter the nucleus, and concluded that “these results provide the first example of impaired organogenesis due to a nuclear localization signal mutation” (*J. Biol. Chem.*, 7 Dec. 2001, p. 46480).

TECHNICAL COMMENT ABSTRACTS

COMMENT ON “Oceanic Rossby Waves Acting as a ‘Hay Rake’ for Ecosystem Floating By-Products”

Peter D. Killworth

The recent suggestion by Dandonneau *et al.* (Reports, 28 November 2003, p. 1548) that apparent waves in ocean color are actually caused by the sensor response to particles swept into convergence zones by Rossby waves is called into doubt, through a demonstration that surface particles in such waves do not move into (propagating) convergence zones.

Full text at

www.sciencemag.org/cgi/content/full/304/5669/390b

RESPONSE TO COMMENT ON “Oceanic Rossby Waves Acting as a ‘Hay Rake’ for Ecosystem Floating By-Products”

Yves Dandonneau, Christophe Menkes, Thomas Gorgues, Gurvan Madec

In his comment, Killworth asserts that floating particles should not concentrate in Rossby wave-induced convergence zones if the Rossby waves propagate faster than the time needed for effective concentration. Observed conditions in our study area in the Southeast Pacific show that in that area, concentration is generally possible, lagging the maximum of convergence by $\pi/4$.

Full text at

www.sciencemag.org/cgi/content/full/304/5669/390c