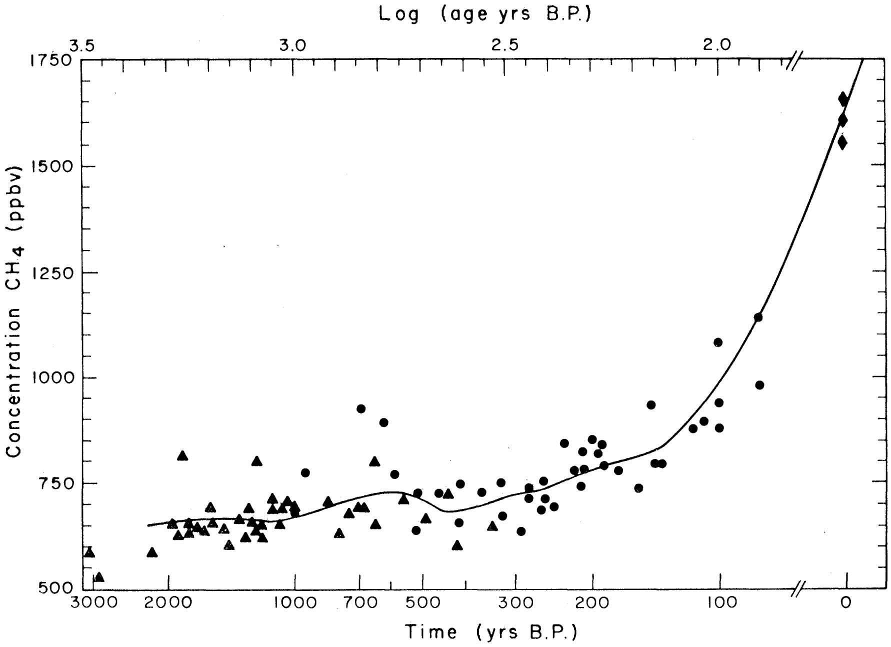
Doubling of Atmospheric Methane Supported

The apparent doubling of methane during the past few hundred years suggests that the current increase will continue, adding to the greenhouse warming

Recent analyses of Greenland and Antarctic glacial ice suggest that something, presumably humankind, has upset a system of geochemical recycling that had kept atmospheric methane concentrations steady for at least 25,000 years. The observed increase of the past few years is apparently the most recent part of a rise that began only a few hundred years ago and has since doubled atmospheric methane abundances. Aside from helping to push the delicate balance of atmospheric chemical interactions out of kilter, the methane increase will mean an even larger greenhouse warming when the amount of atmospheric carbon dioxide doubles in the next century.

Analyses of two kinds of samples have suggested a long-term, continuing growth of atmospheric methane. Five different research groups have analyzed air, collected mainly since 1978, and found a methane concentration of about 1.5 parts per million by volume, which is increasing at a rate of 1 to 2 percent per year. Without a longer record, no one could tell whether that was something to worry about or just a short-term fluctuation about a steady mean concentration. To find out, researchers analyzed air samples that had been "collected" hundreds and thousands of years ago. Fallen snow on glaciers in Greenland or Antarctica slowly compresses under its own weight until it turns into solid ice, trapping tiny bubbles of air as it does so. Drilling down into a glacier is like reaching back in time.

In ice from Greenland containing air ranging from 500 to 27,000 years old, Harmon Craig and C. C. Chou of the Scripps Institution of Oceanography found a methane concentration of only about 0.7 part per million, about half the present value. They found increasingly higher values in younger ice, up to 1.25 parts per million in ice containing 25-year-old air.



The end of natural control of atmospheric methane

The concentration of atmospheric methane (CH_4)*, as determined from analysis of air bubbles trapped in glacial ice, began rising sharply a few hundred years ago after at least 27,000 years of stability. These analyses of Antarctic (triangles) and Greenland (circles) ice cores (expressed in parts per billion by volume) by R. Rasmussen and A. Khalil of the Oregon Graduate Center show methane concentrations to have been roughly constant for almost 3000 years. Less than 200 years ago they began a sharp increase. The triangles represent analyses of present-day air. The exact timing of the increase has not been determined to the satisfaction of all analysts, but its general coincidence with a sharp increase in human population suggests that environmental alterations—everything from forest clearing and rice cultivation to smokestack pollution—are probably involved.*

Earlier workers had assumed that low values reflected a loss of methane during or shortly after ice formation, but in recent work Craig and Chou have seemingly eliminated one of the two more likely routes for methane losses. The exponential decrease in methane content of the ice with increasing age might have reflected the diffusion of methane from the ice. To check this possibility, Craig and Chou encased some cores in gas-tight containers immediately after coring in order to catch all of the core's helium, a lighter gas that moves through ice far more readily than methane. The protected samples showed that the ice had lost no helium, and thus by inference no methane, during compression of the snow into ice.

Another possible loss mechanism is biological. Certain microbes live by oxidizing methane to carbon monoxide. If they could survive in the ice, they would have plenty of time to consume half the methane there. That "seems very unlikely," says microbiologist Mary Lindstrom of the University of Washington, "but it can't be ruled out." Everything would be working against such microbes. The temperature is below freezing, as cold as −20°C. There is no evidence of pockets of liquid water, an essential requirement for any bacteria thriving in ice. And it is not certain that any methane-oxidizing microbe can make use of methane at such low concentrations, even under the best of conditions. Despite the remote possibility of a biological drain on ice methane, analysts are urging further study. A check of the carbon isotopic composition of the methane in older ice will help to determine if microbes have been at work.

Analyses of 80 ice core samples by Reinhold Rasmussen and Aslam Khalil of the Oregon Graduate Center have drawn a more detailed picture of the methane increase. Like Craig and Chou, they found about 0.7 part per million methane in ice that was up to 3000 years old, in their case samples from both Greenland and Antarctica. Methane concentrations did start creeping up about 300 years ago, but the rapid increase did not begin until about 180 years ago, according to their best interpretation of the ages of the ice samples. This was about the time that world population began skyrocketing, they point out. Craig and Chou, on the basis of fewer samples and a different interpretation of ice core ages, have reported that the increase began about 400 years ago.

Except for the suggestion of population-related environmental pressures, researchers still do not know what is behind the methane increase. If the strongly oxidizing atmosphere of Earth had its way, there would be no methane at all, but bacteria-mediated fermentation of organic matter under low oxygen conditions manages to produce hundreds of millions of tons of this reduced form of carbon each year. The problem for researchers is that such fermentation goes on everywhere from termite guts (there may be more termites with increased forest clearing), to rice paddies (which have been expanded to feed a larger population), cows' stomachs, and natural wetlands. Biomass burning and natural gas leakage contribute as well. Part of the methane increase could even be a response to its reduced removal from the atmosphere by hydroxyl radical, whose abundance might be decreased by reaction with pollutants. All these mechanisms—both those that can add more methane and those that can slow its removal—are plausible and are now behaving so as to increase methane, so most researchers suspect that a combination of them is responsible.

The causes of the increase remain obscure, but at least one of its effects seems clear. Craig and Chou have calculated that, to the extent that any estimates of greenhouse warming are reliable, the methane increase has warmed the atmosphere "0.23°C over the past 400 years, and at the current rate of increase the warming due to methane is about 38 percent of the carbon dioxide warming effect." Methane's greenhouse effect is beginning to rival the collective effect of the chlorofluorocarbons (second behind the effect of carbon dioxide), and the cumulative effect of all trace gases is thought to equal that of carbon dioxide (*Science*, 24 June 1983, p. 1364). Ironically, the additional methane may be helping to protect stratospheric ozone from destruction by chlorofluorocarbons.—**Richard A. Kerr**

Additional Reading

1. H. Craig and C. C. Chou, *Geophys. Res. Lett.* **9**, 477 (1982).
2. M. A. K. Khalil and R. A. Rasmussen, *Chemosphere* **11**, 877 (1982).
3. R. A. Rasmussen and M. A. K. Khalil, *J. Geophys. Res.*, in press.

Frog Genes Jump Species

The discovery a year ago (*1*) of populations of a species of European mouse, *Mus musculus*, whose cells contained the mitochondrial DNA of a neighboring species, *Mus domesticus*, constituted a warning to biologists that an organism's genetic package might not always be what is reasonably expected of it. A second clear example of this type of mixing of genomes has now been brought to light, again in Europe, this time among species of water frogs (*2*). The warning becomes yet more intense that systematists who utilize molecular data to reconstruct genealogies must exercise extreme caution in selecting their raw material.

Mitochondrial DNA has a number of peculiarities, some of which are responsible for this occasional aberrant state of genomic affairs. These include being present in many copies per cell, evolving five to ten times faster than chromosomal DNA, and being maternally inherited. When male and female gametes meet they each contribute half of the chromosomal DNA, but only the egg contains mitochondria that become established in the developing embryo. The high rate of evolution of mitochondrial DNA makes it very useful in molecular tracing of genealogies, especially in the short term. But the mode of inheritance clearly restricts available information to maternal lineages. It is also the maternal mode of inheritance that can, under the right circumstances, lead to the introgression of one species' mitochondrial DNA into the cells of another.

When populations of different but related species are geographically contiguous, a hybrid zone sometimes arises, in which cross-species reproduction gives rise to more or less viable hybrids. In the case of the above-mentioned mice, it is postulated that the present-day *musculus* individuals that contain *domesticus* mitochondria arose from the mating of a female *domesticus* and a male *musculus*, the offspring of which backcrossed with *musculus* mates, thus diluting out the *domesticus* chromosomal genome while the mitochondrial genome was retained (through the female line at least). The Central European water frog case, which is reported by Christina Spolsky and Thomas Uzzell of the Academy of Natural Sciences of Philadelphia, is similar but has important differences that arise from the special biology of these animals.

Spolsky and Uzzell analyzed by restriction enzyme fragmentation the mitochondrial DNA from two water frog species, *Rana ridibunda* and *R. lessonae* from Poland. Although 59 percent of *R. ridibunda* individuals had typical *ridibunda* mitochondrial DNA, designated type A, 41 percent had a distinctly separate mitochondrial genome, type B, which differed by about 8 percent of its nucleotide sequence. The mitochondrial DNA in *R. lessonae*, type C, was virtually identical to *R. ridibunda*'s type B, differing by 0.3 percent of sequence, and seemed to be the source of it. The question was, how did this arise?

Natural hybrids between the two species produce a third species, *R. esculenta*, which nearly always has *lessonae* mitochondria and has the peculiarity of producing only *ridibunda* gametes; the *lessonae* genome is always lost. This process is known as hybridogenesis and is a form of clonal reproduction. Mating between two *esculenta* will therefore produce offspring that are *ridibunda* in their chromosomal genomes and probably *lessonae* in their mitochondria. Although this is one way in which the chromosomal/mitochondrial hybrids observed by Spolsky and Uzzell might arise, they often suffer from deleterious effects of recessive genes that are otherwise masked. *Rana ridibunda* individuals with *lessonae* mitochondria more likely arise through the crossing of a male *ridibunda* with a female *lessonae*. Because the *ridibunda* type B mitochondrial DNA has detectably diverged from *lessonae* type C, Spolsky and Uzzell guess that the event that led to the establishment of the chromosomal/mitochondrial genomic hybrid occurred either some while ago or geographically distant from where they sampled the populations.—**Roger Lewin**

References

1. S. Ferris *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* **80**, 2290 (1983).
2. C. Spolsky and T. Uzzell, *ibid.* **81**, 5802 (1984).