PERSPECTIVES: PALEOCLIMATE

"Frozen" Methane Escapes from the Sea Floor

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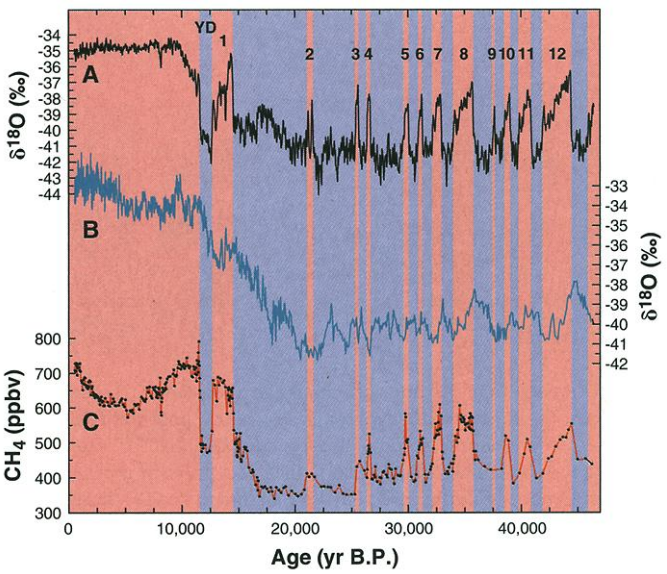
In the late 1980s, ice core records revealed that the drastic climate changes from glacial to warm periods occurring roughly every 100,000 years are paralleled by a rapid increase in the atmospheric concentration of the greenhouse gas methane (CH_4) (*1*, *2*). Initially, these increases were attributed to bacterial processes in wetland environments. Nisbet (*3*) provided an alternative interpretation, based on the enormous amounts of methane stored in permafrost and continental margins in the form of hydrates. He suggested that a massive release of this methane could trigger climate change from glacial to interglacial. On page 128 of this issue, Kennett *et al.* (*4*) provide evidence that fast climate change is indeed associated with the release of methane from hydrates in the Santa Barbara Basin off the California coast.

At high pressure, low temperature, and sufficiently high gas concentration, water molecules form clathrates (also called hydrates), cage structures in which gas molecules are trapped. Huge quantities of methane are stored in this form in the permafrost of polar regions and in sediments of continental margins. How much methane is stored in this way remains highly speculative, with best estimates ranging from 1 to 2 × 10^{19} g of methane, about 4000 times today's atmospheric burden. The very negative carbon isotopic composition ($\delta^{13}C$) of this methane indicates that most of it is produced biogenically, rather than by thermal alteration of organic matter in deeper sediments (*5*).

Gas hydrates are metastable; increased temperature or reduced pressure destabilizes the structure, leading to release of the trapped gas. Today, the major natural source of atmospheric methane is bacterial decomposition in wetland environments (*6*, *7*), and methane hydrates are only a minor source. But it is possible that they have been more important in the past, during the dramatic climate shifts that have characterized the Late Cenozoic (past 65 million years) (*8*).

During the last glacial period, episodes of warmer climate are seen in the temperature records of Greenland ice cores. These warmings (called Dansgaard-Oeschger events) are abrupt and last from several centuries to a few millennia (*9*). Atmospheric methane variations parallel the Greenland warmings, with higher methane concentrations during warm periods (see the figure) (*10*). Dansgaard-Oeschger events are linked to changes of the North Atlantic Thermohaline Circulation (*11*) and therefore affect large portions of the world's climate.



Tracking methane and climate change. $\delta^{18}O$ records, a proxy for temperature, from the GRIP ice core (**A**) (*9*) and from Byrd station, Antarctica (**B**) (*17*). Methane record from GRIP (**C**) (*10*). YD indicates the Younger Dryas; numbers 1 to 12 indicate Dansgaard-Oeschger events.

Kennett *et al.*'s climate record from the Santa Barbara basin covers the past 60,000 years (*4*). The record, which covers both planktonic (surface) and benthic (bottom-dwelling) foraminifera, shows that surface and bottom water temperatures (today at 580-m depth) change in concert with Greenland temperature. Surprisingly, the bottom water temperature leads the surface water temperature by up to 200 years. The benthic record shows the same features as the Greenland temperature record, with lower $\delta^{13}C$ during warmer periods. The low $\delta^{13}C$ values are indicative of biogenic methane from hydrates that were destabilized by the increased water temperature during interglacials. In general, the $\delta^{13}C$ excursions are limited to the benthic foraminifera, indicating that the methane released from hydrates was entirely oxidized in the water column and did not reach the sea surface. Only at the start of Dansgaard-Oeschger events 8 and 11 are spikes of low $\delta^{13}C$ values also present in planktonic foraminifera, which monitor sea surface conditions. Kennett *et al.* suggest that it was huge releases of methane, as a result of sediment slope failure deroofing gas hydrates, that caused these low $\delta^{13}C$ spikes in the planktonic record.

This is the first direct evidence for methane release linked to past climate change. The record shows only four such events, but such events may well have happened in other places, especially during temperature increases. The inhomogeneity and brevity of catastrophic hydrate releases make it difficult to quantify the total release.

Catastrophic hydrate release has the potential to raise the atmospheric methane concentration tremendously (*3*). In contrast to CO_2, CH_4 is chemically removed from the atmposphere, resulting in an atmospheric lifetime of only ~10 years, one order of magnitude less than the atmospheric residence time of CO_2 (*12*). Therefore, elevated concentrations disappear within decades and it is difficult to detect such releases in ice core records with limited resolution. The high-resolution Greenland Ice-Core Project (GRIP) CH_4 record (*13*) shows an overshoot at the Younger Dryas termination compared with the early Holocene that followed (see the figure). This might be a result of a catastrophic methane release. Catastrophic hydrate release may be of some importance in the rapid increase of methane during climate warmings. However, for hydrate releases to maintain an elevated atmospheric methane concentration, they would have to occur very regularly, which is unlikely. Wetland emission thus remains the first candidate for explaining the different methane concentrations in the past.

The succession of bottom warming

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followed by surface warming in Kennett *et al.*'s data suggests a potential lead of catastrophic methane release over Northern Hemispheric warming. Could methane have triggered the climate change from glacial to interglacial? Raynaud *et al.* (*14*) list several points against such an impact of methane. First, deglaciation in Antarctica started several millennia before the fast methane increase (see the figure) (*10*). Second, the contribution of methane to greenhouse warming is much smaller than the one from CO_2, which rises simultaneously with southern temperature (*15*). Further, the methane increase lags the drastic temperature increase in Greenland by up to a few decades (*16*).

Kennett *et al.*'s study shows that methane releases linked to climate change do occur. It is reasonable to assume that such methane release from hydrates intensifies during times of fast temperature increase. However, because of the diversity of the source and its dependence on parameters such as sea level and temperature changes linked to ocean circulation, it is difficult to judge its contribution to fast CH_4 increases in the climate record. The timing of climate and methane changes suggests, however, that methane did not play a more active role in past climate change than has been accounted for so far.

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NOTA BENE: DEVELOPMENT

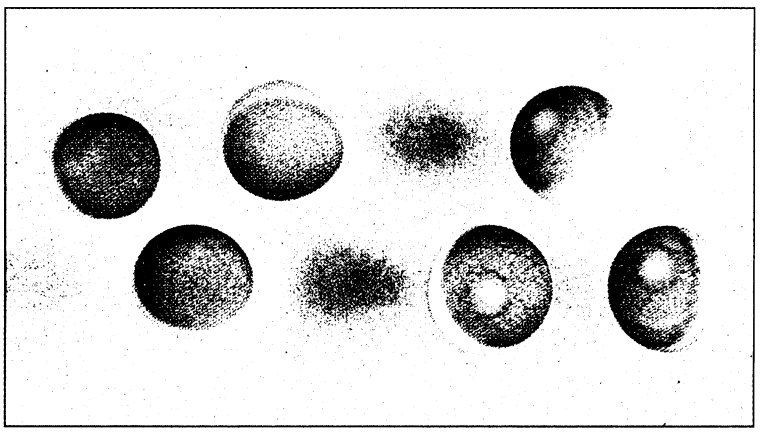
Awakening Aurora

The vertebrate oocyte is a veritable sleeping beauty, for it can remain slumbering in the G_2/M phase of meiosis for months or, in the case of humans, decades. In the frog *Xenopus*, the steroid hormone progesterone is the prince that awakens the oocyte, activating a signaling pathway that enables the oocyte to reenter the cell cycle and to mature into a sperm-responsive egg. Exactly how progesterone awakens the sleeping oocyte (see the figure) is not clear, but a recent report from Richter, Ruderman and their colleagues (*1*) reveals that an elaborate cast of characters helps progesterone in its quest.

Slumbering oocytes contain large stockpiles of ribosomes and mRNAs that encode proteins vital for oocyte maturation and for early development of the embryo after fertilization. Unlike mRNAs in somatic cells, which carry long tails of polyadenylic acid [poly(A)] and are readily translated into protein, these mRNAs have short, stubby poly(A) tails and are not translated. In response to gonadotrophin hormones, follicle cells surrounding the oocyte release progesterone, which binds to an unidentified receptor on the oocyte surface. This results in a rapid decrease in adenylyl cyclase activity, cyclic AMP levels and protein kinase A activity. But the next steps in the signaling pathway that awakens the oocyte are still shrouded in mystery.

Earlier work by the Ruderman group (*2*) on frog oocytes (favored because of their accessibility and large size) reported that activation of *c-mos* mRNA—which encodes the protein kinase Mos, a key component of the MAP kinase signaling pathway—required Eg2 (a serine/threonine kinase of the Aurora family). The researchers found that within 30 minutes of progesterone stimulation, Eg2 became activated through acquisition of a phosphate group (phosphorylation) and then somehow elicited the translation of *c-mos* mRNA into Mos, with subsequent activation of the MAP kinase signaling cascade. This cascade culminates in the activation of M-phase promoting factor (a complex of cyclin B and cdc2), leading to breakdown of the nuclear envelope and reentry of the oocyte into the cell cycle.

But exactly how does Eg2 elicit translation of *c-mos* mRNA? The Ruderman and Richter groups already knew the identity of the key character in the next chapter of the Aurora story: the cytoplasmic polyadenylation element binding factor (CPEB). In their new work (*1*), they discovered that CPEB was phosphorylated at a single site (serine-174) soon after progesterone stimulation but before translation of *c-mos* mRNA; phosphorylation of other CPEB sites occurred much later and depended on Mos activity. The investigators then demonstrated that Eg2 was responsible for the early phosphorylation of CPEB on serine-174, and that this in turn promoted the addition of a long poly(A) tail onto *c-mos* mRNA, resulting in its translation. They suggested that the later Mos-dependent phosphorylation of CPEB might result in its degradation, its task now being complete.



Next, the investigators plan to nail down the identity of the elusive oocyte progesterone receptor, discover the components that connect the receptor to the protein that activates Eg2, and find out how early phosphorylation of CPEB results in recruitment of the enzyme that adds a long poly(A) tail onto *c-mos* mRNA.

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