

OCEANOGRAPHY

The Atlantic heat conveyor slows

Detlef Quadfasel

Computer simulations predict that global warming will weaken the ocean circulation that transports heat from the tropics to higher latitudes in the North Atlantic. Such an effect has now been detected.

The Sun heats the tropics much more than the polar regions, but the resulting extremes of temperature are moderated by compensating heat circulation in the atmosphere and the ocean. Most notably, warm upper waters intrude far into the northern North Atlantic and contribute to the mild European climate. As Bryden *et al.* report on page 655 of this issue¹, that circulation has weakened over the past 50 years, providing worrying support for computer models that predict just such an effect in a world made warmer by greenhouse-gas emissions.

During their journey, the warm waters originating in the tropics release heat to the atmosphere and in consequence become denser. So they sink, and eventually return southwards at depth. This vertical 'overturning circulation' is driven by the north-south contrast in density and is thus vulnerable to processes affecting the densities at either end of the route. Besides changes in temperature, changes in salinity affect water density and so can alter the circulation. One consequence of global warming will be to inject more fresh water into the polar and sub-polar Atlantic², through enhanced precipitation, river run-off and melting of the Greenland ice cap. Increased input of fresh water reduces seawater density at high latitudes. Global atmosphere-ocean circulation models predict a slowdown of the ocean circulation in such circumstances³, with a consequent drop in temperatures over Europe of as much as 4 °C.

Bryden *et al.*¹ have analysed ocean temperature and salinity data, collected at intervals over the past five decades along a section at 25° N across the subtropical Atlantic. Their analysis provides the first observational evidence that such a decrease of the oceanic overturning circulation is well underway. Their approach is straightforward: the northward transport of water in the Gulf Stream system (the part concerned here being the Florida Current between the Gulf of Mexico and the Bahamas) has to be compensated by a return flow. This return flow consists of a wind-driven horizontal cell, which circulates clockwise in the subtropics, and the deep, southerly flow of the vertical overturning circulation (Fig. 1).

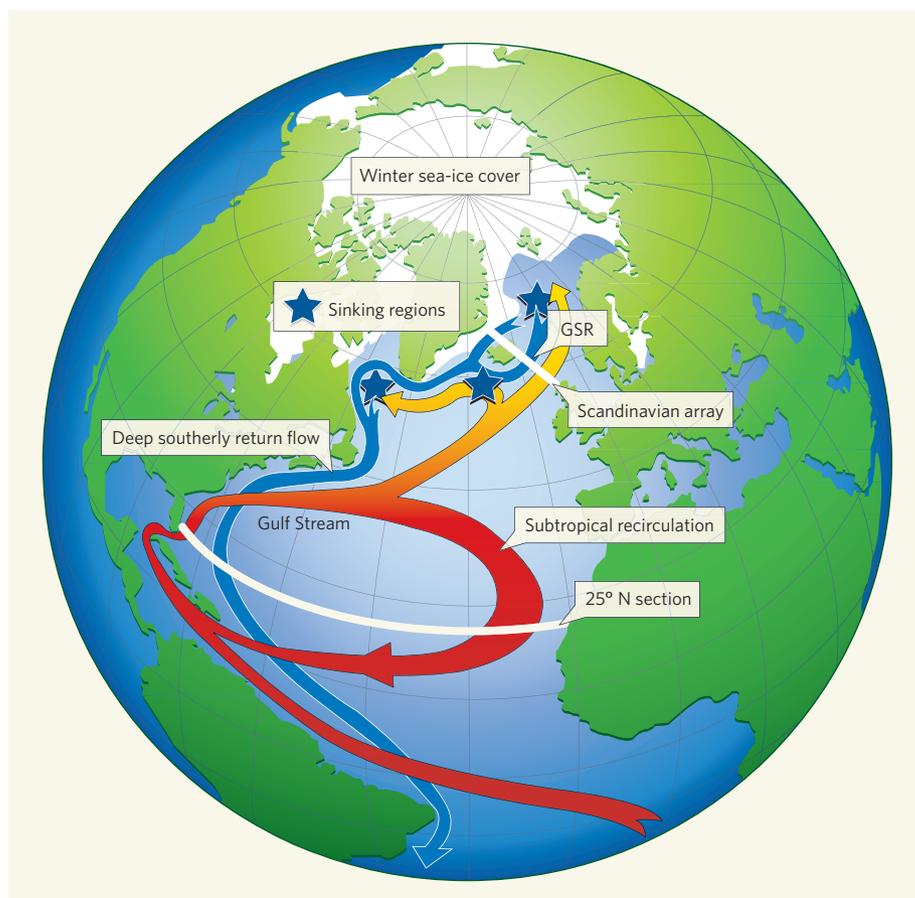


Figure 1 | The North Atlantic heat conveyor. Most warm waters in the upper ocean circulate clockwise in a giant horizontal swirl in the subtropics, but some flow farther north and cross the Greenland-Scotland Ridge (GSR). This branch warms the northern North Atlantic and Europe, and keeps most of the Nordic Seas free of ice. Here the water sinks (indicated by the star) and flows back southwards at depth, mostly down the western edge of the Atlantic basin. The Scandinavian monitoring array tracks only the northern limb of the overturning circulation, but more deep water is added south of the GSR and in the Labrador Sea (stars). The 25° N section covers all of the overturning circulation, and also includes the horizontal recirculation in the subtropics. According to Bryden and colleagues' results¹, the former is weakening and the latter strengthening.

Because of the large temperature difference between its upper and lower branches, the overturning circulation contributes about 90% to the oceanic south-north heat fluxes in the North Atlantic and is thus most significant for European climate and its variability.

Bryden and colleagues estimate the strength of these two circulation cells from

repeated observations of the oceanic density field. They apply the so-called thermal wind relation, in which the internal pressure field is calculated from the density distribution and balanced with the Coriolis force that arises when a fluid is moving on the rotating planet. The result is alarming: a significant shift from the vertical to the horizontal circulation cell

has occurred, with the vertical cell dominating until the early 1990s and the horizontal cell thereafter. Altogether, the overturning circulation has decreased by more than 30%, with the largest effect seen in the lower part of the deep water.

But how solid are these results? The findings are based on just five snapshots of the circulation, taken in 1957, 1981, 1992, 1998 and 2004, and along one latitudinal section. Higher-frequency variability (such as eddies or waves), at the ends of the section at the African coast and the Bahamas, may obscure the detection of long-term change. And the uncertainty of the estimates given is high, so the magnitude of the decline may well be smaller than suggested by the calculations. Against that, the declining trend itself is statistically significant. Also, the observed density structure of the deep waters has changed; this structure is not affected by short-term variability, and so supports Bryden and colleagues' conclusions.

Further support comes from other observations. Based on direct measurements of water flux, along with model calculations, Hansen *et al.*⁴ have reported a 20% reduction in the overflow from the Nordic Seas across the Greenland–Scotland Ridge into the deep North Atlantic over the past 50 years. These overflows contribute about one-third to the overturning circulation and feed the densest part of the vertical cell — the same part in which the largest reduction of water transport was observed at 25° N. At the same time, the overflow waters and in turn the deep waters of the North Atlantic have significantly freshened⁵, thereby reducing the large-scale density gradient driving the overturning circulation.

The implications of these observations are considerable. Palaeoclimate records show that northern air temperatures can drop by up to 10 °C within decades⁶, and that these abrupt changes are intimately linked to switches in the ocean circulation⁷. Increased freshwater input into the Nordic Seas will initially weaken the circulation only slowly. But when a certain threshold is reached, the circulation may jump abruptly to a new state in which there is little or no heat flux to the north. The system is highly nonlinear and will not immediately switch back to the warm mode when the freshwater input weakens.

Although most model studies agree on the way the overturning circulation will develop under global-warming conditions³, direct observations of the relevant fluxes of water volume and heat are still sparse. Scandinavian oceanographers are monitoring the northern limb of the vertical cell⁸, and a basin-wide array of moored temperature and salinity recorders has recently been deployed along the 25° N section⁹. Such observations, combined with modelling activities, are crucial for providing an early warning of a possible breakdown of the overturning circulation — which, if it occurs, would have devastating

effects on socio-economic conditions in the countries bordering the eastern North Atlantic. ■

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BIOPHYSICS

Assembly line inspection

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Many of the biochemical events that occur in a cell are performed by huge complexes of proteins and nucleic acids. A cunning approach promises to show how the components convene to make a functioning 'machine'.

The cell's macromolecular machines contain dozens or even hundreds of components. But unlike man-made machines, which are built on assembly lines, these cellular machines assemble spontaneously from their protein and nucleic-acid components. It is as though cars could be manufactured by merely tumbling their parts onto the factory floor. Knowing how cellular complexes organize themselves is crucial for understanding molecular evolution and for engineering materials that can mimic their properties. In this issue, Talkington and colleagues (page 628)¹ use isotopically labelled proteins and mass spectrometry to follow the assembly of one macromolecular complex — the 30S ribosome — in real time. The elegance of their experimental design should allow it to be adapted to a wide range of such complexes, offering a new approach to the study of cellular dynamics.

Ribosome assembly is fascinating, because its components must form a stable yet flexible platform for protein synthesis. The small (30S) subunit of the 70S ribosome found in bacterial cells consists of the 16S rRNA (1,542 nucleotides) and 20 unique proteins, which interact through highly specific interfaces (reviewed in ref. 2). Actively growing cells demand many thousands of ribosomes, whose synthesis consumes a large fraction of the cell's metabolic energy^{3,4}. So ribosome assembly must be efficient as well as precise.

More than 30 years ago, Nomura and his colleagues⁵ demonstrated that 30S ribosomal subunits could be made *in vitro* from purified proteins and 16S rRNA. By varying the order in which the proteins were mixed with the rRNA, a hierarchy of protein–RNA interactions was defined. This assembly 'map' explained the remarkable specificity of ribosome reconstitution, because only a few

proteins could bind to the naked 16S rRNA and initiate assembly. The binding of these primary initiating proteins then enable the next ones in the hierarchy to bind, and so on. Biochemical and crystallographic experiments showed that this cooperativity of assembly derives mostly from protein-induced changes in the structure of the 16S rRNA, rather than from direct protein–protein contacts (reviewed in ref. 6).

But to fully understand the dynamics of a macromolecular complex, one must follow its components in real time. Until now, the kinetics of 30S ribosome assembly has been studied by monitoring changes in the conformation of the 16S rRNA^{7,8}. Talkington *et al.* took a completely different approach, measuring the rate at which each protein is added to the 16S rRNA *in vitro*. They used a 'pulse–chase' strategy to introduce isotopically labelled proteins within a certain time window (Fig. 1). The 16S rRNA was incubated with a mixture of ribosomal proteins isolated from cells grown in ¹⁵N-containing media, and then excess ¹⁴N-labelled proteins were added (the 'chase'). Fully reconstituted 30S particles were purified to remove any nonspecifically bound proteins. Next, the ratio of ¹⁵N to ¹⁴N protein was measured by subjecting the entire mixture to MALDI–TOF mass spectrometry. Not only were most of the 20 proteins identified in the mass spectrum, but for each protein the ratio of ¹⁵N- to ¹⁴N-labelled polypeptide was accurately determined. By varying the length of the ¹⁵N pulse, the authors obtained rate constants for the association of 17 of the 20 proteins with 16S RNA.

This method of pulse–chase quantitative mass spectrometry (PC/QMS) cleverly sidesteps some of the technical problems that can plague studies of large macromolecular