

CLIMATE CHANGE

Aerosols heat up

Peter Pilewski

Solid particles suspended in the atmosphere have long played second fiddle to greenhouse gases as agents of climate change. A study of atmospheric heating over the Indian Ocean could provoke a rethink.

In the fourth assessment report of the Intergovernmental Panel on Climate Change (IPCC), released earlier this year, the effect on climate of aerosols — small, suspended particles of varying composition, size and shape — since the start of the industrial era was estimated to be about 20% of that of greenhouse gases¹. Aerosols are thought to have a cooling effect on the atmosphere, and therefore to have mitigated some of the expected global warming over this period.

This is, however, a highly uncertain conclusion, in part because the total amount and vertical distribution of solar radiation that is absorbed by aerosol particles is imperfectly known. In this issue, Ramanathan *et al.* (page 575)² report that the aerosol clouds above large regions of Asia actually cause as much warming as greenhouse gases — in contradiction, at first glance, to the notion of aerosol particles as a cooling agent.

The effect of aerosols and greenhouse gases on the climate is usually described as ‘radiative forcing’, an often-used but frequently misunderstood term. Simply put, it is the perturbation to the net rate of radiative energy flow in the atmosphere caused by atmospheric constituents such as clouds, aerosol particles or gases. Aerosol particles, for example, scatter solar radiation in all directions, so more solar radiation should be reflected back into space when aerosols are present. Thus, aerosol particles have a net cooling effect, and their radiative forcing is negative.

Radiative forcing is usually defined at the top of the atmosphere³, or more specifically, at the top of the troposphere (this is the lowest 8–12 km of the atmosphere, which contains most of the aerosol particles, clouds and water vapour). Thus calculated, radiative forcing is a useful parameter in climate modelling both because the globally averaged temperature at Earth’s surface responds linearly to forcing, and because a model’s response can be tested and compared in the absence of feedback mechanisms and independently of the forcing agent³.

But for aerosol particles that absorb radiation (for example, soot produced by combustion), top-of-atmosphere forcing tells only part of the story. When solar radiation is absorbed, it heats the atmospheric layer in which the particles

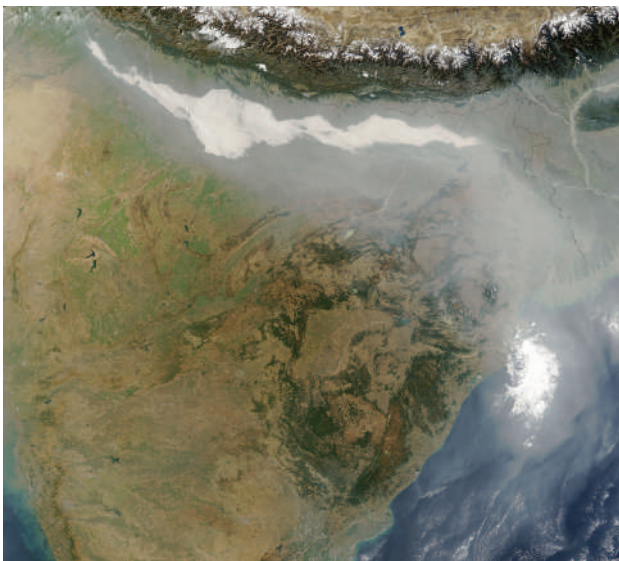


Figure 1 | Hazy days. Smog drifts down India’s populous Ganges valley and out into the Bay of Bengal. This is the source of ‘atmospheric brown clouds’ over the Indian Ocean, and the climatic effect of its constituent aerosol particles is investigated by Ramanathan and colleagues².

atmospheric column may still be cooling.

Ramanathan *et al.*² obtained the crucial data missing from model- and satellite-derived forcing estimates that are needed to determine the extent of this heating of the lower atmosphere. They deployed three small unmanned aerial vehicles (UAVs) carrying instruments to measure aerosol-particle concentrations, aerosol absorption and solar radiation near the remote Indian Ocean island of Hanimaadhoo, in the northern Maldives. Such UAVs are promising tools for airborne science, particularly for radiation studies in which simultaneous, vertically aligned observations are needed to examine the profile of radiative energy absorption. The small UAVs used by the authors were developed 15 years ago⁴ to measure parameters such as air temperature and pressure, and are used in much the same way that weather balloons are used to gather the data for forecast models. Unlike balloons, UAVs can be directed to probe specific regions of interest.

For their ‘Maldives autonomous campaign’ (MAC)², the authors let their UAVs fly in coincident vertical formations between 0.5 and 3 km above sea level throughout March 2006. This is the middle of the region’s annual dry season and is typified by low-level pollution moving from the Asian continent to the north-

Two distinct sets of results were identified during the campaign. The first half of March was dominated by a marine airmass, whereas in the second half air arrived from south Asia that had higher aerosol-particle concentrations and aerosol absorption. During this second, pollution-dominated period, atmospheric heating increased by more than 50%, a finding validated by model studies using data acquired at a climate observatory

on Hanimaadhoo. Most of the heating increase occurred in the visible part of the electromagnetic spectrum, confirming that the elemental carbon in soot was primarily responsible.

Although the direct observations occurred over a relatively small area and over a short period, they are representative of widespread plumes of pollution, known as atmospheric brown clouds, that blanket much of south Asia during the dry season (Fig. 1). To account for the variability of these plumes in time and space, Ramanathan *et al.* relied on satellites and a network of surface observations from an earlier study⁵ covering 2000–03. The regional variation in total aerosol concentration and absorption between pollution-dominated and pollution-free cases throughout this period was in close agreement with the detailed MAC study.

In addition, Ramanathan *et al.* determined how aerosol particles are distributed with altitude in the atmospheric brown clouds using data from the recently launched cloud-aerosol lidar and infrared pathfinder satellite (CALIPSO). CALIPSO revealed that the highest concentration of pollution is at altitudes between 1 and 3 km, again confirming the MAC flight measurements. The authors therefore infer that the MAC results are representative of the larger-scale regional forcing that affects global climate.

To assess the longer-term picture, Ramanathan and colleagues simulated heating caused by atmospheric brown clouds during the period 1950–2000 by imposing the estimated forcing during 2000–03 on the US National Center for Atmospheric Research’s general circulation model CCM3. They determined that warming due to greenhouse gas during that period was between 0.5 and 0.8 °C, about the same as that from the atmospheric brown clouds. The trend in total warming is an increase of about 0.25 °C per decade, twice the rate of warming at the surface, and it has been confirmed by satellite-based microwave measurements. These trends have substantial implications for the elevated region of the Himalaya, where observed warming of 0.15–0.3 °C during the past several decades

These findings² might seem to contradict the general notion of aerosol particles as cooling agents in the global climate system, but they also emphasize the importance of resolving how aerosol radiative forcing varies with altitude. Even though the global view depends on satellite- and ground-based observation networks, intensive studies from airborne platforms, which have become more versatile and efficient with the advent of UAVs, are essential for advancing climate research. Small fleets of UAVs could be used in other regions of the globe to examine the climatic impacts of, for example, regional pollution outflow from urban areas, airborne dust and effects from cloud–aerosol interactions.

A further perspective is that from space. In late 2008, NASA is scheduled to launch the Glory mission, which will fly an aerosol polarimeter sensor with advanced capabilities of retrieving aerosol particle information, including composition and absorption, not attainable from current space-based

instruments⁶. Together with ground- and air-based observations, Glory should help us to assess the contribution of aerosols to global climate. ■

Peter Pilewski is at the Laboratory of Atmospheric and Space Physics, University of Colorado at Boulder, Boulder, Colorado 80309-0590, USA. e-mail: peter.pilewski@colorado.edu

1. Forster, P. *et al.* in *Climate Change 2007: The Physical Science Basis. Fourth Assessment Report of the Intergovernmental Panel on Climate Change* http://ipcc-wg1.ucar.edu/wg1/Report/AR4WG1_Pub_Ch02.pdf (2007).
2. Ramanathan, V. *et al.* *Nature* **448**, 575–578 (2007).
3. Ramaswamy, V. *et al.* in *Climate Change 2001: The Scientific Basis. Contribution of Working Group I to the Third Assessment Report of the Intergovernmental Panel on Climate Change* (eds Houghton, J. T. *et al.*) 349–416 (Cambridge Univ. Press, 2001).
4. Holland, G. H. *et al.* *Bull. Am. Meteorol. Soc.* **82**, 889–901 (2001).
5. Chung, C. E., Ramanathan, V., Kim, D. & Podgorny, I. A. *J. Geophys. Res.* **110**, doi:10.1029/2005JD006356 (2005).
6. Mishchenko, M. I. *et al.* *Bull. Am. Meteorol. Soc.* **88**, 677–691 (2007).

persisted for weeks to months. In general, there was no discernible pattern of abundant species or temporal mode of acquisition of particular organisms in different individuals. The two infants whose microbiotas were the most similar to each other were fraternal twins. These babies share both similar genetics and a similar environment. But their microbial profiles were no more like those of their own parents than they were to those of the parents of the other infants, implying that environment may play a greater role than genetics.

To try to identify the origin of the early colonizers, Palmer *et al.* investigated two relevant sources — the microbiotas of maternal vaginal fluid and of breast milk. The lactobacilli that predominate in the vaginal microbiota were not abundant in the early faecal samples, and the bacterial sample of only one infant ‘clustered’ with the vaginal microbiota of its mother, and then only during the first day after birth. So it seems that vaginal birth does not make a lasting contribution to an infant’s intestinal microbiota. All babies in this study were breast-fed to some extent, but their intestinal microbiotas did not cluster with those of their mother’s milk. Surprisingly, bifidobacterial species turned out to be only minor components: it is generally accepted that these bacteria are abundant in the stool samples of breast-fed infants, and that they are beneficial to their host.

Although the early microbiota of the gut seems largely to result from chance microbial encounters, by one year old there was a consistent convergence towards that of an adult-like microbiota, often coinciding with the introduction of solid food. Therefore, despite the absence of a programmed succession of early organisms, factors such as diet, gut development and environmental changes (possibly induced by the early colonizers) eventually result in the stable colonization of characteristic members of the adult microbiota. A notable exception was the lack of methanogenic archaea in the one-year samples. These organisms are abundant in the adult intestinal microbiota⁷, where they consume methane produced by bacterial members.

Palmer and colleagues’ methods¹ could be used to identify differences in the microbiotas of specific groups of infants and young children. A couple of examples suggest themselves.

First, an aspect only briefly mentioned in this paper is the effect of antibiotic treatment on microbial composition: although some antibiotics severely reduced the microbial load, the authors did not identify any consistent consequences of such treatment. Given the frequent use of antibiotics in children, this is a topic well worth following up with more focused and comprehensive analyses.

Second, it has been proposed that the increased prevalence of chronic inflammatory disorders in industrialized countries is associated with improved sanitation resulting in a reduced microbial burden, or with reduced

MICROBIOLOGY

The inside story

Laurie E. Comstock

The human intestine is home to trillions of bacteria. Investigation of the colonization of the infant gut by these microorganisms is a prelude to understanding how they may act in both health and disease.

At birth, babies emerge from a sterile environment into one that is laden with microbes. The infant’s intestine then rapidly becomes home to one of the densest populations of bacteria on Earth. Writing in *PLoS Biology*, Palmer *et al.*¹ report the most comprehensive analysis to date of the bacteria that first take up residence in the human intestine.

Interest in this ecosystem stems in part from the discovery of numerous benefits that arise from our intestinal microbiota: these bacteria help in extracting nutrients from food, and are instrumental in the development of the gut^{2,3} and the immune system⁴ after birth. However, gut microbes have also been linked to several disease states, including inflammatory bowel diseases and colon cancer, and less directly to maladies such as asthma, rheumatoid arthritis, atopic dermatitis and even autism^{5,6}. An accurate and comprehensive analysis of the microbes present in the developing microbiota of the infant is an essential first step towards understanding which of them may affect the health of the host.

Palmer *et al.*¹ analysed the microbial composition of the intestinal ecosystem of 14 infants by sampling their faeces. Sampling began with the first stool after birth, and was followed by 25 further samples from each infant over

quantifying the bacterial composition avoided the need to culture the bacteria. It involved use of a comprehensive DNA microarray that differentiated and quantified the distinct taxonomic groups present in the samples.

There are 22 broad taxonomic groupings, or phyla, of bacteria, but the bacteria abundant in the infant intestine fell into only three of them: the Gram-positive bacteria (Firmicutes and Actinobacteria), the Bacteroidetes and the Proteobacteria. Given the broad nature of these taxonomic groupings, the results are not entirely surprising — most of the bacteria known to associate with humans fall into these three major groupings. A previous analysis of the intestinal microbiota of healthy adults demonstrated the abundance of only two of these three phyla⁷, with members of the Proteobacteria being only minor components. Proteobacteria are facultative anaerobes — that is, they can grow in the presence or absence of oxygen. They may be early settlers that are necessary to create the reduced environment required for the ensuing colonization by obligate anaerobes, which require oxygen-free conditions.

Contrasting with the similarity in the infants’ microbiota at the phylum level, Palmer *et al.* found a remarkable degree of species-level variation, especially during the first few months.