The more weakly a particle interacts, the earlier it detaches itself from the primordial plasma. Weakly interacting neutrinos, for instance, decoupled when the Universe was only about a second old. Because the gravitational force is so very small in the realm of elementary particles, the interaction of gravitational waves with the primordial plasma is negligible — they have been propagating freely ever since they were generated. In particular, gravitational waves produced during the Big Bang would carry a genuine picture of the Big Bang itself, providing information that no other messenger can carry.

LIGO, together with its European counterpart VIRGO near Pisa, Italy, is the most ambitious project to date to search for gravitational waves. It consists of three detectors, two on a site in Washington (Fig. 1) and one, 3,000 kilometres away, on a site in Louisiana. The passage of a gravitational wave would cause a tiny delay in the passage of laser beams reflected up and down LIGO's 4-kilometre-long detector arms. Although LIGO has not made a positive detection of gravitational waves, the upper bound on the intensity of a random background is an interesting result in its own right.

The strength of the gravitational-wave background is quantified by its energy density, ρ_{gw}. In cosmology, there is a natural unit for energy density, the critical density for 'closing' the Universe, ρ_c. If the Universe's density is greater than ρ_c, the force of its own gravity will at some point cause it to begin contracting, ending in a reverse of the Big Bang, the Big Crunch; if, however, it is smaller than this critical density, the Universe's expansion will continue unchecked for ever. It is thus convenient to use the 'normalized' energy density, $\Omega_{gw} = \rho_{gw}/\rho_c$. LIGO's latest upper bound[1] for the stochastic gravitational-wave background is $\Omega_{gw} < 6.5 \times 10^{-5}$.

This experimental limit is interesting because it represents a sensitivity at which current models of cosmology tell us the detection of gravitational waves is not excluded. Upper bounds on Ω_{gw} can be deduced from various astrophysical and cosmological observations[3]. In the frequency range accessible to LIGO, the most important limit comes from the production of light elements other than hydrogen in the first few minutes of the Universe, known as Big-Bang nucleosynthesis. The abundance of these light elements is fixed by the balance between the rate of the nuclear reactions that produce them and the expansion rate of the Universe, which dilutes them.

The latter rate is determined, through the equations of general relativity, by the total energy density of the Universe. This consists of the energy density carried by the known elementary particles, plus the energy density carried by any other more exotic form of matter — or indeed by gravitational waves. When only the known elementary particles are included in the computation, theory and observation agree beautifully. The energy density of any other

extra particle, and of gravitational waves, at the epoch of nucleosynthesis, is then constrained in order not to spoil this agreement. This puts an upper bound on Ω_{gw} at the level of a few times 10^{-5}, which is comparable to LIGO's new upper bound[1].

Certain cosmological models predict values of Ω_{gw} that could be almost as large as is allowed by the nucleosynthesis bound. In particular, a pre-Big-Bang model that includes the low-energy effects of string theory[4] predicts a stochastic background of gravitational waves that, for some values of its input parameters, approaches this bound[5]. Such cosmological models are thus now seeing experimental constraints.

The data from LIGO's S4 run that have now been published[1] were taken over a period of one month, between February and March 2005. The duration of the data-taking is a major factor because of the way the stochastic background is extracted by correlating the data of two detectors. This procedure allows the gravitational-wave signal to be extracted from the much greater effect of noise local to the detectors — laser fluctuations, seismic rumblings and so on. This signal-to-noise

ratio scales as the square-root of the total observation time.

LIGO is now engaged in its fifth period of data-taking (S5), which will collect one year of coincident data between its detectors, with an improved sensitivity over the S4 data[1]. The combination of better sensitivity and the longer run is expected to improve the sensitivity to Ω_{gw} by a factor of a further 10–100. In a few years, an upgrade of the experiment, known as Advanced LIGO, should eventually reach sensitivities between 10^{-8} and 10^{-9}. That should allow us to penetrate deep into a totally unknown region, where the answers to fundamental questions could well be waiting. ■

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DISEASE ECOLOGY

The silence of the robins

Carsten Rahbek

A continent-wide analysis suggests that West Nile virus has severely affected bird populations associated with human habitats in North America. The declines parallel patterns of human disease caused by the virus.

Scenes reminiscent of those described in Rachel Carlson's *Silent Spring*[1] have been occurring in suburban America. This time, it is not pesticides that are to blame for a decline in bird populations, but outbreaks of West Nile virus[2]. A study by LaDeau and colleagues[3] on page 710 of this issue shows that reductions in bird populations correlate with the prevalence of the virus, that these patterns are upheld across years and throughout the continent, and that the patterns are geographically correlated with epidemics of human infection by West Nile virus*.

West Nile virus emerged in New York City from the Old World in 1999, and then spread rapidly across the entire continent. The primary hosts of the virus are birds, in which virus numbers are also amplified before the virus is transmitted by mosquitoes to the next victim. Besides birds, the virus can infect other vertebrates, including humans, and has caused the death of as many as 1,000 people[4] in the United States alone, as well as uncounted casualties in birds and other vertebrates[2,4] (Box 1).

LaDeau and colleagues have dealt with several analytical challenges to demonstrate that West Nile virus is indeed the main factor behind the observed large-scale declines in bird populations. Continent-wide fluctuations of this kind have been documented previously[5,6], but they have been explained by changes in the local environment related to habitat, land use and climate. LaDeau and colleagues had to disentangle virus-induced mortality from these confounding effects.

To do so, they designed species-specific predictive models based on knowledge of the prevalence of the virus, exposure to mosquitoes and overall mortality for 20 different bird species, each species representing a specific combination of urban (human) association and susceptibility to the virus. The model was applied to 26 years of population data for six geographical regions to construct probability distributions for the expected abundance of each bird species in a given region before and after the arrival of the virus.

The results are revealing: significant population changes in seven of the 20 species were in agreement with specific expectations

*This article and the paper concerned[3] were published online on 16 May 2007.

Box 1 | West Nile virus in the Old and New Worlds

West Nile virus was first isolated in 1937 in the West Nile province of Uganda[10], an area known for other mosquito-transmitted diseases such as malaria, schistosomiasis, dengue and yellow fever. It has apparently only recently caused serious illness among humans[11], and largely outside the tropics.

The first documented human epidemic occurred in Israel in 1951–54, with another in 1957. Major outbreaks occurred in South Africa (1974) and Israel (2000),

with minor incidences in France (1962), Algeria (1994), Romania (1996) and Russia (1999), but only one in central Africa (1998).

Following its detection in the New World in 1999, West Nile virus spread quickly[9] during the dry summer of 2002, and now occurs throughout North and Central America, and in the Caribbean[4]. It has killed individuals of almost 200 bird species in North America, as well as other wild and domestic animals[2,4]. By contrast, it seems

that infected Old World birds rarely show adverse symptoms[12].

The Old World human epidemics have generally been local and short-lived. But, as is the case with birds, the human effects of the virus in the New World are much more severe. Between 1999 and 2006, 23,974 cases were reported in the United States: 14,125 were of the mild West Nile fever, and 9,849 of the severe West Nile meningitis or encephalitis (inflammation of the spinal cord and brain),

including 962 deaths[4]. There is currently no vaccine for humans.

The different effects of West Nile virus in the Old and New Worlds could be an example of host–parasite coevolution, in which the virus has coevolved with birds and humans in tropical Africa in particular, and so has a less lethal effect on its hosts[12]. If so, evolutionary adaptation might occur among New World species, which will minimize the virus's future impact. **C.R.**

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based on the direct adverse impact of virus infections. Although this may seem a modest effect, LaDeau and colleagues' analyses deliberately included tolerant bird species that were unlikely to be greatly affected for various ecological reasons. For the species thought to be susceptible to West Nile virus, there was a disturbingly consistent general relationship between the predicted effects of the virus and the observed declines in population abundance. The correlation was far from perfect. But it suggests that West Nile virus could potentially change the composition of bird communities across the entire continent.

Strikingly, the seven bird species that are most clearly affected by the virus are all 'peri-domestic' — that is, they are associated with human populations, in this case those in town and city suburbs. Among the disappearing species is an icon of North American garden birds, the American robin (*Turdus migratorius*; Fig. 1). It is also thought-provoking that no fewer than 13 of the 20 species experienced a 10-year population low following the human epidemics of West Nile virus in 2002–03 in the United States[3]. This is a notable observation in light of the debate about the spread of the highly pathogenic avian influenza virus (H5N1 strain), and the potential role of migratory, peridomestic and domestic birds as reservoirs and dispersers of this disease.

LaDeau *et al.*[3] caution against oversimplified interpretations of their results. The spatial patterns of disease that they detected may still reflect regional differences in the intensity of viral transmission, and these may be linked to spatial patterns in habitat, land use and climate — all of which are traditionally used to explain large-scale patterns of changes in bird populations.

The authors partly incorporated the potential influence of the El Niño/Southern Oscillation in their models as a crude measurement of climate variability, but their analysis does not include environmental or climatic parameters at the appropriate spatial scale. This may explain why, with the exception of the American crow (*Corvus brachyrhynchos*), the results are qualitatively rather inconsistent for individual species. But the results for

the crow are compelling, not least given the geographical correlation with human infection shown in Figure 2 of the paper[3].

More detailed analyses and studies on further species will be needed to fully understand the impact of West Nile virus on large-scale changes in North American bird populations. But even as it stands, this research reminds

Figure 1 | Viral victim: the American robin. Populations of this bird and of the American crow are among the seven species most clearly identified by LaDeau *et al.*[3] as suffering from mortality caused by West Nile virus. The other five species for which there is a robust correlation between population declines and virus infection are the blue jay (*Cyanocitta cristata*), tufted titmouse (*Baeolophus bicolor*), house wren (*Troglodytes aedon*), chickadee (*Poecile* spp.) and Eastern bluebird (*Sialia sialis*).

us once more of the threat of infectious diseases to both biodiversity and human health. The migratory passenger pigeon (*Ectopistes migratorius*) of North America, once the most abundant bird of its time with an estimated population of between 3 billion and 5 billion, was driven to extinction within a century by human agency and, possibly, diseases[7]. The disappearance of such an abundant species must have had a considerable effect on the communities in which it occurred. Indeed, it has been suggested that the rise in incidence of Lyme disease in humans is a delayed consequence of the removal of the passenger pigeon from the ecosystems of North America[7,8].

We are witnessing the emergence of novel diseases at an unprecedented rate[9]. Epstein and colleagues[9] have argued that human-induced changes in ecological systems and climate are now triggering "a barrage of emerging diseases that afflict humans, livestock, wildlife, marine organisms, and the very habitat we depend upon". LaDeau and colleagues' study is a timely example of the effect that such diseases can have on communities of wild species and humans alike, even at a continental scale. ■

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