

Figure 2 Neighbour-joining protein distance tree for the 151 amino-acid residues encoded by a 454-base-pair fragment⁶ of the DNA-polymerase gene. Sequences were aligned by using ClustalW and analysed with PROTDIST and NEIGHBOR programs in PHYLIP. One hundred replica samplings were subjected to bootstrap analysis (SEQBOOT). Branch lengths are proportional to the evolutionary distance (scale bar) between the taxa. GenBank accession numbers for the new chimp and gorilla KSHV-like sequences are respectively AF250879, AF250880, AF250881, AF250882 and AF250886.

ed polymerase chain reaction and degenerate primers⁵: this was 476 base pairs long and encoded a fragment of the conserved herpesvirus DNA polymerase. Comparative analysis with all the other available related herpesvirus sequences (Figs 1, 2) revealed the existence of two new chimpanzee KSHV-like viruses (which we named PanRHV1a and PanRHV1b, for pan-rhadinoviruses 1a and 1b) and a new gorilla KSHV-like virus (GorRHV1, for gorilla rhadinovirus 1). These new sequences from great apes appear to be outside the natural range of KSHV-sequence variations found in humans.

Phylogenetic analysis by different methods placed these three viruses in the rhadinovirus genus, which, with the KSHV, the macaque RFHVMm and RFHVMn and African green monkey ChRV1 strains, forms a new clade of Old World viruses that is supported by high bootstrap values (Fig. 1).

A second analysis, restricted to all the available primate rhadinovirus DNA-polymerase genes (Fig. 2), indicated that there are five separate lineages among these γ_2 -herpesviruses, one for the New World monkeys (HVS and HVA3), two for the macaques (comprising RFHVMm, RFHVMn, RRV, *Macaca mulatta*, *M. nemestrina* and *M. fascicularis*) and the African green monkeys (ChRV2 and ChRV1), one for the new PanRHV1b strains, and one that includes KSHV and the new PanRHV1a and GorRHV1 strains. Among the chimpanzees, none of the new strains seems to be associated with a genetic

subspecies as they were found to occur nonspecifically in *Pan troglodytes vellerosus* and *Pan troglodytes troglodytes* by mitochondrial-DNA analysis.

The increased contact between great apes and humans in central Africa generated by hunting and butchering for local meat and/or the 'bushmeat trade', as well as by recent socio-economic change such as intense commercial logging, provides more opportunity for interspecies viral transmission⁸. Such infectious events, although rare, may lead to a dead-end infection, as reported for foamy viruses after monkey bites⁹. Alternatively, and more probably in the case of herpesviruses, they may cause persistent infection, with a possible founder effect in restricted populations, leading under particular circumstances to endemic or epidemic dissemination within larger human populations.

The two human retroviruses HIV-1 and HTLV-1, at least some subtypes of which probably originated from the central African chimpanzee viruses SIV/CPZ and STLV-1, provide two examples of infection that has been zoonotically transmitted in this way, albeit with a different epidemiological fate and pathogenicity in humans^{6,10,11}. Our discovery of the new KSHV-related rhadinovirus sequences in chimpanzees and gorillas will enable their likely human counterparts to be identified.

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Addendum

Fish do not avoid survey vessels

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Nature **404**, 35–36 (2000)

Our title has led some readers to misinterpret our conclusions. Questions have also been raised regarding the speed at which the observations were carried out.

Autosub-1, the Autonomous Underwater Vehicle that we compared with the fisheries research vessel *Scotia*, had an operating speed of 3 knots. Vessel noise is usually thought to increase with speed, but the noise signature of *Scotia* (Fig. 1) shows that she makes a similar amount of noise at a low speed and at the normal survey speed of 10 knots. Our conclusions are, therefore, valid at the usual survey speed for this vessel.

Our paper's title has, in some cases, been taken to imply that avoidance is not a problem for any research vessel, without considering the qualifications we thought had been made explicit in the text. The *Scotia* is very quiet: she was the first vessel to be built to the International Council for the Exploration of the Sea's specifications for limiting noise¹ (Fig. 1). We believe that our findings, valid only for such noise-reduced vessels, endorse this objective and justify the 5–10% increase in build cost. Our research shows that fisheries research vessels should be built to the same noise specification as *Scotia* in order to ensure that avoidance is not a source of bias.

1. Mitson, R. B. *ICES Co-op. Res. Rep.* **209**, 1–61 (1995).

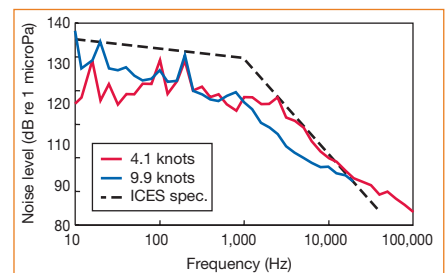


Figure 1 Noise levels of the *Scotia* at different speeds compared with the noise specification recommended by the International Council for the Exploration of the Sea.

no indication that the 15 novel small predictions are coding, and the hexamer algorithm suggests that 12 of the 15 are non-coding. The remaining seven GlimmerM predictions form part of gene models that we consider to be borderline and are validating experimentally before inclusion in the chromosome annotation.

Pertea *et al.* suggest that peer-reviewed bioinformatics methods are essential. Certainly, if the diverse outputs of multiple gene-prediction algorithms can be included, then the annotation should be good, but that does not make the gene prediction correct — it remains a prediction and not a confirmed gene model.

Overreliance on the output of a predictive tool can lead to erroneous prediction and bad annotation. The well-established tools used in the analysis of chromosome 3, Genefinder, hexamer and ACEDB (P. Green and L. Hillier, unpublished software; R. Durbin, unpublished software) have a proven track record in eukaryotic gene prediction³.

Our analysis of chromosome 2 using Genefinder/hexamer indicates that 40 modifications need to be made to the original gene predictions (20 per cent of gene models). Although these new predictions require confirmation, they highlight the inaccuracy of first-pass annotation from uncharacterized genomic DNA. We encourage re-analysis of genomic data to increase sequence accuracy: Genefinder, hexamer and GlimmerM all have roles to play in the (re)annotation of *P. falciparum* chromosomes and in improving the interpretation of sequence data.

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1. Bowman, S. *et al.* *Nature* **400**, 532–538 (1999).
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Oceanography

Fish do not avoid survey vessels

The precarious condition of the world's fisheries is making ever-greater demands of the scientific assessment of fish stocks. Traditional assessments that rely on commercial catch statistics can have major shortcomings¹ (as shown, for example, by the collapse of Canada's northern cod stock²), increasing the need for more fishery-independent data. Acoustic surveys can provide such information³, but ocean-going research vessels have high operating

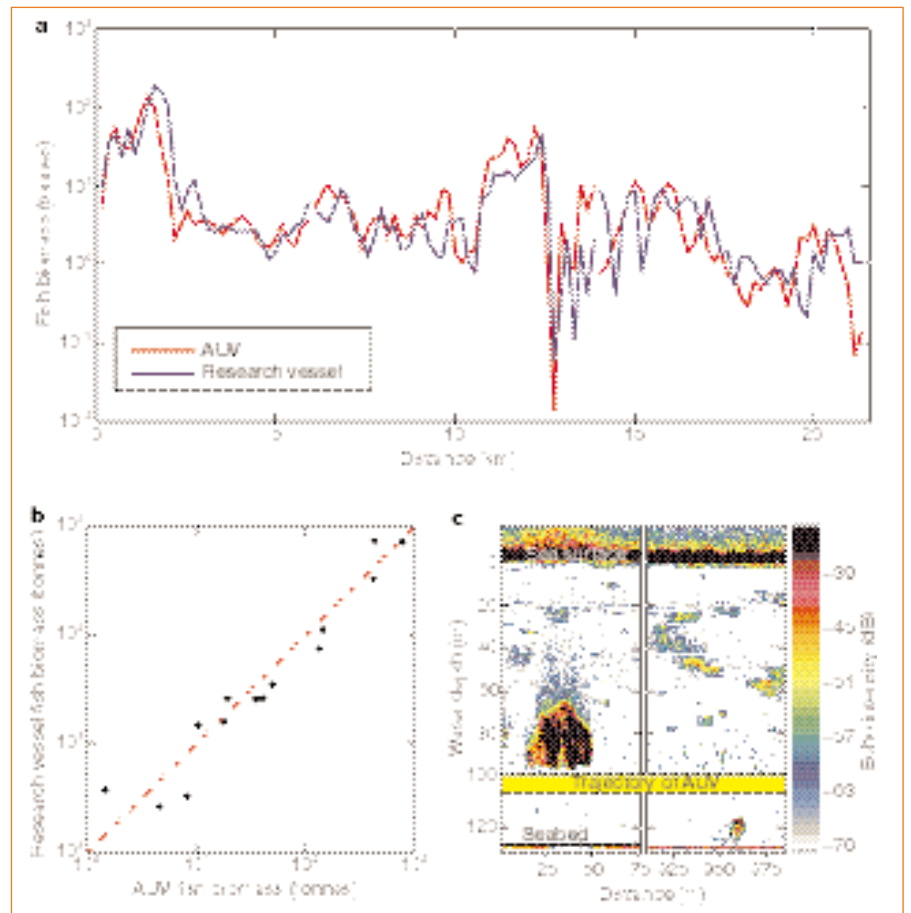


Figure 1 Comparison of acoustic data collected by an autonomous underwater vehicle (AUV) and a research vessel. **a**, Fish biomass at integrated intervals of 186 m along three transects on 21 July 1999; fish were identified as herring (*Clupea harengus*) by trawling. **b**, Strata-averaged biomass estimates from the AUV and research vessel were significantly correlated ($r=0.935$, $P<0.001$), lying around the (dotted) one-to-one line (Wilcoxon signed-rank test, $P>0.05$). **c**, Composite echogram collected by the AUV at 105 m (equipped with upward- and downward-looking transducers) as it passed less than 7 m beneath a large midwater herring school (left) and only 10 m above another close to the sea bed (right).

costs, and there is also widespread concern that fish avoid these vessels because of the noise they make, thereby biasing abundance estimates⁴. Here we present new data gathered by an autonomous underwater vehicle (AUV) showing that vessel avoidance is not a significant source of bias. Our investigation also heralds the arrival of AUVs as effective survey platforms.

During acoustic surveys, sound pulses are transmitted vertically downwards into the water at regular intervals (typically 1 s) from a survey vessel travelling along defined transects. Fish density is calculated by integrating the intensities of the returning echo⁵, and is then interpolated to give an estimate of the abundance in the survey area³.

We deployed the AUV *Autosub-1* (ref. 6) 200–800 m ahead of the research vessel *Scotia* on eight transects in water 60–180 m deep during an acoustic survey of herring in the North Sea. Herring have the most sensitive hearing of the commercially exploited species examined so far⁷ and are more likely than any to react to vessel noise. *Autosub-1* is unmanned and follows pre-programmed

mission trajectories. In comparison to the 68-m *Scotia*, it is small (torpedo shaped, 7 × 1 m) and extremely quiet (being propelled by an electric motor).

Avoidance of *Autosub-1* by herring is minimal: passing unprecedentedly close to a school (Fig. 1c), the vehicle caused only the localized school compression that typically occurs on close approach of predators⁸. *Autosub-1* was equipped with the same type of 38-kHz scientific echosounder as *Scotia*, and gathered equivalent acoustic data before the research vessel arrived. If fish avoided the *Scotia*, then it should have detected fewer fish than *Autosub-1*.

At the integrated resolution, there are small-scale temporal and spatial differences between the AUV and research-vessel data (Fig. 1a), but the underlying similarity in magnitude and trend is clear. For statistical comparison, data from each source were aggregated into independent strata of equivalent geographical area.

The amount of fish detected by the research vessel was not significantly different from that detected by the AUV (Fig. 1b). *Scotia* is very quiet, having been built

to guidelines intended to limit noise emission⁷. Our data show that for such vessels, avoidance is not a source of bias.

We also deployed *Autosub-1* on eight fully autonomous missions. This was the first time that any AUV had operated successfully beyond the control range of a support facility. These missions provided over 76 h (420 km) of additional survey data which, also for the first time, span the whole water column (Fig. 1c).

AUV technology is now sufficiently robust for effective fish-stock monitoring⁹, and could advance fisheries surveys by allowing acoustic detection closer to the target species. This could improve the assessment of groundfish, such as cod, and deep-water fish, and may also facilitate more extensive high-frequency zooplankton studies¹⁰. Reductions in battery costs and improvements in the acoustic identification of species using multifrequency¹¹ and broadband¹² techniques may eventually enable AUVs to replace research vessels as acoustic sampling platforms.

Autosub-1's unique capabilities are being used in a variety of other marine-science programmes¹³, from studies of ocean turbulence to marine geochemistry. We plan to exploit the vehicle's ability further to operate in otherwise impenetrable environments later this year, when we will deploy it under Southern Ocean sea-ice to measure ice thickness, and the abundance and distribution of Antarctic krill.

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Evolution

Migration and speciation

Although migration is a common behaviour, the effects of this annual two-way event on the speciation process are poorly understood, even though birds, which are commonly migratory, played a critical role in the development of speciation theory^{1,2}. Here I propose that new developments^{3,4} in the theory of sympatric speciation — a process whereby new species can arise through population differentiation without spatial isolation — may help to explain the bursts of speciation observed in some seasonal migrant lineages.

Seasonal migrants, particularly those travelling long distances, have few recognized limits to their ability to disperse into new environments^{5,6}. These colonizations can foster the production of new species flocks — examples include nearctic *Catharus* thrushes (Fig. 1), some palaeartic *Phylloscopus* warblers, and the irruptive migrant specialists red crossbills (*Loxia curvirostra*)^{7–9}. I suggest that migration itself can be viewed as a key innovation that occasionally enables lineages to radiate in new environments.

Migration is a complex mode of dispersal, promoting the colonization of new areas, but also their regular re-colonization and gene flow. Spatial segregation — the linchpin of most speciation theory — becomes less and less likely with increasing migratory tendencies. Achieving true geographic isolation from other populations, thereby allowing differentiation to occur in the absence of gene flow, seems particularly unlikely among long-distance migrants, whose movements regularly encompass entire continents and oceans.

But here we have a conundrum: while migration opens the door to differentiation in new ecological and geographic space, it apparently slams it shut again through denial of geographic isolation and the promotion of gene flow.

Until now, migration was considered to counter differentiation¹⁰. Scenarios proposed to explain migrant speciation have had to invoke geographic isolation and, by implication, mechanisms such as lower historic levels of migration and greater levels of natal philopatry — neither of which fits the evidence^{11–13}. Although it is true that the origins and losses of migration have occurred independently in many lineages, it is unrealistic to suggest that the associated complex life-history characteristics were somehow held in temporary abeyance across entire lineages or clades.

Recent developments in speciation theory^{3,4} offer a theoretical framework to escape such ill-fitting scenarios, and species flocks of migrants could provide a testing ground for these theories. Phenotypic evidence in



Figure 1 Hermit thrush (*Catharus guttatus*; top) and Swainson's thrush (*C. ustulatus*; bottom), two nearctic–neotropical migrants from a highly migratory clade. These two species and three close relatives comprise a group of neotropical origin. They have trans-continental breeding distributions in temperate- and high-latitude nearctic forests, and wintering distributions centred on neotropical North and South America.

birds suggests that sexual selection may operate only as a distant second to resource competition and perhaps reinforcement (adaptations to prevent hybridization) in driving speciation events among many migratory animals.

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Correction

Arsenic poisoning in the Ganges delta

T. R. Chowdhury *et al.*; reply from J.M. McArthur
Nature **401**, 545–547 (1999)

The form of citation of one of the references given in this exchange (ref. 10 of Chowdhury *et al.*, ref. 6 of McArthur) was misleading and should have been written as “British Geological Survey/Mott MacDonald Ltd *Groundwater Studies for Arsenic Contamination in Bangladesh* (1999).” This is because it is the final report of Phase 1: *Rapid Investigation Phase*, not of the overall project, for which the final report will appear in 2000.