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BRIEF COMMUNICATIONS

Fruit bats as reservoirs of Ebola virus

Bat species eaten by people in central Africa show evidence of symptomless Ebola infection.

The first recorded human outbreak of Ebola virus was in 1976, but the wild reservoir of this virus is still unknown¹. Here we test for Ebola in more than a thousand small vertebrates that were collected during Ebola outbreaks in humans and great apes between 2001 and 2003 in Gabon and the Republic of the Congo. We find evidence of asymptomatic infection by Ebola virus in three species of fruit bat, indicating that these animals may be acting as a reservoir for this deadly virus.

Human Ebola outbreaks that occurred between 2001 and 2005 in Gabon and the Republic of the Congo were linked to concurrent outbreaks that devastated local gorilla and chimpanzee populations^{2,3}. To identify the viral reservoir, we undertook three trapping expeditions in areas close to infected gorilla and chimpanzee carcasses, just after their discovery (Fig. 1a). In total, 1,030 animals were captured, including 679 bats, 222 birds and 129 small terrestrial vertebrates, and were tested for evidence of infection by Ebola virus (for details, see supplementary information).

Of the infected animals identified during these field collections, immunoglobulin G (IgG) specific for Ebola virus was detected in serum from three different bat species (4 of 17 Hypsignathus monstrosus, 8 of 117 Epomops franqueti and 4 of 58 Myonycteris torquata). Two of the principal organs targeted by Ebola virus are the liver and spleen4. Viral nucleotide sequences were detected in these organs in other bats from the same populations (4 of 21, 5 of 117 and 4 of 141, respectively). No viral RNA was detected in kidney, heart or lung in these animals after amplification by polymerase chain reaction (PCR) and no viral nucleotide sequences were revealed in any of the other animal species tested.

Nucleotide-sequence analysis of purified PCR products identified seven different fragments amplified from the 13 PCR-positive animals, all clustering phylogenetically within the Zaire clade (Fig. 1b). The fragments differed not only from one collection to another, but also within a given collection, among the three bat species, and within a given species. The need to use nested PCR indicated that the viral RNA load in tissues was extremely low, which probably explains why we failed to isolate the virus itself.

Surprisingly, none of the IgG-positive animals was PCR-positive, and none of the PCR-positive animals was IgG-positive. This may

be because PCR-positive bats were recently infected and were tested before they developed a detectable immune response. Alternatively, it could be that differences in the virulence of Ebola virus strains led to different immunological responsiveness and viral replication patterns. Of the bat species collected at Mbomo in February 2003, 7 of 31 (22.6%) and 0 of 10 (0%) were PCR-positive and IgG-positive, respectively, but five months later the corresponding results were 4 of 184 (2.2%) and 12 of 160 (7.5%). These opposite trends in the PCR and serological results are consistent with the first hypothesis.

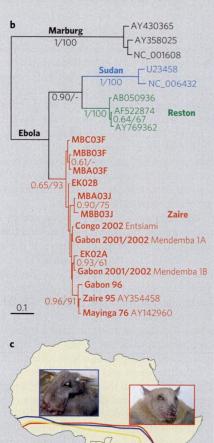
Each of the three bat species has a broad geographical range that includes regions of Africa where human Ebola outbreaks occur⁵ (Fig. 1c). Our findings support results of previous investigations that identify bats as candidate reservoirs for Ebola and Marburg viruses^{1.6}, and as reservoirs for the virus families *Paramyxoviridae* and *Rhabdoviridae*⁷⁻⁹, which are genetically related to Ebola.

Mortality among great apes from Ebola infection can increase during the dry seasons³ when fruit is scarce in the forest — conditions that foster contact between animals as they compete for food. Immune function in bats also changes during these periods¹0, for example as a result of food scarcity or pregnancy, which would favour viral replication and — aided by aggressive interactions — increase infection among great apes. These factors may contribute to the episodic nature of Ebola outbreaks.

Although other bat and animal species may also act as Ebola virus reservoirs, insight into

Figure 1 | Fruit bats as potential carriers of Ebola virus. a, Dates and locations of animal-trapping sites (blue) and of Ebola virus outbreaks among humans (red stars) in Gabon and the Republic of the Congo. b, Phylogeny of Ebola viruses inferred from RNA polymerase sequences. Values below branches are bayesian posterior probabilities (left of slash; values less than 0.5 not shown); bootstrap percentages were obtained by maximum parsimony (right of the slash; values under 50% not shown). (GenBank accession numbers, DQ 205409-205415.) Sequences of the subtype Zaire (red) share five nucleotide signatures in positions 1,755 (T), 1,800 (G), 1,857 (T), 2,002 (A) and 2,003 (C) of the complete coding sequence of the gene encoding RNA polymerase. c, Geographic distribution (inside coloured lines) of the fruit bats Hypsignathus monstrosus (blue), Epomops franqueti (red) and Myonycteris torquata (yellow).





the behavioural ecology of the bat species identified here should help to improve protection of the great apes from Ebola virus. Human infection directly from fruit bats might in part be countered by education, as these animals are eaten by local populations living in the outbreak regions.

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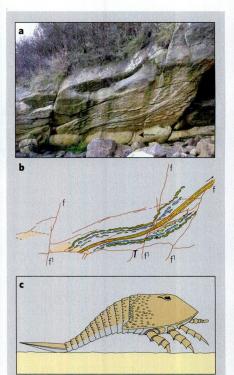
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PALAEOECOLOGY

A gigantic fossil arthropod trackway

A unique, complex trackway has been discovered in Scotland: it was made roughly 330 million years ago by a huge, six-legged water scorpion that was about 1.6 m long and a metre wide. To my knowledge, this is not only the largest terrestrial trackway of a walking arthropod to be found so far, but is also the first record of locomotion on land for a species of *Hibbertopterus* (Eurypterida). This evidence of lumbering movement indicates that these giant arthropods, now extinct, could survive out of water at a time when the earliest tetrapods were making their transition to the land.

The trackway (Fig. 1a, b) is exposed on a bedding plane close to the base of a sandstone section in a non-marine sequence. It is 6 m long, 0.90–0.98 m wide and consists of sinuous, paired belts of appendage prints flanking a sub-central groove. The trace-maker had at least three pairs of appendages of different lengths (heteropodous), which moved in phase. The longest, outer limbs left elongated crescent-shaped prints (series A in Fig. 1b, green), which overlap slightly or coalesce into a linked series of arcs. The stride length is therefore less than the series-A print length (average, 0.27 m) and indicates that the animal was crawling extremely slowly.

Lines of elongate, crescentic or sigmoidal prints (series B in Fig. 1b, blue) lie inside series A, and further elliptical prints (series C in Fig. 1b, yellow), made by the shortest appendages, can be detected inside these. In places, the series-C prints have been erased by the central groove, which was made by the posterior part of the animal. This is trapezoidal in cross-section and its base is deeper at the margins and slightly raised in the centre. Occasional oblique lineations on the sides and base of the groove indicate that the motion

was jerky. The sinuous curve of the groove is smaller in amplitude than, and out of phase with (by about 0.5–0.6 m), the trackway margins, which reveals the direction of locomotion (Fig. 1a, b). The slow, stilted progression, together with the dragging of the posterior, indicates that the animal was not buoyant and that it was probably moving out of water.

There are several groups of Lower Carboniferous (Asbian) arthropods that might have been capable of leaving large trackways¹, but only the water scorpions, or eurypterids¹, are likely to have left the trackway described here. The pattern and character of the limb prints is most consistent with a relatively short-limbed and markedly heteropodous hibbertopteroid eurypterid^{2–5} (Fig. 1c). The double-keeled underside of the terminal tail plate of these animals^{4,5} matches the character of the central groove.

Fragmentary exoskeletal remains of *Hibbertopterus* and related forms are relatively well known from Scottish Lower Carboniferous rocks^{2–5} and were first described from West Lothian in 1831 (ref. 2). The trackwaymaker (Fig. 1c) would have been comparable in size to the largest known hibbertopteroid body fossils, which have head shields^{3–5} that are 0.65 m wide.

The short length of the relative stride in the trackway emphasizes the extreme slowness of the gait and differentiates it from other eurypterid trackways within the ichnogenus *Palmichnium*^{1,6–9}. This trace is 0.2 m (25%) wider than any other trackway of this type¹. The only larger known invertebrate trackway, although also attributed to a eurypterid, is very different in character and appears to have been made by a swimming animal¹⁰.

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Figure 1 | Hibbertopteroid trackway from Lower Carboniferous (Asbian) rocks in Scotland.

a, View of the trackway on the undersurface of an overhanging sandstone bed, which is dipping at 45° away from the viewer. The hammer (arrowed) in the photograph is 30 cm long, but the oblique view affects scale and relative proportions. b, Interpretive diagram showing track features, position of a second, smaller (0.80 m wide) trackway and the position in the rock of microfaults (f-f1), joints and bedding traces (red lines). Arrow indicates movement direction of the animal. Trackway: orange, central groove; series A, B and C are shown in green, blue and yellow, respectively. c, Reconstruction of the hibbertopteroid eurypterid trackway-maker. This arthropod was about 1.6 m. long (for clarity, the limbs on the left of the body are omitted).

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