

and Hölldobler [4], which considers only recent common ancestry, kin selection remains the best explanation for altruism in eusocial groups because most are families [3,6]. Unrelated ant and wasp queens do found nests together [2,4], but this is a mutualistic interaction that can work at $r=0$ [3]. Workers are typically related to the individuals that they altruistically help. Even when relatedness is close to zero in unicolonial ants [3], relatedness was >0 when the altruistic worker caste first evolved. Furthermore, theory predicts that family relatedness is more likely to produce stable altruism than are other forms of relatedness, such as green-beard genes [3]. This suggests that it is selection acting through family relatedness that explains the altruism of eusocial species. We are unconvinced by E.O. Wilson's recent ideas, but are in full agreement with his earlier view: 'How can altruism, which by definition reduces personal fitness, possible evolve by natural selection? The answer is kinship...' [18].

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Letters

Molecular cryptozoology meets the Sasquatch

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Most mainstream scientists believe that few species of large mammal remain to be discovered. Nevertheless, there are countless unverified reports of a large, non-human, bipedal primate from Asia (the 'Yeti') and North America ('Sasquatch' or 'Bigfoot'). Thus far, none of these reports has been convincingly verified by modern scientific methods [1]. However, new species inhabiting remote areas are occasionally described that were previously known only from local and traditional knowledge. The most recently described large mammal could be the sao la *Pseudoryx nghetinhensis*, which became known to science in 1992 from three sets of horns found in the possession of hunters in the Vu Quang Nature Reserve in Vietnam [2]. Subsequent surveys and the morphometric and DNA analysis of >20 specimens revealed that the sao la was a previously undescribed 100-kg bovid distinct from all described genera. More recently, in

2003 a new species of African monkey (*Lophocebus kipunji*) was discovered in southern Tanzania, based on sightings, photographs and recorded distinctive vocalizations [3]. Discoveries such as these fuel hope in the cryptozoology community for the existence of more enigmatic creatures, such as the Sasquatch.

Several high-profile Sasquatch sightings have recently been reported in Canada. In April 2005, a Manitoba ferry operator videotaped a large, dark, indistinct creature moving along a riverbank, which made international news. In July 2005, nine residents of Teslin, Yukon, witnessed through a kitchen window a large bipedal animal moving through the brush. The next morning, they collected a tuft of coarse, dark hair and also observed a footprint measuring 43 cm in length and 11.5 cm in width. The tuft of hair was sent to Philip Merchant, a wildlife technician of the Government of Yukon Department of Environment who, based on structural features, identified it as probably originating from bison *Bison bison*. We

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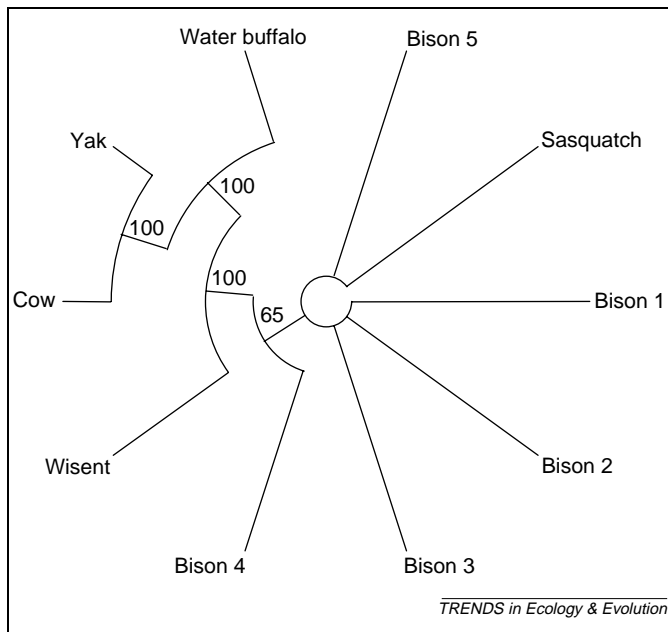


Figure 1. Maximum parsimony tree illustrating the position of the Sasquatch hair sample. Bootstrap support values are given at the nodes. The species and GenBank accession numbers are water buffalo *Bubalus bubalis* (AF197216), yak *Bos mutus* (AY521157), cow *Bos taurus* (AB065127), wisent *Bos bonasus* (AY748759), and North American bison *Bison bison* (1, AY748758; 2, U12947; 3, AY748757; 4, AY748478; 5, AY748620).

offered to shed the hard light of modern science onto this case using a DNA test to eliminate any remaining uncertainty.

We extracted DNA from the hair follicles of ten roots using DNeasy columns (QIAGEN Inc.; <http://www.qiagen.com/>) and amplified the hypervariable region I of the control region (also known as the D-loop) using primers that have conserved sequence in mammals [4]. Alignment of a 429-bp DNA

fragment to DNA databases [5] produced high probability matches to 2058 sequences, all of which were from the infraorder Pecora (horned ruminants). The top 58 matches were from *B. bison*, all with 99–100% sequence identity. A total of 1641 hits were to the Bovinae (mostly to *Bos* spp.) and the remainder to members of the Cervidae (e.g. moose *Alces alces*). The phylogenetic position of the unknown sequence derived from a maximum parsimony analysis of an alignment of representative taxa places the sample in the same clade as North American bison (Figure 1).

There are several possible explanations for these results. First, as suggested from molecular analysis of hair from a suspected Yeti [1], the Sasquatch might be a highly elusive ungulate that exhibits surprising morphological convergence with primates. Alternately, the hair might have originated from a real bison and be unrelated to the Sasquatch. Parsimony would favor the second interpretation, in which case, the identity and taxonomy of this enigmatic and elusive creature remains a mystery.

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Megafaunal extinction: climate, humans and assumptions

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Recently in *TREE*, Burney and Flannery reviewed the role of colonizing humans in prehistoric extinctions [1]. Their treatment is informative and we applaud the broad assertion that realistic explanations will not be found in simple, single-cause paradigms. However, despite some qualification, the authors strive to present human influences as primary in all instances: '...a more interesting

extinction debate lies within the realm of potential human-caused explanations and how climate might exacerbate human impacts' [1]. We question an underlying assumption that evidence from remote islands can be extrapolated to continents, and challenge suppositions underpinning human causation for extinctions in Australia and the Americas, where most megafaunal losses occurred.

Most prehistoric extinctions have been of birds on remote islands within the past few thousand years [2]. The

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