SCIENTIFIC CORRESPONDENCE-

Here be Komodo dragons

SIR-For as long as mankind has been discussing dragons, it has been difficult to distinguish fact from fiction; the recent article by Diamond¹ concerning the very real Komodo dragon is no exception.

The giant monitor lizard of Pleistocene Australia, Megalania prisca, although not well known, is not likely to have reached 2,000 kg in body weight. Neither of the references cited by Diamond support this figure. I am aware of only two quantitative estimates. Rich and Hall² (cited by Diamond) suggested that Megalania could have had eight times the mass of the Komodo dragon. The largest reported dragon3 was apparently 132 kg, therefore Megalania might have just exceeded 1,000 kg. Hecht⁴ estimated a lower figure of 600-620 kg. Both of these figures are within the normal range for large crocodiles of similar dimensions - for example, Crocodilus porosus and C. niloticus^{5,6}

Megalania was not the only large carnivore in Australia during the Pleistocene. It has been suggested 7 that the ziphodont crocodile Quinkana fortirostrum, which was possibly terrestrial, shared this niche with Megalania and no doubt C. porosus. The possible importance of large pythons such as the 5-m-long Wonambi naracoortensis⁸ should not be discounted.

As to the problem of what oras ate before the arrival of humans and their associated mammals, Diamond has confused the approximate dates for the introduction of domesticated species with the minimum estimates for the arrival of man. Humans were present in the region at least 35,000-40,000 years ago9 and in Australia are known to have shared the continent with the megafauna until about 6,000 years ago¹⁰. Because fossil dragons are recorded from the Pleistocene in both Timor and Java it is reasonable to assume that any of the large animals found in

ELEPHANTOS ET DRACONES

CAIUS PLINIUS SECUNDUS' EDICOP NACUPA.



have peceived a copy, sip, of ... YOUP RECENT PUBLICATION ... CONCLINING AN ACCOUNT OF THE .. RELACIONSHIP BECWEEN ELEPHANCS and dragons in Lands to the EAST OF INDIA. I THOUGHT I Should OPAW YOUP ACCENCION TO & PASS-AGE IN MY NACUPAE hiscopiae' LIBRO VIII, CHAC YOU MAY COMMUNI-CACE IT TO PROFESSOR DIAMOND. ... SED MAXIMOS INDIA BELLANCESQUE CHM his

DEDDEEUN DISCORDIN OPACONES CANCHE MINC. NICUDINUS EC IPSOS UC CIRCUMPLEXU FACILI ... mopicup ex dimicatio, victusque conpuens - conplexum elidic pondepe."

AS TO OPACONS IN AUSTRALIA, I KNOW NOT ... of that place, sip, but if there be dracons. then supely too elephants?

ι with assistance γρου με mitchell, school of experi-schools, με αναμαρία υπανερίας, με ωι τον Australia, Σιπανολ, με πλαταρί του ματαγμάτιστας του ματαγμάτι η μαλίπλατ, με τρακές μέτας ματαγμάτι μιατορίς του πι α βιακόπλανα καλ προγορό μια γρόες, μείοι

these and adjacent islands may have been available as prey. These include11; Elphas as well as Stegodon, a number of pigs, the pig deer (Babyrousa babyrussa), endemic 'wild cattle' (Anoa depressicornis), several large rats and a giant tortoise (Geochelone atlas).

If indeed Wallace had been able to visit the region at any time between perhaps 6,000 and 50,000 years ago, he would have found humans as well as dragons. In Australia the dragons probably shared the top carnivore niche with crocodiles of similar size (about 1,000 kg) and in Wallacia their diet was possibly more varied than just pygmy elephant.

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Disputed African origin of human populations

SIR-In a recent paper. Cann et al.¹ proposed a fascinating interpretation of the comparison between mitochondrial (mt)DNA polymorphisms in different geographic human populations. Their data certainly improve our knowledge of the molecular evolution of humans. However they do not provide a conclusive demonstration of the African origin of Homo sapiens sapiens.

The most important reason for this is that their parsimonious tree is not a phylogenetic tree: ambiguous character polarities do not yield safe trees². Cladistic approaches34 have shown that to be phylogenetic, a tree must be rooted after an estimate has been made of which are ancestral, and which derived, states. The widely used out-group criterion gives the polarity and is suitable for computing programs. In this system, a character state shared by both in-group and out-group is primitive. Unfortunately, for the populations of Homo sapiens sapiens, first, we do not have any out-group comparison; second, we do not know in a DNA sequence if a given base is primitive or derived, and third, the mtDNA polymorphism frequencies in populations are estimated from very small samples, for example by using 18 black American and 2 African individuals to estimate the genetic diversity of the African population as a whole.

Even by using the 'midpoint rooting technique' the authors cannot convert their unrooted network of different mtDNA types into a phylogenetic tree of the human populations. From a methodological viewpoint, the midpoint method has certain flaws. For a given data matrix, the midpoint technique does not always give the same tree as the phylogenetic tree rooted either by an out-group or an ancestor. If a supplementary terminal taxon with only primitive characters (that is, identical to the ancestor) is added to the analysed taxa, it does not necessarily appear in an external or ancestral position in the tree rooted by the midpoint method

No single hypothesis is certain as long as there is a possible alternative that cannot be proved to be false. Many other interpretations of the data of Cann et al. are possible as long as multiple hypotheses exist about relative rates of evolution along the branches of the tree, and as long as selective pressures, admixture, migration and bottleneck effects cannot be included in intraspecific models. To test such models, more than 9% of the mtDNA of 147 individuals must be tested, the mtDNA itself being 0.048% of the whole human genome. In this field, the best is yet to come.

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CANN ET AL. REPLY-Saitou and Omoto¹ argued that comparisons to mitochondrial (mt) DNA do not yield reliable trees relating populations to one another. We agree that population trees can be unreliable, especially when only a few individuals are sampled per population and when the extent of mtDNA divergence within populations nearly equals that between populations. For these reasons, we chose not to present a population tree in the article²

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Cann, R.L., Stoneking, M. & Wilson, A.C. Nature 325, 31-36(1987).