may be at least 150 species in total. Thus, the synonymy rate here is most probably below 5%.

These examples show that different groups may have widely different synonymy rates. Long lists of synonyms may be expected for large, easily collected organisms with extensive geographical ranges and conspicuous individual variation. Conversely, hard to find, minute species with restricted ranges and uninteresting external appearance are likely to have none or few. Synonymy rates are affected by changing species concepts and improved analytical tools, rather than by continuous, predictable error of taxonomists.

Estimates of global biodiversity should therefore not rely on the number of described species, as this parameter is too

uncertain to provide any consistent estimate. Clearly, there is a need for more updated, robust taxonomic revisions, but taxonomy is a scientific discipline relevant on its own, able to contribute significantly to the preservation of biodiversity^{3,9}. Because the true extent of diversity in these three groups of molluscs has been unrecognized until now, these animals have been largely ignored by conservationists. It is sad indeed that many of these species, often still undescribed, are threatened or already extinct.

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acetoacetyl-CoA: acetate/butyrate:CoA-transferase, one of the two enzymes involved in the final steps of acetone formation. We obtained a hybridization signal with the 210-kb linearized plasmid forms of *C. acetobutylicum* Weizmann, but no signal with WDS1 (see figure), indicating that the plasmid carries the *sol* operon locus. This plasmid was named pWEIZ.

Our finding raises an obvious question: what is the natural selective pressure for the maintenance of pWEIZ? The answer is probably linked to the fact that all the *C. acetobutylicum* strains that have lost pWEIZ also do not sporulate. It is tempting to speculate that an essential gene(s) needed for sporulation might be carried by the plasmid.

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Solvent-forming genes in clostridia

SIR — The Weizmann process¹, in which the bacterium *Clostridium acetobutylicum* converts corn starch into acetone and butanol, was used during the First World War to produce the acetone needed for smokeless gunpowder. The loss of the Weizmann strain's capacity to produce solvents after repeated subculture (degeneration)² is still not understood from the molecular viewpoint³. We show here that the solventogenic genes^{4,5} encoding the enzymes required for acetone and butanol formation are carried on a 210-kilobase (kb) plasmid (pWEIZ), and that three degenerate strains lack both these solventogenic genes and pWEIZ.

To investigate the molecular basis of degeneration, we isolated three spontaneous degenerate mutants (WDS1, 2 and 3) of *C. acetobutylicum* ATCC 4259 (the Weizmann strain used in warfare⁶) through serial subculturing. None of the mutants produced any detectable amounts of butanol or acetone, nor did they sporulate. DNA from the wild-type and mutant strains was prepared in agarose plugs and analysed by pulsed-field gel electrophoresis (PFGE).

Below a band of sheared chromosomal DNA in our gels, we always observed an extra band at 210 kb in the wild-type strain which was absent from all the degenerate mutants (see figure). DNA from the Weizmann strain digested by *Sma*I, *Apa*I or *Sst*II (see figure for the *Sma*I digest only) has a considerably higher-intensity 210-kb band than has the uncut DNA, whereas there is no 210-kb band for WDS1 DNA digested by the same enzymes. Because circular DNA cannot enter the gel in PFGE⁷, our data demonstrate: first, that *C. acetobutylicum* Weizmann contains a 210-kb plasmid (linearized by *Apa*I, *Sma*I and *Sst*II); second, that a small portion of it is linear in uncut DNA preparation; and third, that it is lost in the degenerate strains.

The genes encoding the enzymes required for the last steps of acetone and butanol production are clustered in the *sol* operon locus^{4,5}. To check whether these genes are carried on the plasmid, we used as a probe *ctfA* and *ctfB* genes (from *C. acetobutylicum* Weizmann), amplified by the polymerase chain reaction (PCR), encoding the two subunits of the

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Mammal bones in Dominican amber

SIR — When and how did land vertebrates colonize the Greater Antilles, West Indies, during the Cenozoic? Were colonization events sporadic and fortuitous, or were they tightly clustered in time, suggesting the operation of a common cause (see ref. 1)? Fossils should help with these enquiries, but discoveries in conventional palaeontological contexts on these islands are exceedingly rare².

To a certain extent, this deficiency is made up by finds in Dominican amber, specimens of which occasionally contain small lizards and frogs. However, evidence for the presence of larger vertebrates, especially birds and mammals, has so far been limited to isolated (and rather undiagnostic) feathers and hair strands. We now report the discovery of the first mammal bones in Dominican amber (*A*, *B* in the figure), the identification of which provides additional evidence for the view³ that most mammalian colonizations were clustered early in the Tertiary.

The amber piece, containing six vertebrae and portions of several ribs in partial articulation, is reliably reported to have been collected from the La Toca group of amber mines in the La Cumbre region of the northern Dominican Republic. It lacks features indicative of forgery⁴, and we conclude that it is authentic. Recent re-analy-

Ethidium bromide-stained unrestricted (lanes 1, 2) and *Sma*I-digested (lanes 3, 4) DNA from *C. acetobutylicum* Weizmann (odd lane numbers) and WDS1 (even lane numbers) after separation by PFGE. The 1% agarose gel was run in $\times 0.5$ Tris-borate EDTA buffer for 18 h at 200 V (6 V cm^{-1}) using a linear ramp of pulse time from 10 to 50 s. Autoradiogram obtained, after hybridization with the PCR-amplified *ctfA* and *B* genes used as a probe, for unrestricted (lanes 5, 6) and *Sma*I-digested (lanes 7, 8) DNA from *C. acetobutylicum* Weizmann and WDS1. DNA was blotted on Hybond N⁺ (Amersham). The probe was labelled by random-priming with [α -³²P]-dATP and purified on a Microspin S200 (Pharmacia) column. Hybridization was performed at 65 °C in $5 \times \text{SSC}$, $5 \times \text{Denhardt}$, 0.5% SDS. Blots were washed at room temperature twice for 10 min in $2 \times \text{SSC}$ 0.1% SDS and twice for 30 min in $0.1 \times \text{SSC}$ 0.1% SDS.