theorem[16,4]. Fish in food-sparse environments 1 and 5 (Table 1) stay at the bait source longer than in the more food-rich environments.

This study shows that large organic falls reaching the sea floor are rapidly dispersed at abyssal depths in the Northern Hemisphere. There are significant spatial variations in departure rates depending on abundance of scavengers and prevailing food availability. The range of these demersal fish on a basin-wide scale must be considered when modelling the distribution and fate of natural an anthropogenic inputs to the deep ocean. □

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Is the guinea-pig a rodent?

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THE guinea-pig (*Cavia porcellus*), traditionally classified as a New World hystricomorph rodent, often shows anomalous morphological and molecular features in comparison with other eutherian mammals[1–14]. For example, its insulin differs from that of other mammals in anabolic and growth-promoting activities and in its capability to form hexamers[5,6]. Indeed, the literature about the molecular evolution of guinea-pigs abounds in references to 'convergent evolution', 'extremely rapid rates of substitution', and 'unique evolutionary mechanisms'. These claims are based on the assumption that the guinea-pig is a rodent. Our phylogenetic analyses of amino-acid sequence data, however, imply that the guinea-pig diverged before the separation of the primates and the artiodactyls from the myomorph rodents (rats and mice). If true, then the myomorphs and the caviomorphs do not constitute a natural clade, and the Caviomorpha (or the Histricomorpha) should be elevated in taxonomical rank and regarded as a separate mammalian order distinct from the Rodentia. If, as suggested by recent data[15,16], the myomorphs branched off before the divergence among the carnivores, lagomorphs, artiodactyls and primates, then the new order would represent an early divergence in eutherian radiation.

The Rodentia, which is the most speciose mammalian order, is traditionally divided into three extant suborders: the Sciuromorpha (squirrel-like rodents), the Myomorpha (rat-like rodents) and the Hystricomorpha (porcupine-like rodents)[1]. Whereas the first two suborders are generally considered to be monophyletic, the New World families of the Hystricomorpha (the Caviomorpha or guinea-pig-like rodents) are sometimes thought to have evolved independently of the Old World hystricomorph rodents, and are, thus, regarded as a separate group within the Rodentia[2]. Claims about the peculiarity of guinea-pig genes are usually based on the assumption that the guinea-pig is indeed a rodent. A different taxonomic assignment may resolve or ameliorate many of the paradoxes associated with the evolution of guinea-pig genes.

To infer the taxonomic position of the guinea-pig, we analysed the phylogeny of protein sequence data from the caviomorphs, myomorphs, the primates, the artiodactyls and some outgroup species such as marsupials, birds, or toads. We used the maximum parsimony method[17] and the PROTPARS program of Felsenstein's PHYLIP package (version 3.3) to calculate the number of amino-acid replacements required for each of the alternative trees, and the number of informative sites supporting each of the trees.

We first consider, besides the outgroup, only three eutherian groups: the guinea-pig (or caviomorphs), the myomorphs and the primates. This simplifies the analysis because the branching order of eutherians is not well established. Moreover, it increases the amount of data for analysis because there are more sequence data for the primates than for other orders. If there are more than one sequence available in a group, we choose sequences with known branching order. For example, for the primates we choose the human, an Old World monkey (the rhesus monkey,

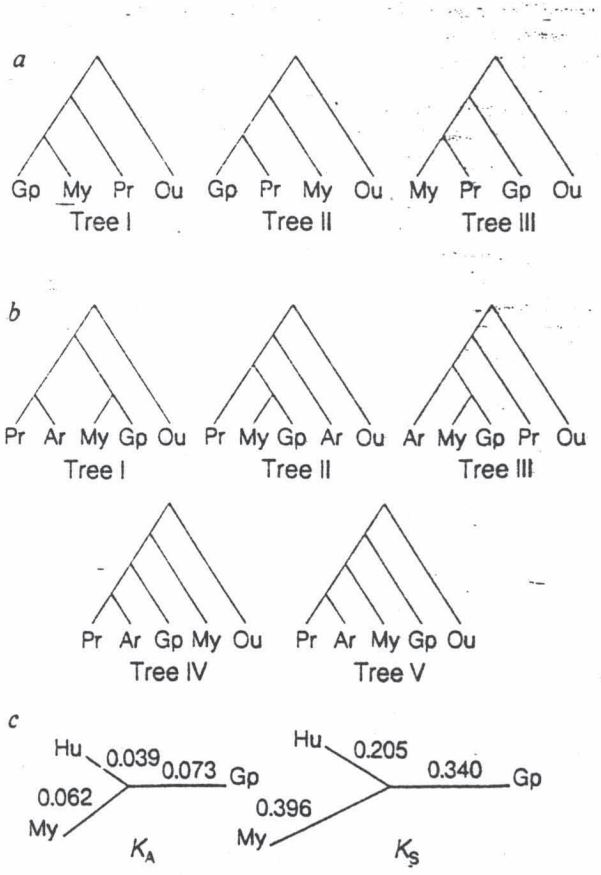

FIG. 1 *a*, Three possible phylogenetic trees for guinea-pigs (Gp), primates (Pr), myomorphs (My), and an outgroup (Ou). Tree I represents the traditional view that the guinea-pig and the myomorphs form one clade. *b*, Five of 15 possible alternative phylogenetic trees for primates, artiodactyls (Ar), myomorphs, guinea-pigs, and an outgroup. *c*, Branch lengths from a common node to humans (Hu), myomorphs (My) and guinea-pigs (Gp) computed from the number of nucleotide substitutions per nonsynonymous site (K_A) and per synonymous site (K_S) given in Table 3.

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TABLE 1 Number of informative sites supporting each of the three possible alternative phylogenetic trees (Fig. 1*a*), and minimum number of amino-acid replacements required for each tree (in parentheses)

		Primates (Pr), guinea-pig (Gp) and myomorphs (My)					Artiodactyls (Ar), guinea-pig (Gp) and myomorphs (My)				
Protein	Out-group	*L**	*I*†	Tree I (Gp-My)	Tree II (Gp-Pr)	Tree III (Pr-My)	*L*	*I*	Tree I (Gp-My)	Tree II (Gp-Ar)	Tree III (Ar-My)
β-globin	MA	145	9	5 (189)	0 (194)	4 (189)	145	11	7 (210)	0 (217)	4 (213)
α-crystallin A chain	MA	162	1	0 (33)	1 (32)	0 (33)	162	1	1 (29)	0 (30)	0 (30)
α-globin	MA	145	9	4 (170)	0 (174)	5 (168)	145	9	2 (190)	1 (191)	6 (185)
α-lactalbumin	MA	120	17	4 (148)	8 (143)	5 (147)	120	12	1 (188)	6 (183)	5 (184)
glucagon	MA	29	0	0 (5)	0 (5)	0 (5)	29	0	0 (5)	0 (5)	0 (5)
pancreatic ribonuclease	MA	122	7	1 (193)	5 (189)	1 (193)	122	5	2 (223)	3 (222)	0 (225)
'big' gastrin	MA	31	1+gap	0 (22)	0 (22)	1+gap(21)	31	1+gap	0 (28)	0 (28)	1+gap(27)
adrenocorticotrophin	OS	39	1	0 (11)	0 (11)	1 (10)	39	1	0 (13)	0 (13)	1 (12)
lipocortin	PG	345	19	4 (179)	4 (179)	11 (172)	25	2	1 (31)	1 (31)	0 (32)
pancreatic polypeptide	CK	36	0	0 (15)	0 (15)	0 (15)	36	1	0 (38)	1 (37)	0 (38)
proinsulin	CK	78	4	1 (74)	1 (74)	2 (73)	78	4	2 (87)	0 (89)	2 (87)
lipoprotein lipase	CK	447	20	2 (206)	6 (202)	12 (196)	447	21	2 (218)	9 (212)	10 (211)
β-nerve growth factor	CK	171	11	5 (84)	1 (88)	5 (84)	123	7	5 (38)	0 (43)	2 (41)
vasoactive intestinal peptide	CK	28	1	0 (8)	0 (8)	1 (7)	28	1	0 (8)	0 (8)	1 (7)
vasopressin-neurophysin precursor	TD	100	2	0 (60)	2 (58)	0 (60)	102	1+gap	1+gap(58)	0 (59)	0 (59)
Total		1,998	102 +gap	26 (1,397)	28 (1,394)	48 (1373) +gap	1,632	77 + 2 gaps	24 (1,364) +gap	21 (1,368)	32 (1,356) +gap

Sequences in this and other tables from the GenBank, EMBL, NBRF-PIR, and Swiss Prot DNA or protein data libraries. The outgroup species used are CK, chicken; OS, ostrich; PG, pigeon; TD, toad (*Bufo japonicus*); and MA, marsupials. Opossum (*Didelphis virginiana*) and red kangaroo (*Macropus rufus*) used for β-globin and α-crystallin A chain; opossum and Eastern grey kangaroo (*M. giganteus*) for α-globin; red-necked wallaby (*M. rufogriseus*) for α-lactalbumin; opossum for glucagon and 'big' gastrin; and red kangaroo for pancreatic ribonuclease. For the caviomorph group, guinea-pig is used in all cases, except that chinchilla, cuis, and capybara are used for pancreatic ribonuclease and guinea-pig and chinchilla are used for 'big' gastrin. For the other three eutherian groups the species used are: human, rhesus monkey, spider monkey, mouse, rat, golden hamster, cow, goat, and Bactrian camel (*Camelus bactrianus*) for the β-globin; human, rhesus monkey, galago (bush baby), mouse, rat, golden hamster, cow, camel (*Camelus dromedarius*) and pig for α-crystallin A chain; human, baboon, spider monkey, mouse, rat, golden hamster, cow, camel and pig for α-globin; human, rat, cow, goat and camel for α-lactalbumin; human, rat and pig for glucagon; human, mouse, rat, golden hamster, cow, camel, and giraffe for pancreatic ribonuclease; human, rat, cow and pig for 'big' gastrin; human, rat, cow and pig for pancreatic polypeptide; human, mouse, rat, cow and pig for adrenocorticotrophin; human, rat and pig for lipocortin; human, mouse, rat, cow and pig for proinsulin; human, mouse and cow for lipoprotein lipase; human, mouse and cow for β-nerve growth factor; human, rat and pig for vasoactive intestinal peptide; human, rat, cow and pig for vasopressin-neurophysin precursor. Informative sites are all those amino-acid positions at which the number of substitutions required differs among the possible alternative phylogenetic trees. An informative site is said to support a tree if that tree requires the least number of subsitutions at that site in comparison with the alternative possible trees. Note that the number of informative sites supporting trees I and II are 26 and 28, but tree I requires 3 additional substitutions. This is because replacement of an amino acid by another at a certain site may sometimes require more than one nonsynonymous nucleotide substitution at the DNA level.

* *L*, number of aligned amino-acid sites.

† *I*, number of informative sites.

for instance), and a New World monkey (spider monkey). The species used are given in Table 1. With these three groups and an outgroup (which may comprise more than one species) there are three possible phylogenetic trees (Fig. 1*a*). Tree I represents the presently accepted taxonomic scheme, in which the guinea-pig and the myomorphs are clustered to form a clade. In tree II, the guinea-pig and the primate lineages form one clade, with the two groups more closely related to each other than either is to the myomorphs. In tree III, the guinea-pig is an outgroup to both primates and myomorphs.

Table 1 presents the results of this analysis for 15 protein sequences with a total of 1,998 aligned amino-acid sites. There are 102 informative sites, of which 48 sites support tree III, whereas only 26 and 28 sites support trees I and II, respectively. The probability that tree III is wrong is roughly $P < 0.05$ (refs 18, 19); the test is rough because it assumes rate-constancy and equal weights for all informative sites. (Although 48% of the sites supporting tree III are due to lipocortin and lipoprotein lipase, this is not much higher than the contribution (40%) of these two proteins to the 1,998 sites analysed.) The molecular evidence against the traditional view (tree I) is very strong, for it is supported by only 26 of the 102 informative sites. The amino-acid sequence of gastrin[8] provides additional support for tree III. The 'big' gastrins of dogs, cats, cows, sheep, goats, humans, rats and rabbits are of 34 amino acids. In comparison, the 'big' gastrins of two New World hystricomorphs, guinea-pig and chinchilla (*Chinchilla brevicaudata*), are of only 33 amino acids, lacking a glutamic acid near their terminus. The same feature was noted in the gastrin of opossum (*Didelphis virginiana*), a marsupial.

TABLE 2 Number of amino-acid differences between an outgroup (OU) and humans (HU), myomorphs (MY) and guinea-pigs (GP)

Protein		OU-HU	OU-MY	OU-GP
Outgroup: marsupial				
α-globin		27	33	36
pancreatic ribonuclease		42	42	46
α-lactalbumin		55	66	66
α-crystallin		16	14	15
β-globin		38	45	44
glucagon		2	2	6
'big' gastrin		6	10	10
pancreatic polypeptide		5	10	5
	Total	191	222	226
Outgroup: chicken				
β nerve growth factor		71	80	74
lipoprotein lipase		104	104	122
vasoactive intestinal polypeptide		4	4	6
insulin		41	37	51
	Total	220	225	253

TABLE 3 Number of substitutions per nonsynonymous site (K_A) and synonymous site (K_S) between guinea-pigs and humans (GP-HU), guinea-pigs and myomorphs (GP-MY), and humans and myomorphs (HU-MY)

Gene	N	K_A			K_S		
		GP-HU	GP-MY	HU-MY	GP-HU	GP-MY	HU-MY
preproinsulin	330	0.208	0.211	0.102	0.700	0.854	0.673
apolipoprotein E	906	0.149	0.176	0.175	0.387	0.771	0.618
preproglucagon	540	0.044	0.061	0.043	0.464	0.660	0.560
α-lactalbumin	411	0.170	0.241	0.174	0.550	1.112	0.848
lipoprotein lipase	1,335	0.065	0.071	0.029	0.653	0.671	0.607
pancreatic polypeptide	213	0.149	0.193	0.155	0.958	0.789	0.486
N-*ras* proto-oncogene	564	0.002	0.009	0.007	0.284	0.516	0.462
factor IX	804	0.116	0.125	0.097	0.366	0.676	0.525
insulin-like growth factor I	604	0.210	0.292	0.224	0.861	0.846	0.666
Weighted average		0.112	0.136	0.101	0.545	0.736	0.601

Next, we replace the primate group by the artiodactyl group. The data set now becomes smaller (1,632 aligned sites) and the number of informative sites is reduced to 77. The number of sites supporting tree III is 32 whereas those supporting trees I and II are only 24 and 21, respectively. Therefore, the result again supports the view that the guinea-pig has branched off earlier than did the myomorphs.

Finally, we consider the guinea-pig, the myomorphs, the primates and the artiodactyls together. The first three trees in Fig. 1*b* represent the traditional view that the guinea-pig and the myomorphs belong to one clade. We compare these trees with tree V, which is suggested by the above analyses and the study of Li *et al.*[16], and also with tree IV, which is a modification of tree V with the order of My and Gp reversed. The minimum numbers of amino-acid replacements required for each of the five trees are 1,460, 1,457, 1,458, 1,457, and 1442. Thus, tree V requires at least 15 steps fewer than trees I, II and III, which are only as parsimonious as tree IV. In this analysis, the sites used are the same as those used in the second analysis of Table 1, but the differences in steps between the most parsimonious tree and the other trees have become larger as a result of including the primate group. The result strengthens our hypothesis that the guinea-pig branched off earlier than the myomorphs and also the suggestion of Li *et al.*[16] that the myomorphs are an outgroup to the primates and artiodactyls.

Thus our analyses suggest that the guinea-pig represents a separate evolutionary lineage from the myomorph rodents, and should not be classified in the same order. It is not yet possible to decide which species besides the caviomorphs belong to the new mammalian order represented by the guinea-pig. Although controversial, the caviomorphs are commonly regarded as a subgroup of the hystricomorphs, and this is supported by limited molecular data[20]. We therefore tentatively suggest that the hystricomorphs represent a new order.

A new taxonomic assignment for the guinea-pig resolves or ameliorates many of the paradoxes associated with the evolution of its genes. For example, consider lipocortin. Under the assumption that the guinea-pig is a rodent or at least a sister group of the rodents, one must assume that at least 15 amino-acid replacements have occurred in parallel in pigeons and in guinea-pigs. The number of parallel substitutions is reduced to 8 if the new taxonomic position of the guinea-pig is accepted.

In many studies the rate of substitution in guinea-pig genes relative to that in myomorph species has been computed by using the relative rate test[21] with human or bovine genes as an outgroup; that is, tree I in Fig. 1*a* is assumed to represent the true phylogeny. For many genes the conclusion was that the guinea-pig lineage evolves much faster than the myomorph lineage. For example, the α- and β-globin chains evolved roughly two to four times faster in the guinea-pig than in mice or rats[22]. By contrast, under our proposed phylogenetic position for the guinea-pig, the two sequences seem to have evolved at about the same rate in both the caviomorph and the myomorph lineages. Table 2 lists the number of amino-acid differences between an outgroup, on the one hand, and humans, myomorphs or guinea-pigs, on the other. For the group of proteins for which the outgroup is a marsupial, there seems to be no difference in the number of replacements between myomorphs and guinea-pigs. For the group of proteins for which chicken serves as the outgroup, the guinea-pig seems to have accumulated an excess of amino-acid replacements in comparison to myomorphs. The excess, however, can be entirely attributed to insulin and lipoprotein lipase, both of which seem to have evolved much faster in the guinea-pig than in other mammals (refs. 5, 6, 23; W.A.H. and W.-H.L., unpublished results). We therefore conclude that claims of large differences in the rate of evolution between guinea-pigs and myomorphs may have been exaggerated in many cases as a result of an erroneous phylogenetic assumption. But there is evidence that both the caviomorph and myomorph lineages have evolved faster than the human lineage (Table 2).

Several DNA sequences are available for computing the genetic distance between guinea-pigs, on the other hand, and myomorphs or humans, on the other (Table 3). The number of substitutions per nonsynonymous site (K_A) and per synonymous site (K_S) were estimated by the method of Li *et al.*[24]. In almost all cases, the values of both K_A and K_S between guinea-pigs and humans are smaller than the corresponding values between guinea-pigs and myomorphs. The only exceptions are the K_S values for pancreatic polypeptide and insulin-like growth factor I. Therefore, even if tree I in Fig. 1*a* represents the true branching order, the genetic distances between guinea-pigs and myomorphs are large enough to warrant a separate ordinal status for the Caviomorpha. Again, the results indicate that myomorph genes evolve 1.5–2.0 times faster than human genes (Fig. 1*c*).

The proposed new evolutionary position of the guinea-pig needs to be re-examined in the future using more sequence data, particularly by replacing those bird sequences by marsupial sequences as references. If the hypothesis turns out to be false, and the guinea-pig is indeed a rodent, then the genetic distances in Table 3 imply a much faster rate of nucleotide substitution in guinea-pig and myomorph genes than in human genes and the data in Table 1 provide a dramatic example that unequal rates of evolution can consistently mislead parsimony inferences[25], even when the characters are from amino-acid sequences. □

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