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How to cite:

Haresnape, Janet (2010). Darwin and evolution: a set of activities based on the evolution of mammals. *School Science Review*, 91(337) pp. 75–86.

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# Darwin and evolution: a set of activities based on the evolution of mammals

*Janet M. Haresnape*

**ABSTRACT** These activities, prepared for key stage 5 students (ages 16–18) and also suitable for key stage 4 (ages 14–16), show that physical appearance is not necessarily the best way to classify mammals. DNA structure is examined to show how similarities and differences between DNA sequences of mammals can be used to establish evolutionary relationships. Some real DNA sequences are compared to illustrate that the whale is surprisingly closely related to mammals such as the hippo, camel and cow, a relationship confirmed by fossil evidence. Finally, an analysis of haemoglobin sequences of primates shows the close relationship between humans and other great apes such as the chimpanzee.

Darwin made extensive observations on a great many creatures, including mammals, and noticed that species fell into natural groups. For example, lions, tigers and leopards have many similarities and resemble cats. On the basis of his observations, he was able to place mammals in distinct groups. His work has been continued, and we now recognise that all mammals evolved from a common ancestor and have branched into many different taxonomic orders (Figure 1).

The activities described here provide students with an opportunity to compare species on an anatomical and biochemical level. Information available to Darwin, such as fossil evidence and observation of the physical appearance of animals, is considered alongside the molecular evidence that is available now. Students examine genuine molecular evidence in the form of DNA and amino acid sequences, and use this to deduce evolutionary relationships between different mammals. The importance of looking at evidence from different sources, such as morphological, fossil and molecular, is emphasised. These problem-solving exercises allow small groups of students to think through the evolutionary relationships between mammalian groups, and to realise that physical appearance is not always the best way to classify mammals. The activities have been successfully trialled with a group of year 9 students (ages 13–14) as well as with key stage 5 (ages 16–18) students for whom they were

prepared. They take approximately two hours to complete, but this could be spread over two or more lessons. Where appropriate ‘blank’ versions of tables and figures are provided which can be copied for students to complete.

## Activity 1: Odd one out

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The first activity involves an examination of four well-known mammals: the rhinoceros, hippopotamus, elephant and whale.

We begin by asking which of the four is the ‘odd one out’. Models or pictures of these four mammals should be presented if possible, and students asked to consider which one appears at first sight to be most different from the other three.

Students are likely to suggest that the whale is the odd one out on the basis of its habitat, as it lives in the sea, and also on the basis of its appearance, as it has no legs. Others may suggest the rhino, as it is the most endangered, or the elephant, as it has a trunk. A good argument can be made for any answer. However, in evolutionary terms, it is the elephant that is most different from the others, as it has a different evolutionary origin from the other three. (It is in the purple section, in Figure 1, whereas the rhino, hippo and whale are all in the blue section.) The physical appearance of animals does not necessarily indicate which are most closely related.

We now turn to look at some fossil evidence that tells us about the evolutionary history

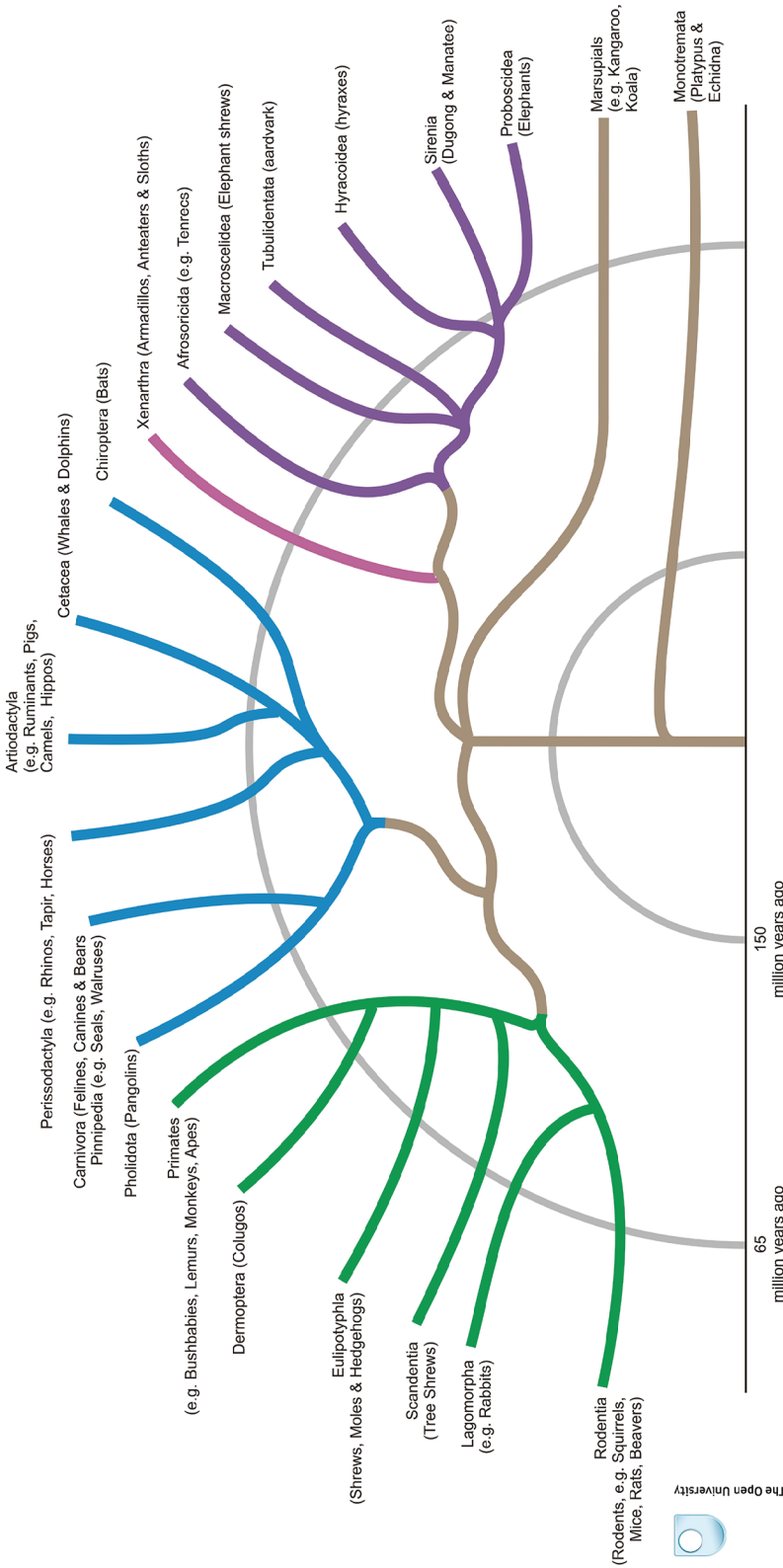
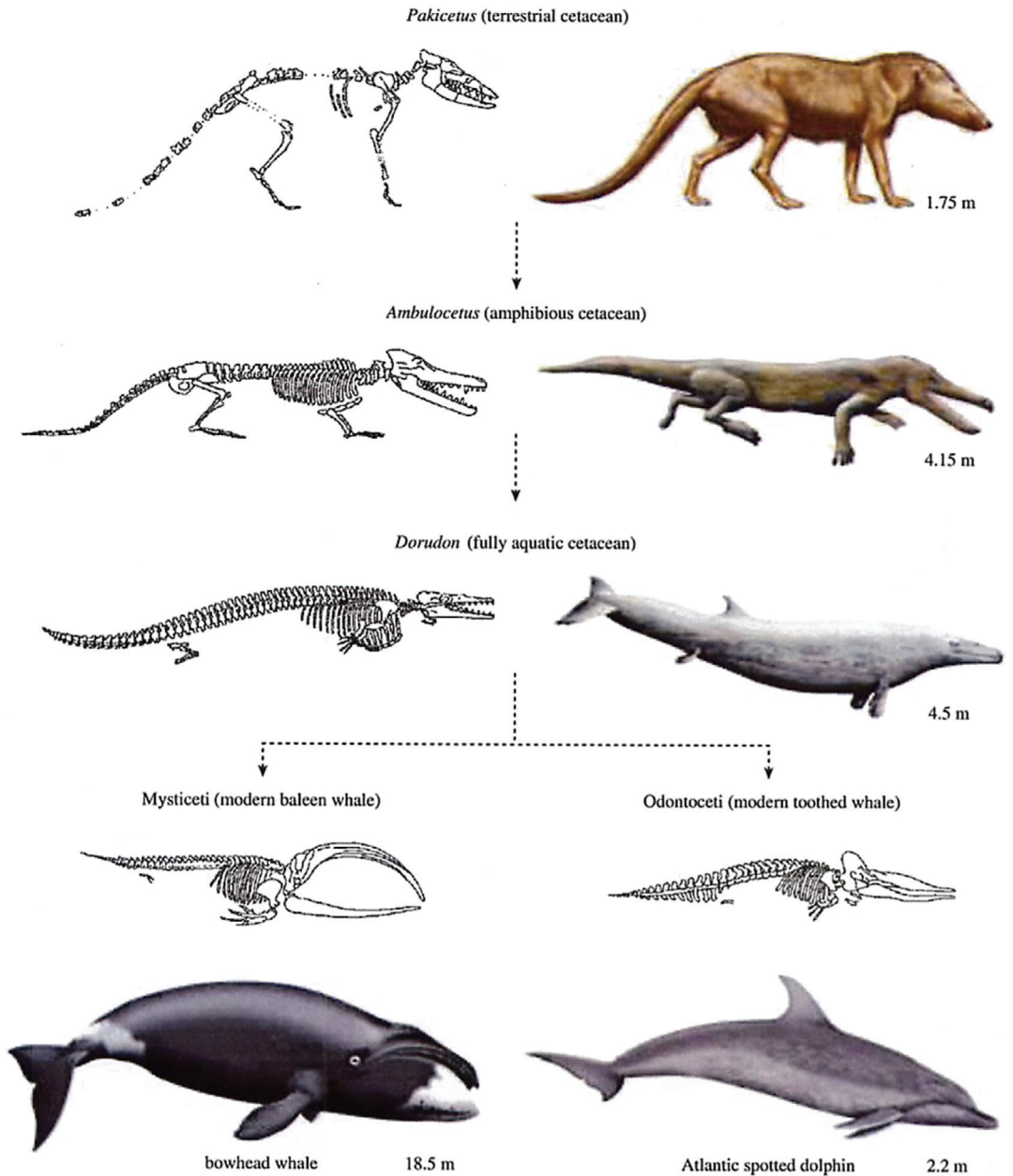


Figure 1 Evolutionary tree showing the origin of the main mammalian groups. (Adapted from MacDonald, 2001.)

of modern whales. Figure 2 summarises the evolutionary origin of whales and dolphins, and shows that they evolved from land creatures with four legs, gradually losing their legs and becoming more streamlined. Note that fossils of ancestral

whales have an ankle bone, even though the animal had no legs, showing that it was descended from animals which did have legs. This is clearly visible in the fully aquatic Dorudon (Figure 2) and can still be seen in the skeletons of modern whales.

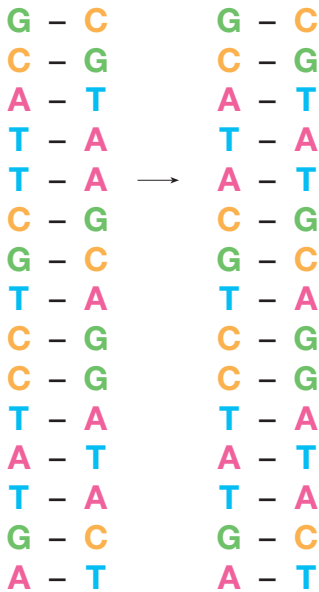


**Figure 2** Some representative mammals in the evolutionary history of modern whales. Imaginative reconstructions of the fossil species are shown, suggesting how they might have looked in life. Note these are not drawn to scale, and the measurements refer to body length. (Figure 7.5 from Thomas, 2003, reproduced with grateful permission.)

This fossil evidence, together with the evolutionary tree (Figure 1), shows that the whale is more closely related to the hippo than the hippo is to the elephant, or even the rhino, despite its very different outward appearance.

### Activity 2: Spot the difference

We now turn to look at how molecular evidence can be used to investigate evolutionary relationships. This activity involves examining two models of double-stranded DNA, with one difference in base sequence between them. This illustrates what is meant by a mutation, or difference in base sequence. If models are not available, a diagram such as that shown in Figure 3 can be used. This activity provides an opportunity to discuss complementary base pairing in double-stranded DNA, and the fact that closely related species have similar DNA. The number of mutations or differences between the DNA of different species can give an indication of how long ago they diverged from a common ancestor.



**Figure 3** Two short sequences of double-stranded DNA with just one base difference. Bases are A (adenine), C (cytosine), G (guanine) and T (thymine). In the fifth base pair from the top, A has been replaced by T and T has been replaced by A.

### Activity 3: DNA sequence evidence

Table 1 shows the DNA sequence of a small stretch of the gene for a particular milk protein called casein in a number of different mammals. The sequence differs from one mammal to another, and those shown are from two species of whale, several familiar ungulate species (members of the order Artiodactyla, including hippo, pig, cow, sheep, goat, deer and camel, plus zebra and tapir from the order Perissodactyla), and the leopard (Carnivora). All these are in the blue section of the evolutionary tree shown in Figure 1. Also included are some more distantly related mammals, from orders in the green section of the tree: human, rabbit and mouse. Ideally, these sequences would be presented as strings of coloured beads, with one colour representing each of the four bases, A, T, C and G. Alternatively, Table 1 could be printed in colour and cut into strips for comparison of sequences from different species.

The task is to count how many differences there are in this stretch of DNA between the whale and each of the other mammals (students can be given a copy of Table 2a to complete). If the sequences are represented as strings of beads, or as strips of paper, the calculation can be done fairly easily by lining them up against each other and counting the number of colour differences. The differences are shown in the last column of Table 2b, and confirm that whale DNA closely resembles that of the members of the order Artiodactyla and that the whale is therefore closely related to them. Here whales appear to be most closely related to the hippo, cow or camel, as there are only three differences between their base sequences in this stretch of DNA.

Note that the difference between the whale DNA and that of the human, rabbit or mouse is much larger than between the whale and other mammals in the table. These mammals are more distantly related, being in the green section as opposed to the blue section of the evolutionary tree shown in Figure 1.

More detailed studies of this kind, looking at much longer sequences from many different genes, have confirmed that whales and dolphins do have their evolutionary origin within the Artiodactyla, and this is in agreement with the evidence from fossils. Their closest living relative is actually believed to be the hippo.

Astute students may note with surprise that the number of differences between the whale and the

**Table 1** DNA sequences from part of the casein gene of selected mammals. This is a 50 base sequence taken from exon 7 of the gene for beta-casein. Bases are A (adenine), C (cytosine), G (guanine) and T (thymine). (From Gatesy *et al.*, 1996.)

	Toothed whale	Baleen whale	Hippopotamus	Cow	Camel	Giraffe	Sheep	Goat	Peccary	Pig	Deer	Tapir	Zebra	Leopard	Human	Rabbit	Mouse
1	A	A	A	T	A	T	T	T	A	A	T	A	A	A	G	G	G
2	G	G	G	G	G	G	G	G	G	G	G	G	G	G	A	G	C
3	A	A	A	A	T	A	A	A	A	A	A	T	T	T	T	T	T
4	G	G	G	G	G	G	G	G	G	G	G	G	G	G	A	C	C
5	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
6	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	G
7	C	C	C	C	C	C	C	C	T	T	C	C	C	C	C	C	C
8	T	T	T	T	T	T	T	T	T	T	T	T	T	C	T	T	C
9	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
10	T	T	T	T	T	T	T	T	T	T	C	T	T	T	T	T	C
11	A	A	A	A	A	A	A	A	G	G	G	T	T	T	T	G	A
12	T	T	C	C	C	C	C	C	T	T	C	C	C	T	T	T	T
13	T	T	T	T	T	T	T	T	T	G	T	T	T	T	G	T	A
14	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	A
15	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
16	A	A	A	A	A	A	A	A	A	A	A	A	A	C	C	C	C
17	A	A	A	A	A	A	A	A	G	G	G	C	C	A	C	T	T
18	G	G	G	G	G	G	G	G	G	G	G	G	G	G	C	C	C
19	C	C	G	C	C	C	C	C	C	C	C	C	C	C	T	T	T
20	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
21	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
22	G	G	G	G	G	G	G	G	G	G	G	A	A	A	A	A	A
23	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
24	G	G	G	G	G	G	G	G	G	G	G	T	T	T	T	T	T
25	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	T	C
26	C	C	C	C	C	C	C	C	C	C	C	T	T	G	C	C	C
27	T	T	T	T	T	T	T	T	T	T	T	T	T	T	C	T	C
28	G	G	G	G	G	G	G	G	A	A	G	G	G	G	A	G	C
29	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
30	C	C	C	C	C	C	C	C	C	C	C	A	A	A	A	A	G
31	T	T	T	T	C	T	T	T	T	T	T	T	T	A	A	T	C
32	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
33	T	T	T	T	T	T	T	T	T	T	T	C	C	T	T	T	T
34	C	C	T	C	G	C	C	C	C	C	C	C	C	C	C	C	T
35	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	G
36	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	G	C
37	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	G	C
38	G	G	G	G	G	G	G	G	G	G	G	A	A	G	G	G	A
39	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	G
40	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	G	T
41	C	C	C	G	C	G	G	G	T	T	G	G	G	C	C	A	C
42	T	T	T	T	T	C	T	T	T	T	T	G	G	T	T	T	T
43	T	T	T	C	T	T	T	T	C	T	T	T	T	T	T	G	T
44	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	A	G
45	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	C
46	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	T
47	A	A	A	A	A	A	A	A	A	G	A	A	A	A	A	A	A
48	A	A	A	A	A	A	A	A	G	T	A	A	A	A	A	A	A
49	T	T	T	T	T	T	G	G	T	C	C	T	T	T	T	T	T
50	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C

**Table 2** DNA sequence differences between the whale and each of the other species for the stretch of the gene shown in Table 1. (a) For students to complete, (b) completed.

(a)

Mammal species	Order	Number of differences in this stretch of DNA between this species and the whale
Toothed whale	Cetacea	
Baleen whale	Cetacea	
Hippopotamus	Artiodactyla	
Cow	Artiodactyla	
Camel	Artiodactyla	
Giraffe	Artiodactyla	
Sheep	Artiodactyla	
Goat	Artiodactyla	
Peccary	Artiodactyla	
Pig	Artiodactyla	
Deer	Artiodactyla	
Tapir	Perissodactyla	
Zebra	Perissodactyla	
Leopard	Carnivora	
Human	Primates	
Rabbit	Lagomorpha	
Mouse	Rodentia	

(b)

Mammal species	Order	Number of differences in this stretch of DNA between this species and the whale
Toothed whale	Cetacea	0
Baleen whale	Cetacea	0
Hippopotamus	Artiodactyla	3
Cow	Artiodactyla	3
Camel	Artiodactyla	3
Giraffe	Artiodactyla	4
Sheep	Artiodactyla	4
Goat	Artiodactyla	4
Peccary	Artiodactyla	5
Pig	Artiodactyla	7
Deer	Artiodactyla	7
Tapir	Perissodactyla	11
Zebra	Perissodactyla	11
Leopard	Carnivora	9
Human	Primates	15
Rabbit	Lagomorpha	18
Mouse	Rodentia	25

leopard is less than between the whale and zebra or tapir. This is because the length of DNA under consideration is only 50 bases long, and analysis of longer sequences has established that the relationships shown in Figure 1 are correct.

If time permits, a more detailed analysis of the sequences shown in Table 1 could be undertaken; for example, comparing more of the DNA sequences in a pairwise manner. A possible comparison could involve the mammals shown in Table 3. Of these, the sheep and goat form the most closely related pair, with no DNA sequence differences in this particular 50 base stretch of DNA. The zebra is more distantly related than the mammals within the order Artiodactyla, as would be expected as it is a member of the order Perissodactyla (Figure 1). The DNA evidence in Table 3b confirms that the whale is more closely related to the Artiodactyla species than any of those within the order Artiodactyla are to the zebra. If time is short, it might be more worthwhile to omit this analysis and move on to Activity 4, which is a similar problem-solving exercise.

**Activity 4: Haemoglobin sequences of primates**

Here we take seven species of primate and consider our relationship to other primate groups by comparing the sequence of the first 130 amino acids of the beta-haemoglobin chain found in each of them. In addition to humans, we consider the great apes (chimpanzee and gorilla), a lesser ape (gibbon), an Old World monkey (rhesus monkey), a New World monkey (squirrel monkey) and a lemur. Students might first be asked to predict which of these primate species are most closely and most distantly related on the basis of their appearance. Pictures or models of the species could be provided. It is likely that they will suggest that the two species of monkey (rhesus monkey and squirrel monkey) are more closely related than the different species of great ape (gorilla, chimpanzee, human).

After consideration of this question, students could be shown the haemoglobin sequences of the seven primates, shown in Table 4. Those amino acids which are the same for all primate species are shown in grey, so only those that differ are identified here. Each amino acid in the positions where there is variation is represented by a different colour, identified in the key. Again, these



**Table 3** Pairwise comparison of DNA sequence differences between the whale, five species from the order Artiodactyla (hippo, cow, camel, sheep and goat) and the zebra from the order Perissodactyla. (a) For students to complete, (b) completed.

(a) Number of DNA sequence differences between pairs of mammals							
	Whale	Hippo	Cow	Camel	Sheep	Goat	Zebra
Whale							
Hippo							
Cow							
Camel							
Sheep							
Goat							
Pig							

(b) Number of DNA sequence differences between pairs of mammals (completed)							
	Whale	Hippo	Cow	Camel	Sheep	Goat	Zebra
Whale		3	3	3	4	4	12
Hippo			4	4	5	5	13
Cow				4	1	1	11
Camel					5	5	11
Sheep						0	11
Goat							11
Pig							

sequences are best shown as strings of coloured beads, with grey beads for the invariant sites, and a different colour for each amino acid, in order to make the comparisons easier. However, as in Activity 3, it would be possible to print a colour version of Table 4 and cut it into strips for pairwise comparison of species.

As with DNA sequences, analysis of the similarities and differences between the amino acid sequences in the same protein from different mammals can give an indication of how closely related they are. Most striking in Table 4 are the similarities between the amino acid sequences of beta-haemoglobin in all primates, shown by all the positions coloured in grey. Ninety-five of the 130 amino acids in this part of the chain (73%) are the same for all primates.

Detailed analysis of the differences in amino acid sequence can be made by counting the

differences between pairs of primate species and recording them in a copy of Table 5a. Table 5b is a completed version of the table. If there is insufficient time for this, students could simply look at the number of differences between the human sequence and each of the other primates. Either way, it is clear from this evidence that humans are very closely related to the great apes, such as the gorilla and chimpanzee. The amino acid sequences of beta-haemoglobin in humans and chimpanzees are identical, and there is only one difference between the sequences in humans and gorillas.

From a completed version of Table 5, the evolutionary relationships between these seven species of primate can be deduced, and are shown in Figure 4. It is worth pointing out that the number of differences between the sequence of an Old World monkey (rhesus monkey) and that of a New World monkey (squirrel monkey)



**Table 4** Amino acid sequence of beta-haemoglobin in seven species of primate. These could be presented in any order, but are here given in order of the closeness of their relationship to humans. Grey positions represent those amino acids which are the same for all these primates. (Adapted from Banister-Marx, J. The National Health Museum activities exchange.)

Position in chain	Primate species						
	Human	Chimp	Gorilla	Gibbon	Rhesus monkey	Squirrel monkey	Lemur
1	VAL	VAL	VAL	VAL	VAL	VAL	THR
2	HIS	HIS	HIS	HIS	HIS	HIS	LEU
3							
4	THR	THR	THR	THR	THR	THR	SER
5	PRO	PRO	PRO	PRO	PRO	GLY	ALA
6	GLU	GLU	GLU	GLU	GLU	ASP	GLU
7							
8	LYS	LYS	LYS	LYS	LYS	LYS	ASP
9	SER	SER	SER	SER	ASN	ALA	ALA
10	ALA	ALA	ALA	ALA	ALA	ALA	HIS
11							
12	THR	THR	THR	THR	THR	ALA	THR
13	ALA	ALA	ALA	ALA	THR	ALA	SER
14							
15							
16							
17							
18							
19							
20							
21	ASP	ASP	ASP	ASP	ASP	GLU	GLU
22	GLU	GLU	GLU	GLU	LEU	ASP	LYS
23							
24							
25							
26							
27							
28							
29							
30							
31							
32							
33	VAL	VAL	VAL	VAL	LEU	VAL	VAL
34							
35							
36							
37							
38							

Position in chain	Primate species						
	Human	Chimp	Gorilla	Gibbon	Rhesus monkey	Squirrel monkey	Lemur
39							
40							
41							
42							
43							
44							
45							
46							
47							
48							
49							
50	THR	THR	THR	THR	SER	THR	SER
51							
52	ASP	ASP	ASP	ASP	ASP	ASP	SER
53							
54							
55							
56	GLY	GLY	GLY	GLY	GLY	ASN	SER
57							
58							
59							
60							
61							
62							
63							
64							
65							
66							
67							
68							
69	GLY	GLY	GLY	GLY	GLY	GLY	SER
70							
71							
72							
73	ASP	ASP	ASP	ASP	ASP	ASP	GLU
74							
75							
76	ALA	ALA	ALA	ALA	ASN	THR	HIS
77							
78							
79							
80	ASN	ASN	ASN	ASP	ASN	ASN	ASN
81							
82							
83							
84							

Position in chain	Primate species						
	Human	Chimp	Gorilla	Gibbon	Rhesus monkey	Squirrel monkey	Lemur
85							
86							
87	THR	THR	THR	LYS	GLN	GLN	GLN
88							
89							
90							
91							
92							
93							
94							
95							
96							
97							
98							
99							
100							
101							
102							
103							
104	ARG	ARG	LEU	ARG	LYS	ARG	LYS
105							
106							
107							
108							
109							
110							
111	VAL	VAL	VAL	VAL	VAL	VAL	SER
112	CYS	CYS	CYS	CYS	CYS	CYS	ALA
113	VAL	VAL	VAL	VAL	VAL	VAL	GLU
114	LEU	LEU	LEU	LEU	LEU	LEU	SER
115	ALA	ALA	ALA	ALA	ALA	ALA	GLU
116	HIS	HIS	HIS	HIS	HIS	HIS	LEU
117							
118							
119							
120	LYS	LYS	LYS	LYS	LYS	LYS	HIS
121	GLU	GLU	GLU	GLU	GLU	GLU	ASP
122	PHE	PHE	PHE	PHE	PHE	PHE	LYS
123	THR	THR	THR	THR	THR	THR	SER
124							
125	PRO	PRO	PRO	GLN	GLN	GLN	ALA
126	VAL	VAL	VAL	VAL	VAL	LEU	VAL
127							
128							
129							
130	TYR	TYR	TYR	TYR	TYR	TYR	PHE

Key to amino acids in Table 4

Abbreviation	Amino acid
ALA	alanine
ASN	asparagine
ARG	arginine
ASP	aspartic acid
CYS	cysteine
GLN	glutamine
GLY	glycine
GLU	glutamic acid
HIS	histidine
LEU	leucine
LYS	lysine
PHE	phenylalanine
PRO	proline
SER	serine
TYR	tyrosine
THR	threonine
VAL	valine

**Table 5** Number of amino acid differences between different pairs of primates. (a) For students to complete, (b) completed.

(a) Number of amino acid differences between beta-haemoglobin chains

	Human	Chimp	Gorilla	Gibbon	Rhesus monkey	Squirrel monkey	Lemur
Human							
Chimp							
Gorilla							
Gibbon							
Rhesus monkey							
Squirrel monkey							
Lemur							

(b) Number of amino acid differences between beta-haemoglobin chains (completed)

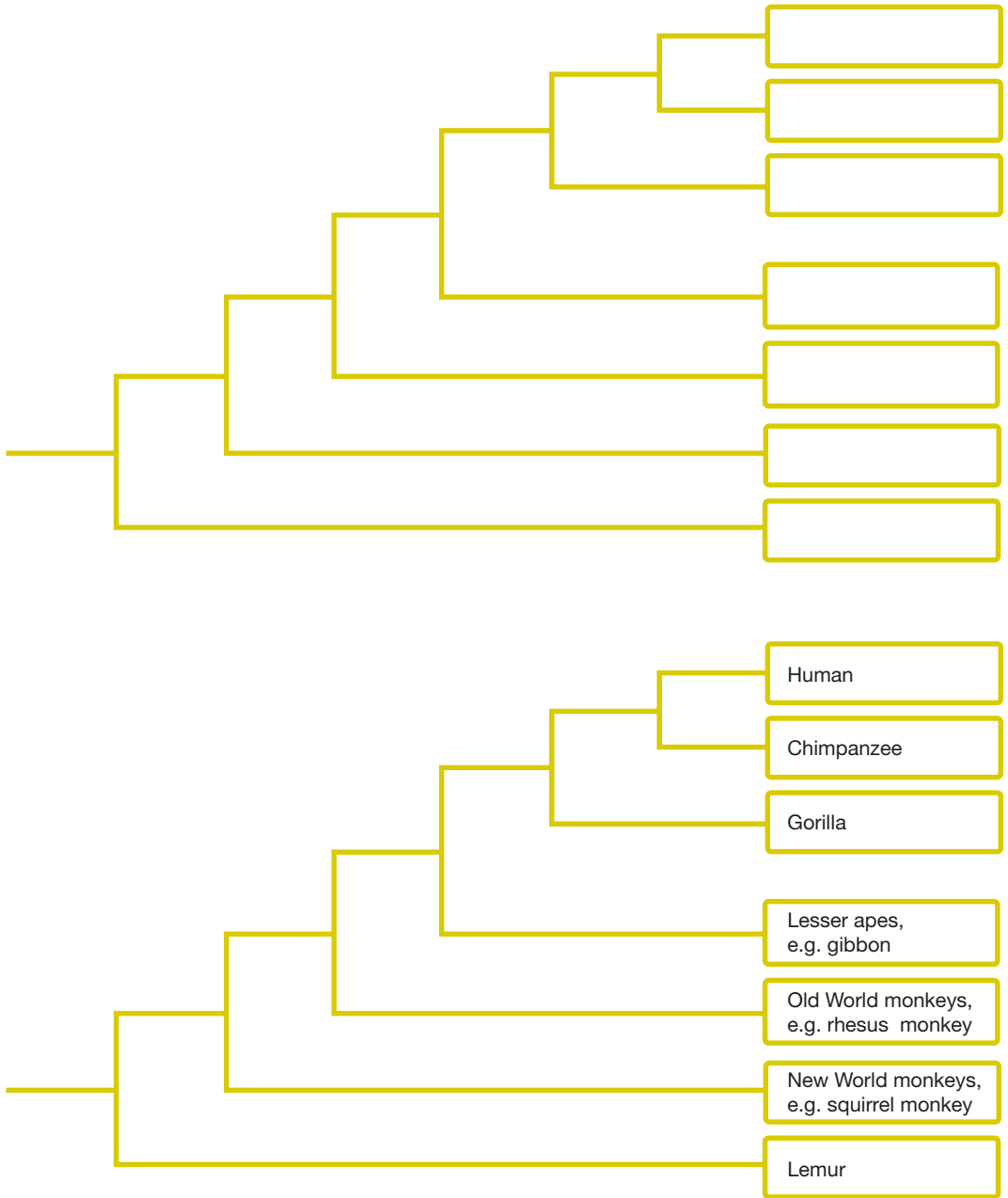
	Human	Chimp	Gorilla	Gibbon	Rhesus monkey	Squirrel monkey	Lemur
Human		0	1	3	10	10	30
Chimp			1	3	10	10	30
Gorilla				4	10	12	30
Gibbon					9	11	31
Rhesus monkey						13	29
Squirrel monkey							30
Lemur							

is more than between humans and apes. This is because these two groups of monkeys diverged longer ago than humans diverged from other apes. So although they seem more similar in outward appearance than humans and other great apes, they are much more distantly related. By examining evidence from fossils, and molecular and anatomical data, it has been deduced that human and chimpanzee lineages diverged about 6 million years ago, whereas Old World and New World monkeys diverged about 13 million years ago.

Similar amino acid sequences of a protein indicate that similar DNA sequences code for

them. Overall, 99% of the DNA of humans and chimpanzees is identical. The 1% of the DNA which is different is crucial in determining what makes us human, and accounts for all the differences between humans and chimpanzees. The remaining 99% is responsible for all the attributes of chimpanzees which are similar to those of humans. We are much more similar to chimps than we might think.

To see how you might have looked millions of years ago, go to [www.openuniversity.co.uk/darwin](http://www.openuniversity.co.uk/darwin) and morph your own face using the Open University’s fun face morph tool, ‘Devolve me’.



**Figure 4** Evolutionary relationships between primate groups, as deduced from amino acid sequence evidence. (a) For students to complete, (b) completed.

Some of these activities are available online in the Science and Nature section of the Open University’s *OpenLearn* website (Haresnape, 2010).

**Acknowledgements**

Thanks to Martin Scott and Linda Hurst (Open

University in the South) for help with preparing Figure 1, and to the referees for their helpful comments. This work was developed at the Open University and has been adapted for *School Science Review* with permission.

