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Homo divinus: The ape that bears God's image

Some Christians believe that to allow room for God they must disallow room for evolution. However, aspects of the evolutionary paradigm have been established conclusively, and can be adduced to demonstrate the complementarity that exists between scientific and theological views of the world. Randomly formed, unique genetic markers shared by similar species establish that these species are descendents of a common ancestor in which the unique markers arose. Three features that demonstrate the common ancestry of humans and other higher primates are discussed. The chromosome set of one species can be rearranged into those of other species by cutting and pasting chromosomes, reflecting familiar genetic processes. The presence of unique non-functional gene relics (pseudogenes), and of unique packets of genetic information known as retrotransposons (both of which we share with other primate species) represent genetic markers which can have arisen only once, in a common ancestor. This compelling genetic evidence must inform our understanding of what it means for God to create, of the place of chance in the creative work of God, and of the nature of humanity. It illustrates the way in which God works, and demonstrates his grace as seen in creation and redemption.

Key words: Evolution; genetics; chromosomal rearrangements; pseudogenes; retrotransposons; creation; chance and design.

Debate over the evolutionary paradigms of science continues to divide the church and distract it from its essential commission. This task is to serve God in society and the world, making known the good news of reconciliation through Christ. The scientific ideas debated in these controversies extend over the range of natural science. To many people, the issues seem irresolvable. By their very nature, the artifacts of a remote past seem unable to provide straightforward interpretations that could satisfy the sceptics and allow Christians unitedly to address more substantial matters.

Is there no truly tractable issue, in which some aspect of evolutionary science could be demonstrated beyond reasonable doubt, and so illuminate authentically biblical faith? Of course, to the confirmed sophist, no demonstrations carry any weight if they threaten to overthrow cherished *a priori* commitments. But it is hoped that people who are motivated by a 'love that comes from a pure heart, a clear conscience, and a genuine faith' (1 Tim.1:5; GNB) could sustain a search for truth, even if they are anxious about what they may

find.

With the advance of the exact science of human genetics, one such key issue presents itself. Christians hold to the biblical assertion that people are created by God in his own image (Gen.1:26-27; 9:6; James 3:9). This status ascribed to humanity is a non-negotiable basis of the biblical world-view. *Theologically* we are creatures who share vital characteristics with God. But it is now clear that we must hold this conviction together with the sure knowledge that we are an evolved species. This knowledge arises from recent genetic advance, which has established conclusively that we are closely related to the (other) great apes, with which we share many unambiguous genetic markers.¹ *Biologically*, we are apes. Hence the title of this paper.²

The establishment of this test case should dispel the basis of all theologically-motivated conflict over evolution. It will allow our exegetes to approach the Scriptures afresh, knowing that the plain meaning of the biblical narratives cannot include physical anthropology. We are free to learn what they teach us about God's purposes for his creatures, and the basis of the relation between God and humanity.³

Two striking facts present themselves when we compare ourselves with the chimpanzees. The first fact is our extraordinary similarity to them. The other is our vast difference from them. The Bible points to this polarity in our nature by teaching that we are made in the image of God and formed of the dust of the earth (Gen.2:7). This indicates our utter dependence on God:

...the LORD has compassion on those that fear him;

...he remembers that we are dust (Psa. 103:13; 90:3; cf. 104:29).

That we are 'made of earth', 'came from the earth', 'belong to the earth' and 'are like the one who was made of earth' (1Cor. 15:47-48) stresses our creatureliness, our membership of a fallen race, and our mortality.

1. The fact of our evolution

We share the carbon-based biochemistry of every known life form. We are vertebrates, because we have backbones. We are eutherian mammals, because we are warm-blooded, have hair, are nourished by a placenta during embryonic development and feed on mothers' milk. We are primates, because we have close affinities with the monkeys. And we are numbered among the great apes. In particular the chimps and gorillas share our genetic information to a

1 Hacia, J.G. 'The ape genome', *Trends Genet* (2001) 17, 637.

2 the term *Homo divinus* is borrowed from Stott, J.R.. *Understanding the Bible*, London: SU (1984), pp. 48f.

3 Kidner, D. *Genesis*, London: Tyndale Press (1967), p.26; Poole, M.W. and Wenham, G.J. *Creation or Evolution: a False Antithesis?* Oxford: Latimer House (1987), p.31.

remarkable extent.⁴

The order of relatedness of humans to the other great ape species has been established by comparing the nucleotide sequences of mitochondrial⁵ and nuclear⁶ DNA (see Glossary at the end of the article for explanations of technical terms). Human and chimpanzee sequences are 98-99% identical for nuclear DNA (>98.3% for non-coding and ~99.5% for coding DNA). At most genetic loci, we are most closely related to chimps, but at some loci, chimps and gorillas are the closest.⁷ A high degree of genetic similarity implies close relatedness, which in turn implies descent from a common ancestor. Evidence establishing such biological roots will be summarised under three headings. (1) Our chromosomes have taken shape by familiar processes of cutting and pasting. (2) We share with other species uniquely rearranged genes. (3) We share with other species unique random additions to our DNA.

1.1 Cutting and pasting chromosomes

Chromosome structure is studied in the science of *cytogenetics*. Humans possess 24 different chromosomes, including 22 autosomes (the same for females and males) and 2 sex (X and Y) chromosomes. Closely related species have similarly structured chromosomes. The chromosome sets of the great apes including humans look strikingly similar.⁸

The main difference in the chromosome sets of humans compared to the other great apes is that our chromosome number 2 is an end-to-end (*telomere-to-telomere*) fusion of two chromosomes which are separate in all the other great apes. Telomeres are the extreme ends of chromosomes and consist of a highly repeated sequence, (TTAGGG)_n. Near the middle of the human chromosome 2 (at band 2q13) is the site where the ancestral ape chromosomes fused. Two telomeric sequences are arranged head-to-head at this site.⁹ Adjacent *sub-telomeric* sequences are the same as those of the corresponding ape chromo-

4 King, M.-C. and Wilson, A.C. 'Evolution at two levels in humans and chimpanzees', *Science* (1975) 188, 107.

5 Ruvolo, M., Pan, D., Zehr, D. *et al.* 'Gene trees and hominid phylogeny', *Proc Natl Acad Sci USA* (1994) 91, 8900; Horai, S., Hayasaka, K., Kondo, R. *et al.* 'Recent African origin of modern humans revealed by complete sequences of hominid mitochondrial DNAs', *Proc Natl Acad Sci USA* (1995) 92, 532; Gibbons, A. 'Our chimp cousins get that much closer', *Science* (1994) 250, 376.

6 Goodman, M. 'Molecular evolution '99: the genomic record of humankind's evolutionary roots', *Am J Hum Genet* (1999) 64, 31; Fujiyama, A., Watanabe, H., Toyoda, A. *et al.* 'Construction and analysis of a human-chimpanzee comparative clone map', *Science* (2002) 295, 131.

7 Gibbons, A. 'Which of our genes make us human?', *Science* (1998) 281, 1432.

8 Yunis, J.J. and Prakash, O. 'The origin of man: a chromosomal pictorial legacy', *Science* (1982) 215, 1525; Jauch, A., Weinberg, J., Stanyon, R. *et al.* 'Reconstruction of genomic rearrangements in great apes and gibbons by chromosomal painting', *Proc Natl Acad Sci USA* (1992) 89, 8611.

9 Ijdo, J.W., Baldini, A., Ward, D.C. *et al.* 'Origin of human chromosome 2: an ancestral telomere-telomere fusion', *Proc Natl Acad Sci USA* (1991) 88, 9051. Humans share many such *interstitial telomeres* with other apes and old world monkeys.

somes.¹⁰ The genetic content of human chromosome 2 is co-linear with that of the two great ape chromosomes from which it is derived.¹¹ At band 2q21 lie the remains of the redundant centromere of one of the ancestral chromosomes.¹² Such *telomeric fusions* are familiar phenomena, arising by naturally occurring mechanisms (Figure 1).

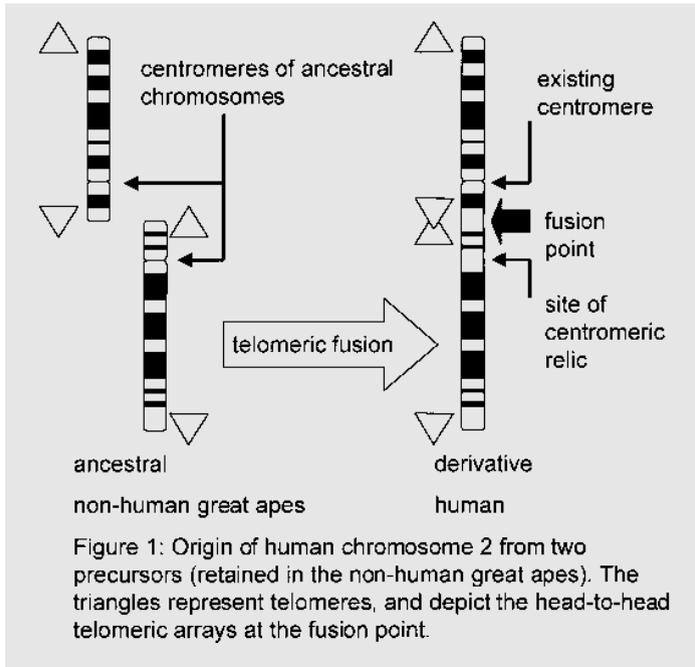


Figure 1

Humans and chimpanzees also differ by rearrangements *within* chromosomes. In these *inversions*, a chromosome breaks in two places, the intervening segment is flipped 180°, and the bits are joined again. An inversion distinguishing human chromosome 17 from the chimp equivalent has been characterised at nucleotide resolution. Sequencing of the breakpoints has shown that the human chromosome retains the ancestral form, and the chimp equivalent is derivative.¹³ Work on the breakpoints that distinguish human chromosomes

10 Martin, C.L., Wong, A., Gross, A. *et al.* 'The evolutionary origin of human subtelomeric homologues – or where the ends begin', *Am J Hum Genet* (2002) 70, 972.

11 except for a translocation and an inversion in the gorilla chromosomes; see de Pontbriand A., Wang, X.-P., Cavaloc, Y. *et al.* 'Synteny comparison between apes and human using fine-mapping of the genome', *Genomics* (2002) 80, 395.

12 Baldini, A., Ried, T., Shridhar, V. *et al.* 'An alphoid DNA sequence conserved in all human and great ape chromosomes: evidence for ancient centromeric sequences at human chromosomal regions 2q21 and 9q13', *Hum Genet* (1993) 90, 577.

13 Kehrer-Sawatzki, H., Schreiner, B., Tanzer, S. *et al.* 'Molecular characterization of the pericentric inversion that causes differences between chimpanzee chromosome 19 and human chromosome 17', *Am J Human Genet* (2002) 71, 375.

4 and 12 from their chimpanzee counterparts is in progress.¹⁴

High resolution cytogenetic mapping has shown how the chromosomes of the great apes (humans, chimps, gorillas, orangutans) may be rearranged to form an ancestral set. The structures of most of the chromosomes belonging to this common ancestor have been unambiguously derived.¹⁵ Blocks of human chromosomal material can be cut-and-pasted to give the chromosome sets of gibbons (lesser apes), macaques (Old World Monkeys)^{15, 16}, or ancestral primates.¹⁷

There is one exception to the conservation of chromosome structure. The Y (male-determining) chromosomes are extensively remodelled.¹⁸ Such shuffling arises during meiosis because Y chromosomes lack a partner with which to undergo side-by-side pairing (which suppresses rearrangement). Some of these rearrangements have been characterised. Humans, alone of the great apes, possess a segment of the X chromosome that has been copied (*transposed*) into the Y chromosome. A part of this introduced DNA was subsequently flipped (inverted) into a distant site.¹⁹ A section of chromosome 1 has been copied into the Y chromosome of humans and the two chimpanzee species, indicating that humans and chimps are descended from a common ancestor in which the shared trait arose.²⁰

Such copied segments of DNA constitute ~5% of the human genome.²¹ Humans and chimpanzees (but not other primates) share duplicated chromosomal segments which have generated two copies of a novel gene,²² and produced the unstable 'CMT' genetic region involved in neurological diseases.²³ These duplications must have been generated in a creature ancestral to humans and chimps. Another duplication inherited by humans, chimps, and

14 Marzarella, R., Viggiano, L., Miolla, V. *et al.* 'Molecular cytogenetic resources for chromosome 4 and comparative analysis of phylogenetic chromosome IV in great apes', *Genomics* (2000) 63, 307; see also Fujiyama *et al.*, ref. 6.

15 Muller, S. and Weinberg, J. "Bar-coding" primate chromosomes: molecular cytogenetic screening for the ancestral karyotype', *Hum Genet* (2001) 109, 85.

16 Schrock, E., du Manoir, S., Veldman, T. *et al.* 'Multicolour spectral karyotyping of human chromosomes', *Science* (1996) 273, 494.

17 O'Brien, S.J., Menotti-Raymond, M., Murphy, W.J. *et al.* 'The promise of comparative genomics in mammals', *Science* (1999) 286, 458.

18 Archidiacono, N., Storlazzi, C.T., Spalluto, C. *et al.* 'Evolution of chromosome Y in primates', *Chromosoma* (1998) 107, 241.

19 Schwartz, A., Chan, D.C., Brown, L.G. *et al.* 'Reconstructing hominid Y evolution: X-homologous block, created by X-Y transposition, was disrupted by Yp inversion through LINE-LINE recombination', *Hum Molec Genet* (1998) 7, 1.

20 Wimmer, R., Kirsch, S., Rappold, G.A. and Schempp, W. 'Direct evidence for the Homo-Pan clade', *Chromosome Res* (2002) 10, 55.

21 Stankiewicz, P. and Lupski, J.R. 'Molecular-evolutionary mechanisms for genetic disorders', *Curr Opin Genet Dev* (2002) 12, 312.

22 Courseaux, A. and Nahon, J.-L. 'Birth of two chimeric genes in the *Hominidae* lineage', *Science* (2001) 291, 1293.

23 Keller, M.P., Seifried, B.A. and Chance, P.F. 'Molecular evolution of the CMT1A-REP region: a human and chimpanzee-specific repeat', *Mol Biol Evol* (1999) 16, 1019.

gorillas is implicated in chromosomal instability giving rise to leukaemias.²⁴

1.2 Gene decay

Our genome contains 6,000 to 10,000 derelict genes or gene fragments (*pseudogenes*) that no longer produce functional proteins²⁵ (Figure 2). Some are dis-

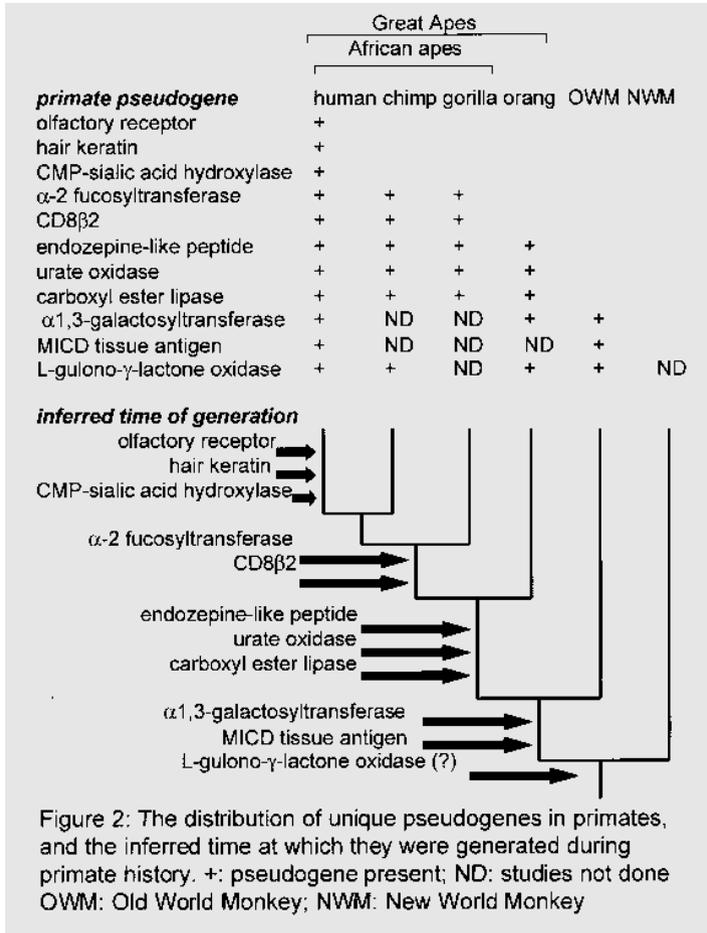


Figure 2

24 Saglio, G., Storlazzi, C.T., Guigliano, E. *et al.* 'A 76-kb duplicon maps close to the BCR gene on chromosome 22 and the ABL gene on chromosome 9: possible involvement in the genesis of the Philadelphia chromosome translocation', *Proc Natl Acad Sci USA* (2002) 99, 9882.

25 Harrison, P.M., Hegyi, H., Balasubramaniam, S. *et al.* 'Molecular fossils in the human genome: identification and analysis of the pseudogenes in chromosomes 21 and 22', *Genome Res* (2001) 12, 272. For a review of pseudogenes, see Mighell, A.J., Smith, N.R., Robinson, P.A., and Markham, A.F. 'Vertebrate pseudogenes', *FEBS Lett* (2000) 468, 109.

abled versions of genes which remain functional in other species. Others are inactive copies or duplicated fragments of functional genes. Each pseudogene is unique. It is the product of a random, unrepeatable originating event (or series of events) that occurred during the history from which humanity arose. Pseudogenes therefore provide unambiguous evidence for the animal ancestry of humans.

Some genes are inactivated in humans only. The olfactory receptor (OR) gene family comprises 1000 members. The proportion of OR genes that are pseudogenes is very high in humans compared to other primates.²⁶ It seems that humans (like dolphins, in which all sampled OR genes are pseudogenes²⁷) no longer require an acute sense of smell. One of the OR pseudogenes that humans have inherited has been shown to be disabled by the mutation of a glutamic acid residue ('E') to an inactivating stop signal (*).²⁸

chimp, gorilla, orang, gibbon	MANENYTKVTEFIFTGLNYN...
human	MANENYTKVT*FIFTGLNYN...

Other genes which are disabled only in humans encode a structural protein²⁹ and an enzyme.³⁰

Some of these genetic fossils are found in humans and other species, and contain the same inactivating lesions in the different species. It is vanishingly unlikely that they would arise independently in two or more species. All the species that possess a particular genetic relic must have inherited it from a common ancestor in which the gene sustained its unique inactivating damage.

For example, the α -fucosyltransferase pseudogene is shared by humans, chimps, and gorillas³¹. A nucleotide triplet CAA (which specifies glutamine, 'Q') has mutated to TAA (a 'stop' signal, *):

gibbon, orang	...SPFDVVFRPQAAFLPEWVG...
human, chimp, gorilla	...SPFNVVFRP*

26 Rouquier, S., Blancher, A. and Giorgi, D. 'The olfactory receptor gene repertoire in primates and mouse: evidence for reduction of the functional fraction in primates', *Proc Natl Acad Sci USA* (2000) 97, 2870; Young, J.M., Friedman, C., Williams, E.M. *et al.* 'Different evolutionary processes shaped the mouse and human olfactory receptor gene families', *Hum Molec Genet* (2002) 11, 535.

27 Freitag, J., Ludwig, G., Andreini, I. *et al.* 'Olfactory receptors in aquatic and terrestrial vertebrates', *J Comp Physiol A* (1998) 183, 635.

28 Rouquier, S., Friedman, C., Delettre, C. *et al.* 'A gene recently inactivated in human defines a new olfactory receptor family in mammals', *Hum Mol Genet* (1998) 7, 1337.

29 Winter, H., Langbein, L., Krawczak, M. *et al.* 'Human type I hair pseudogene *qhHaA* has functional orthologs in the chimpanzee and gorilla: evidence for recent inactivation of the human gene after the *Pan-Homo* divergence', *Hum Genet* (2001) 108, 37.

30 Chou, H.-H., Takematsu, H., Diaz, *et al.* 'A mutation in human CMP-sialic acid hydroxylase occurred after the *Homo-Pan* divergence', *Proc Natl Acad Sci USA* (1998) 95, 11751; Hayakawa, T., Satta, Y., Gagneux, P. *et al.* 'Alu-mediated inactivation of the human CMP-N-acetylneuraminic acid hydroxylase gene', *Proc Natl Acad Sci USA* (2001) 98, 11399.

31 Apoil, P.-A., Roubinet, F., Despiau, S. *et al.* 'Evolution of α 2-fucosyltransferase genes in primates: relation between an intronic *Alu*-Y element and red cell expression of ABH antigens', *Mol Biol Evol* (2000) 17, 337.

As a result of the mutation to a stop signal, the gene no longer encodes the complete α -fucosyltransferase enzyme. In a further example, humans, chimps, gorillas and orangutans have inherited the same scrambled endozepine-like peptide gene.³² This gene was destroyed in a great ape ancestor when an 'A' was inserted into the genetic sequence, obliterating the downstream protein sequence ('xxxxx').

macaque	...ALKQLKGPVSDPEKLLIYG...
chimp, gorilla, orang	...ALKQLKGTVCDQEKxxxxx...
human	...ALKQLKGTVCDQERxxxxx...

The urate oxidase gene was also inactivated in a great ape ancestor when a C to T (italicised) mutation generated a 'TGA' ('stop') signal (underlined).³³

four monkey species	...ATT <u>CAG</u> CGAGATGGAAAATAT...
human, chimp, gorilla, orang	...ATT <u>CAG</u> <u>TG</u> AGATGGAAAATAT...

The apes and Old World Monkeys (OWMs) derive from a common ancestor, as they share unique pseudogenes such as those for α -1,3-galactosyltransferase³⁴ and the tissue antigen MICD.³⁵ Most primates lack the enzyme L-gulonono- γ -lactone oxidase, which is required for the biosynthesis of ascorbic acid (vitamin C). Humans share with other apes and OWMs a relic of the gene for this enzyme, containing a common inactivating mutation (loss of an 'A').³⁶

rat	...TCACCCGAGGCGATGACA...
macaque	...TCACCCA_AGCGATGACA...
orang	...TCACCCA_GACGATGACA...
human, chimp	...TCACCTG_GACGATGACA...

Some pseudogenes are uniquely structured *copies* of active genes. Such deranged genes can have arisen only once, and yet we share many such scrambled genes with other primates. Mitochondria (the cellular power stations) possess a tiny chromosome, over 600 fragments of which have been copied into the human (nuclear) genome.³⁷ The events generating each shared pseudogene

32 Ivell, R., Pusch, W., Balvers, M. *et al.* 'Progressive inactivation of the haploid expressed gene for the sperm-specific endozepine-like peptide (ELP) through primate evolution', *Gene* (2000) 255, 335.

33 Oda, M., Satta, Y., Takenaka, O. and Takahata, N. 'Loss of urate oxidase activity in hominoids and its evolutionary implications', *Mol Biol Evol* (2002) 19, 640.

34 Kioke, C., Fung, J.J., Geller, D.A. *et al.* 'Molecular basis of evolutionary loss of the α 1,3-galactosyltransferase gene in higher primates', *J Biol Chem* (2002) 277, 10114.

35 Seo, J.W., Walter, L. and Gunther, E. 'Genomic analysis of MIC genes in rhesus macaques', *Tissue Antigens* (2001) 58, 159.

36 Ohta, Y. and Nishikimi, M. 'Random nucleotide substitutions in primate non-functional gene for L-gulonono- γ -lactone oxidase, the missing enzyme in L-ascorbic acid biosynthesis', *Biochim Biophys Acta* (1999) 1472, 408.

37 Bensasson, D., Zhang, D.-X., Hartl, D.L. and Hewitt, G.M. 'Mitochondrial pseudogenes: evolution's misplaced witnesses', *Trends Ecol Evol* (2001) 16, 314. Surveys of human mitochondrial pseudogenes are provided by Woischnik, M. and Moraes, C.T. 'Pattern of organization of human mitochondrial pseudogenes in the nuclear genome', *Genome Res* (2002) 12, 885; Tourmen, Y., Baris, O., Dessen, P. *et al.* 'Structure and chromosomal distribution of human mitochondrial pseudogenes', *Genomics* (2002) 80, 71.

must have occurred in a creature ancestral to all the existing species that possess it.

<i>species sharing a particular pseudogene</i>	<i>pseudogene copied from</i>
human, chimp, gorilla	CD8b-chain-2 gene ³⁸
human, chimp, gorilla, orang	carboxyl ester lipase gene ³⁹
human, chimp, gorilla, orang, gibbon	mitochondrial D loop ⁴⁰
human, chimp, gorilla, orang, [gibbon], OWM	mitochondrial 16S rDNA ⁴¹ and cytochrome b genes ⁴²

1.3 Random events: accumulation of DNA

DNA is copied (“transcribed”) into RNA, which functions during protein synthesis. Rarely, RNA can be copied back into DNA (“reverse transcribed”) by enzymes called *reverse transcriptases*, which are produced by virus-like genetic entities that exist within cells (Figure 3). Reverse transcribed DNA can be inserted into chromosomal DNA. Each insertion event is random and creates a unique structure, which typically includes short duplications flanking the insert.

These reverse transcribed cassettes occasionally become integrated into the DNA of the germline. They are then transmitted to future generations, providing unambiguous markers of genetic history. Over 40% of our DNA consists of cassettes of genetic material that have been reverse transcribed and spliced into chromosomal DNA. This parasitic DNA includes human endogenous retroviruses (HERVs), long and short interspersed nuclear elements (LINEs, SINEs), and processed pseudogenes.⁴³

38 Delabre, C., Nakauchi, H., Bontrop, R. *et al.* ‘Duplication of the CD8 beta-chain gene as a marker of the man-gorilla-chimpanzee clade’, *Proc Natl Acad Sci USA* (1993) 90, 7049.

39 Madeyski, K., Lidberg, U., Bjursell, G. and Nilsson, J. ‘Characterisation of the gorilla carboxyl ester lipase locus, and the appearance of the carboxyl ester lipase pseudogene during primate evolution’, *Gene* (1999) 239, 273.

40 Zischler, H., Geisert, H. and Castresana, J. ‘A hominoid-specific nuclear insertion of the mitochondrial D-loop: implications for reconstructing ancestral mitochondrial sequences’, *Mol Biol Evol* (1998) 15, 463.

41 Zischler, H. ‘Nuclear integrations of mitochondrial DNA in primates: inferences of associated mutational events’, *Electrophoresis* (2000) 21, 531.

42 Schmitz, J., Ohme, M. and Zischler, H. ‘The complete mitochondrial sequence of *Tarsius bancanus*: evidence for an extensive nucleotide compositional plasticity of primate mitochondrial DNA’, *Mol Biol Evol* (2002) 19, 544.

43 Smit, A.F.A. ‘Interspersed repeats and other mementos of transposable elements in mammalian genomes’, *Curr Opin Genet Dev* (1999) 9, 657; Li, W.-H., Gu, Z., Wang, H. and Netrutenko, A. ‘Evolutionary analyses of the human genome’, *Nature* (2001) 409, 847; Weiner, A.M. ‘SINEs and LINEs: The art of biting the hand that feeds you’, *Curr Opin Cell Biol* (2002) 14, 343; Deininger, P. L. and Batzer, M. A. ‘Mammalian retroelements’, *Genome Res* (2002) 12, 1455.

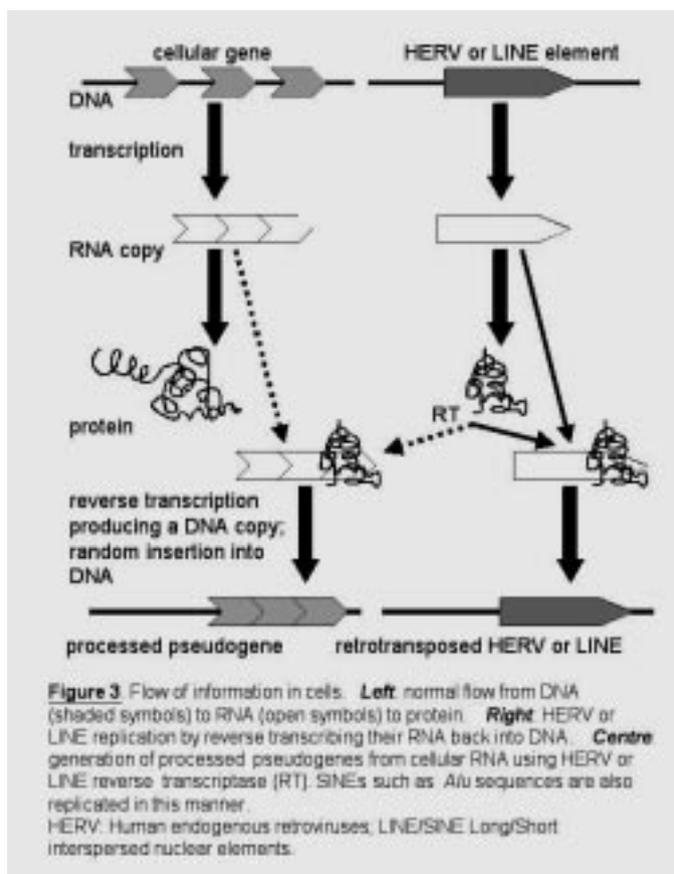


Figure 3

<i>Repetitive element</i>	<i>no. in the genome</i>	<i>proportion of genome, %</i>
HERVs and related elements	300,000	8
LINEs, total	1,400,000	19
LINE, L1 family	500,000	17
SINEs, total	1,800,000	13
SINE, <i>Alu</i> family	1,100,000	11
processed pseudogenes	10,000	<1

Reverse transcribed elements such as LINEs, SINES and processed pseudogenes are intracellular parasites that replicate within a single lineage of cells and are severely restricted in their ability to travel into the DNA of other species. Patterns of inheritance are not obscured by transmission as infectious

agents. If one of these elements is inserted at the same site in the DNA of different species, then those species must have inherited that insert from the same ancestor. All the species containing the particular cassette are descendants of the one creature in which the unique insertion event occurred.

Our genome is a graveyard of inherited *HERVs*.⁴⁴ Several years ago, evidence was presented suggesting that each of several endogenous retroviruses in human and chimp DNA was the product of the same insertion event.⁴⁵ It is now clearly established that humans and other primates possess common retroviruses.⁴⁶ In a seminal study, three *HERVs* were localized to unique sites common to the African great apes, and three to the OWMs (including the great apes).⁴⁷

Many proviruses of the *HERV-K*⁴⁸ and *HERV-H*⁴⁹ families in primate genomes have been identified, and the distribution of individual proviruses in different species defined:

<i>species sharing a particular provirus</i>	<i>number of proviruses</i>	
	<i>HERV-K</i>	<i>HERV-H</i>
human	13	
human, chimp	1	
human, chimp, gorilla	10	3
human, chimp, gorilla, orang	7	2
human, chimp, gorilla, orang, gibbon	4	

Representative insertion sites are shown in Table 1. Each unique provirus present in different species establishes that those species are descended from

44 Leib-Mosch, C., Brack-Werner, R., Werner, T., *et al.* 'Endogenous retroviral elements in human DNA', *Cancer Res* (1990) 50, 5636s; Lower, R., Lower, J. and Kurth, R. 'The viruses in all of us: characteristics and biological significance of human endogenous retroviruses sequences', *Proc Natl Acad Sci USA* (1996) 93, 5177.

45 Bonner, T.L., O'Connell, C. and Cohen, M. 'Cloned endogenous retroviral sequences from human DNA', *Proc Natl Acad Sci USA* (1982) 79, 4709; Mariani-Constantini, R., Horn, T.M. and Callahan, R. 'Ancestry of a human endogenous retrovirus family', *J Virol* (1989) 63, 4982.

46 Sverdlov, E.D. 'Retroviruses and primate evolution', *BioEssays* (2000) 22, 161; Bromham, L. 'The human zoo: endogenous retroviruses in the human genome', *Trends Ecol Evol* (2002) 17, 91.

47. Johnson, W.E. and Coffin, J.M. 'Constructing primate phylogenies from ancient retrovirus sequences', *Proc Natl Acad Sci USA* (1999) 96, 10254.

48 Hughes, J.F. and Coffin, J.M. 'Evidence for genomic rearrangements mediated by human endogenous retroviruses during primate evolution', *Nature Genet* (2001) 29, 487; Barbulescu, M., Turner, G., Seaman, M.I. *et al.* 'Many human endogenous retrovirus K (*HERV-K*) proviruses are unique to humans', *Current Biology* (1999) 9, 861; Barbulescu, M., Turner, G., Su, M. *et al.* 'A *HERV-K* provirus in chimpanzees, bonobos and gorillas, but not humans', *Current Biology* (2001) 11, 779. The *HERV* integration site is situated in a *LINE* element common to great apes and macaques.

49 de Parseval, N., Casella, J.-F., Gressin, L. and Heidmann, T. 'Characterization of the three *HERV-H* proviruses with an open envelope reading frame encompassing the immunosuppressive domain and evolutionary history in primates', *Virology* (2001) 279, 558; Lindskog, M., Mager, D.L. and Blomberg, J. 'Isolation of a human endogenous retroviral *HERV-H* element with an open reading frame', *Virology* (1999) 258, 441.

Table1: Insertion sites of HERVs or LTRs in primate DNA^{47-49,55}

<u>HERV</u>	<u>species</u>	<u>insertion site</u>
K105	human	CTCTGGAATTC[HERV]GAATTCATATGT
	chimpanzee	CTCTGGAATTC[HERV]GAATTCATATGT
	bonobo	CTCTGGAATTC[HERV]GAATTCATATGT
K110	human	GAATCTGAGAC[HERV]TGAGACAATAT
	chimpanzee	GAATCTGAGAC[HERV]TGAGACAATAT
	bonobo	GAATCTGAGAC[HERV]TGAGACAATAT
	gorilla	not determined [HERV]TGAGACAGCAT
	orangutan	GAATCTGAGACAATAT
H/env59	human	AAACAATATT[HERV]ATATTATGTT
	chimpanzee	AAACAATATT[HERV]ATATTATGTT
	gorilla	AAACAATATT[HERV]ATAT $\Delta\Delta\Delta$ GTT
	orangutan	AAACAATATT[HERV]ATATTATGTT
	gibbon	AAGGAATATTATGTT
H/env60	human	TCTCCAAATA[HERV]AAATATACTA
	chimpanzee	TCTCCAAATA[HERV]AAATATACTA
	gorilla	TCTCCAAATA[HERV]AAATATACTA
	orangutan	TCTCCAAATA[HERV]AAATATACCA
	gibbon	TCTCCAAATATACTA
H/env62	human	GTTATCCAAC [HERV] CAAACTAAAT
	chimpanzee	GTTATCCAAC [HERV] CAAACTAAAT
	gorilla	GTTATCCAAC [HERV] CCAACTAAAT
	orangutan	GTTATCCAACTAAAT
axin gene	human	CACCCCGG[LTR]CCGGGACG
	chimpanzee	CACCCCGG[LTR]CCGGGACG
	gorilla	CACCCCGG[LTR]CCGGGACG
	orangutan	CACCCCGG[LTR]CCGGGACG
	gibbon	CACCCCGGACG
U2 snRNA	human	TAGCTGAGATAA[LTR]AGATAAGATATA
	chimp	TAGCCGAGATAA[LTR]AGATAAGATATA
	gorilla	TAGCTGAGATAA[LTR]AGATAAGATATA
	orang	TAGCTGAGATAA[LTR]AGATAAGATATA
	baboon	TAATCGAGATAA[LTR]AGGTAAGATATA

The nucleotide sequences in which seven endogenous retroviruses have inserted are shown. Underlined nucleotides are short duplications which form at insertion sites. The retroviral element inserted into the DNA of an ancestor of all the species that possess it. In five cases, the original, uninterrupted sites are shown.

the ancestor in which the provirus spliced itself into the primate genome.

Other unique HERV structures include a HERV-H inserted into a HERV-K provirus (in the African great apes⁵⁰); a cellular gene (*FAM8A1*) inserted into a HERV-K provirus (in apes and OWMs⁵¹); and a HERV inserted into a pseudo-gene (in the great apes⁵²). A fusion between a HERV-H and a HERV-E provirus has produced a chimaera, present in multiple copies in human, chimpanzee, and gorilla. The sequences around the junction are shown below for representative copies.⁵³ Dashes (-) indicate the same nucleotide as that in the top sequence; "Δ" indicates a deletion.

```

human, several proviruses  CTGCCCCCACCCTAG/TCTTGGTTCCCTGAC
human, provirus 1          - - - - - / - - - - - A - - - - -
chimpanzee, two proviruses - - - - - / - - ΔΔ-C - - - - -
gorilla, provirus 1        - - - - - / - - - - - A - - - - -
gorilla, provirus 2        - - - - - / - - - - - T - - - - -

representative HERV-H      - - - - - T - - - - - CTC-C C C - GA -- C - T
representative HERV-E      ACT- GT-- T G - TACA - - - - - G -
    
```

The fusion point ('/') is the same in every case. The sequences to the left of this are derived from a HERV-H; those to the right from a HERV-E. These HERVs became juxtaposed at this site in a unique event. All copies of this hybrid are derived from the original. All species possessing copies of this hybrid are derived from the one creature in which the recombination event happened.

Sometimes most of the proviral DNA can be excised and lost, leaving in place only one of the two end sequences (the 'long terminal repeats', LTRs). Many LTRs are shared between humans and other primates.⁵⁴ Representative insertion sites are indicated (Table 1).⁵⁵ Each element was formed in one insertion event. Different species acquired it by inheritance.

50 Lapuk, A.V., Khil, P.P., Lavrentieva, I.V. *et al.* 'A human endogenous retrovirus-like (HERV) LTR formed more than 10 million years ago due to an insertion of HERV-H LTR into the 5' LTR of HERV-K is situated on human chromosomes 10, 19 and Y', *J Gen Virol* (1999) 80, 835.

51 Jamain, S., Girondot, M., Leroy, P. *et al.* 'Transduction of the human gene *FAM8A1* by endogenous retrovirus during primate evolution', *Genomics* (2001) 78, 38.

52 Samuelson, L.C., Phillips, R.S. and Swanberg, L.J. 'Amylase gene structure in primates: retroposon insertions and promoter evolution.' *Mol Biol Evol* (1996) 13, 767.

53 Lindeskog, M., Medstrand, P., Cunningham, A.A. and Blomberg, J. 'Coamplification and dispersion of adjacent human endogenous retroviral HERV-H and HERV-E elements: presence of spliced hybrid transcripts in normal leukocytes', *Virology* (1998) 244, 219.

54 Mamedov, I., Batrak, A., Buzdin, A., *et al.* 'Genome-wide comparison of differences in the integration sites of interspersed repeats between closely related genomes', *Nucleic Acids Res* (2002) 30, e71; and references therein.

55 Ling, J., Pi, W., Bollag, R. *et al.* 'The solitary long terminal repeats of ERV-9 endogenous retrovirus are conserved during primate evolution and possess enhancer activities in embryonic and hematopoietic cells', *J Virol* (2002) 76, 2410; Liao, D., Pavelitz, T. and Weiner, A.M. 'Characterisation of a novel class of interspersed LTR elements in primate genomes: structure, genomic distribution, and evolution', *J Mol Evol* (1998) 46, 649.

The random insertion of *LINEs* and *SINEs* into DNA is usually innocuous, but sometimes damages genes. New insertions appear in human populations with an estimated frequency of one germline insertion per 100 individuals.⁵⁶

Individual *LINEs* with the features of recent insertions are found in human DNA only. Other *LINEs* at unique sites which show slightly older characteristics are shared by humans and chimps, or by humans, chimps, and gorillas. Over 50 older *LINEs* have been identified that are common to the great apes.⁵⁷

The insertion of a *SINE* (such as an *Alu* cassette) into cellular DNA is rare and random. It is highly unlikely that the same *SINE* would insert independently into the same site in different species.⁵⁸ *Alu* sequences are clear markers of evolutionary relationships.⁵⁹ A table depicting the species distribution of individual *Alu* sequences (usually identified by the gene in which they are found) is shown below.

<i>groups with common Alu insert</i>	<i>Alu location</i>
great ape	pseudo-autosomal boundary ⁶⁰
great ape, lesser ape	α -globin 2 gene ⁶¹
great ape, lesser ape, OWM	α -globin genes (six cassettes) ⁶² 'EPL' locus ⁶³
great ape, lesser ape, OWM	<i>RHAG</i> genes (three cassettes) ⁶⁴ <i>FRG1</i> gene (two cassettes) ⁶⁵ interferon- γ gene ⁶⁶
great ape, lesser ape, OWM, NWM	CMT1A-REP locus (two cassettes) ⁶⁷ RHCE blood group gene ⁶⁸ blue opsin gene ⁶⁹ BC200 gene ⁷⁰
great ape, lesser ape, OWM, NWM, tarsiers	ATP synthase β gene, zonadhesion gene, α 1-microglobulin gene ⁷¹

56 see Deininger and Batzer, ref.43; Esnault, C., Maestre, J. and Heidmann, T. 'Human LINE retrotransposons generate processed pseudogenes', *Nature Genet* (2000) 24, 363; Weiner, A.M. 'Do all SINEs lead to LINEs?' *ibid*, 332; Morrish, T.A., Gilbert, N., Myers, J.S. *et al.* 'DNA repair mediated by endonuclease-independent LINE-1 retrotransposition', *Nature Genet* (2002) 31, 159; Eickbush, T.H. 'Repair by retrotransposition', *ibid*, 126.

57 Ovchinnikov, I., Rubin, A. and Swergold, G.D. 'Tracing the LINEs of human evolution', *Proc Natl Acad Sci USA* (2002) 99,10522.

58 Cantrell, M.A., Filanoski, B.J., Ingermann, A.R. *et al.* 'An ancient retrovirus-like element contains hot spots for SINE insertion', *Genetics* (2001) 158, 769; Roy-Engel, A.M., Carroll, M.L., El-Sawy, M. *et al.* 'Non-traditional *Alu* evolution and primate genomic diversity', *J Mol Biol* (2002) 316, 1033.

59 Shedlock, A.M. and Okada, N. 'SINE insertions: powerful tools for molecular systematics', *BioEssays* (2000) 22, 148.

60 Ellis, N., Yen, P., Neiswanger, K. *et al.* 'Evolution of the pseudoautosomal boundary in Old World Monkeys and Great Apes', *Cell* (1990) 63, 977.

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The insertion site of an *Alu* element common to the apes, OWMs and NWMs is provided as an example.⁷² This *Alu* element has resided in primate DNA since the simian common ancestor. The 16 nucleotides shown on each side of the *Alu* cassette represent the duplicated sequences identifying the unique insertion site.

insertion site	TAATAATACAACCTTTT
human	--- A G --- T G ----- [Alu]TAATAATACAACCTTTT
chimpanzee	--- C G ---- G ----- [Alu]- - - - -
gorilla	--- C G ---- G ----- [Alu]- - - - -
orangutan	--- C G ---- G ----- [Alu]- - - - - Δ Δ G - - - - -
gibbon	--- C G ---- G ----- [Alu]- Δ - - - - -
baboon (OWM)	---- G --- A G ----- [Alu]- - - - -
rhesus macaque (OWM)	---- G --- A G ----- [Alu]Δ Δ Δ - - - - - G- - - - -
barbary macaque (OWM)	---- G --- A G ----- [Alu]Δ Δ Δ - - - - - G- - - - -
marmoset (NWM)	- - - - - [Alu]Δ Δ Δ - - - C - - - A - - - C

Alu elements shared between humans and other primates have mediated

61 Knight, A., Batzer, M.A., Stoneking, M., Tiwari, H.K. *et al.* 'DNA sequences of *Alu* elements indicate a recent replacement of the human autosomal genetic complement', *Proc Natl Acad Sci USA* (1996) 93, 4360.

62 Bailey, A.D. and Shen, C.-K. J. 'Sequential insertion of *Alu* family repeats into specific genomic sites of higher primates', *Proc Natl Acad Sci USA* (1993) 90, 7205.

63 Shaikh, T.H. and Deininger, P.L. 'The role and amplification of the HA *Alu* subfamily founder gene', *J Mol Evol* (1996) 42, 15.

64 Huang, C.-H., Liu, Z., Apoil, P.-A. and Blancher A. 'Sequence, organization, and evolution of Rh50 glycoprotein genes in nonhuman primates', *J Mol Evol* (2002) 51, 76.

65 Grewal, P.K., van Geel, M., Frants, R.R. *et al.* 'Recent amplification of the human *FRG1* gene during primate evolution', *Gene* (1999) 227, 79.

66 Ackerman, H., Udalova, I., Hull, J. and Kwiatkowski, D. 'Evolution of a polymorphic regulatory element in interferon- γ through transposition and mutation', *Mol Biol Evol* (2002) 19, 884. This *Alu* sequence integrated into another SINE called a MER33 element, found in all primates sampled – and in the mouse.

67 see ref.23; an unrelated SINE (a mariner-like element) is present in the repeated segment in apes, OWMs, and NWMs.

68 Apoil, P.-A. and Blancher, A. 'Rh gene evolution in primates; study of intron sequences', *Mol Biol Evol* (2000) 17, 127.

69 Shimmin, L.C., Mai, P. and Li, W.-H. 'Sequences and evolution of human and squirrel monkey blue opsin genes', *J Mol Evol* (1997) 44: 378.

70 Kuryshv, V.Yu., Skryabin, B.V., Kremerskothen, J. *et al.* 'Birth of a gene: locus of neuronal BC200 snmRNA in three prosimians and human BC200 pseudogenes as archives of change in the *Anthropoidea* lineage', *J Mol Biol* (2001) 309, 1049. This study identified repetitive elements shared between lorises and lemurs but not tarsiers.

71 Schmitz, J., Ohme, M. and Zischler, H. 'SINE insertions in cladistic analyses and the phylogenetic affiliations of *Tarsius bancanus* to other primates', *Genetics* (2001) 157, 777. Other *Alu* insertions common to apes, OWMs and NWMs, were identified.

72 Crouau-Roy, B. and Clisson, I. 'Evolution of an *Alu* DNA element of type Sx in the lineage of primates and the origin of an associated tetranucleotide microsatellite', *Genome* (2000) 43, 642.

chromosomal rearrangements.⁷³ They have been co-opted as gene regulators⁷⁴ and have been used to assemble new genes.⁷⁵ The strategy of identifying species with common SINE insertions has provided unambiguous evolutionary relationships in various mammalian orders, including primates,⁷⁶ whales and dolphins,⁷⁷ and ruminants (giraffe, bongo, ox, bison, sheep and goats).⁷⁸ How much unnecessary heat has been generated over the question of the giraffe's neck!

Processed pseudogenes arise when RNA arising from normal cellular genes is reverse transcribed (by LINE reverse transcriptase) and stitched back into chromosomal DNA. These genetic fossils typically accumulate mutations and disappear into the genetic background. If a particular processed pseudogene (at a unique integration site) is found in different species, the single, random integration event which gave rise to it must have occurred in an ancestor of all the species possessing that pseudogene. Many processed pseudogenes are common to humans and other primates.⁷⁹ A pseudogene common to humans and rhesus macaques (*Per4*) is itself interrupted by a SINE called a MER-2 element.⁸⁰ The serine hydroxymethyltransferase pseudogene has been shown to be common to 20 primate species including tarsiers.⁸¹ A processed version of the phosphoglycerate mutase gene, investigated in humans and chimpanzees and present in species as remote as the macaque, retains its function.⁸²

2. Some implications

Arguments about evolution continue after 150 years. But the unique genetic markers reviewed above establish unequivocally the fact of our evolution. DNA

73 see refs.13, 23.

74 see ref. 31.

75 see refs. 22, 70.

76 Hamdi, H., Nishio, H., Zielinski, R. and Dugaicyk, A. 'Origin and phylogenetic distribution of *Alu* DNA repeats: irreversible events in the evolution of primates', *J Mol Biol* (1999) 289, 861; Hamdi, H.K., Nishio, H., Travis, J. *et al.* 'Alu-mediated phylogenetic novelties in gene regulation and development', *J Mol Biol* (2000) 299, 931;

Martinez, J., Dugaicyk, L.J., Zielinski, R. and Dugaicyk, A. 'Human genetic disorders: a phylogenetic perspective', *J Mol Biol* (2001) 308, 587.

77 Nikaido, M., Matsuno, F., Hamilton, H. *et al.* 'Retroposon analysis of major cetacean lineages: the monophyly of toothed whales and the paraphyly of river dolphins', *Proc Natl Acad Sci USA* (2001) 98, 7384; see also Wong, K. 'The mammals that conquered the seas', *Scient Amer* (2002, May), 52.

78 Nijman, I.J., van Tessel, P. and Lenstra, J.A. 'SINE retrotransposition during the evolution of the pecoran ruminants', *J Mol Evol* (2002) 54, 9.

79 Nachman, M.W. and Crowell, S.L. 'Estimate of the mutation rate per nucleotide in humans', *Genetics* (2000) 156, 297; Friedberg, F. and Rhodes, A.R. 'Calculation and verification of the ages of retroprocessed pseudogenes', *Molec Phylogenet Evol.* (2000) 16, 127.

80 Gotter, A.L. and Reppert, S.M. 'Analysis of human *Per4*', *Molec Brain Res* (2001) 92, 19.

81 Devor, E.J., Dill-Devor, R.M., Magee, H.J. and Waziri, R. 'Serine hydroxymethyltransferase pseudogene, SHMT-ps1: a unique genetic marker of the order primates', *J Exp Zool* (1998) 282, 150.

82 Betran, E., Wang, W., Jin, L. and Long, M. 'Evolution of the *phosphoglycerate mutase* processed gene in human and chimpanzee revealing the origin of a new primate gene', *Mol Biol Evol* (2002) 19, 654.

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markers called microsatellites are used for forensic purposes. They establish guilt or innocence, and resolve questions of paternity beyond reasonable doubt even though they are not unique markers like pseudogenes and retrotransposed sequences.⁸³ The assertion that we have evolved is established beyond reasonable doubt. These findings must deal to the hermeneutic paradigm of biblical literalism what Galileo's findings dealt to the Aristotelian paradigm of his day. When we surrender the expectation that the Bible teaches physical anthropology, we become free to rediscover its liberating message about the nature of God and his redemptive purposes.

2.1 Creation

The findings of primate genetics illuminate the Bible's theological statements regarding the creative work of God. That God created human beings (Gen.1:27; Psa.100:3) does not imply instantaneous action. God's creation of humanity encompasses past primate history, the present, and whatever is to come. The sweep of human evolution illustrates how God's work of creation is a continuing relationship of dependence between the world and God,⁸⁴ a continuing act of God's will;⁸⁵ an eternal covenantal relationship.⁸⁶

This should not surprise us. God is worshipped as the creator of Israel (Isa.43:1,15; 44:2; Psa.149:2), but this does not refer to one or a few discrete events. God created Israel through the entire continuum of Israel's history. In fact, the work continues (Gal.6:16; Eph.2:15), and completion is future (Rom.11:26). Similarly, God is the creator of each individual person (Psa.119:73; 139:13; Eph.2:10; 1Pet.4:19). This creative work cannot be restricted to any event. It encompasses the continuum of our development from fertilisation to ultimate transformation (1Cor.15:42f; Phil.3:21).

2.2 Chance

Our genetic history is constituted by myriad chance (random, unpredictable, unrepeatable) events, unique milestones that mark stages of our evolutionary past. Is the demonstration that *chance* events have formed our genome compatible with the biblical assertion that we are created by God? This issue illuminates the distinction between two broad meanings of 'chance'.⁸⁷

83 Bennett, P. 'Microsatellites', *J Clin Pathol: Mol Pathol* (2000) 53, 177.

84 MacKay, D.M. *The Clockwork Image* (London: IVP, 1974) 69; Boyd R.F.L., 'The space sciences', in Henry, C.F.H. *Horizons of Science* (New York etc: Harper and Row, 1978) 6.

85 Polkinghorne, J. *One World* (London: SPCK, 1986) 66; *Science and Creation* (London: SPCK, 1988) 54.

86 Van Till, H.J. *The Fourth day* (Grand Rapids: Eerdmans, 1986) 226.

87 as discussed variously by MacKay, D.M., ref. 84, 48f; Forster, R. and Marston, V.P. *Reason and Faith* (Eastbourne: Monarch, 1989) 400f; Alexander, D. *Rebuilding the Matrix* (Oxford: Lion, 2001) 332f.

Chance in a physical sense is a technical term used to describe aspects of the behaviour of components of the material world. It analyses the unpredictability of events in parlance appropriate to scientific analysis. Chance in a metaphysical (quasi-religious) sense indicates the absence of design or of personal, causal agency.

Randomness of molecular events (physical chance) bears no necessary connection with a metaphysical presupposition that denies purpose in the universe (metaphysical chance). The randomness of brownian motion is directed into the ordered processes of biochemistry by the energy present in biological molecules. 'The idea of generating order by 'selecting' from random variations is hardly new. It is the fundamental idea of Darwin's theory of natural selection.'⁸⁸

Chance as an aspect of the intelligibility of God's creation 'is not an alternative to design but a creative part of it',⁸⁹ an aspect of God's creativity.⁹⁰ God has ordained random processes as a means of generating novelty. In the interaction between freely-acting, contingent chance and constraining, directing necessity, God has chosen to create the creature which would bear his image.⁹¹ A writer in this journal has said 'order is essential together with chance in the evolution of the universe.' God has created the forces of physics 'with prescient precision'.⁹² The fruitful interplay of novelty-generating chance and lawful necessity in the universe evinces divine design. Chance is a part of the anthropic fruitfulness of the universe.

2.3 The status of humanity

Our close genetic similarity to the chimpanzees is an extraordinary concomitant of vast differences in mental capacity. We are connected genetically to primate antecedents. There is intense interest in identifying qualitatively altered genes which (it is stated) 'make us human'.⁹³ They may have remodelled brain structure,⁹⁴ modified brain sugar biochemistry,⁹⁵ or conferred the ability to

88 Oster, G. 'Darwin's motors' *Nature* (2002) 417, 25. Ordered functions emerging from brownian randomness include movement of motors along intracellular rail tracks, protein secretion through membranes, interactions between substrates and catalytic sites, and the F_0F_1 ATPase that generates ATP. In molecular engines, 'brownian motion drives both the power and exhaust strokes'.

89 Forster, R and Marston, V.P., ref.87, 416.

90 Peacocke, A. *God and the New Biology* (London, Melbourne: Dent, 1986) 62,99.

91 see Polkinghorne, J. *The Way the World Is* (London: SPCK, 1983) 11-12; *Science and Creation*, 47f; Wright, J. *Designer Universe* (Crowborough: Monarch, 1994) 42.

92 Burge, T. 'What else does physics tell us about God?' (Correspondence). *Science and Christian Belief* (2002) 14, 79.

93 Gibbons, A., ref. 7.

94 Balter, M. 'What made humans modern?' *Science* (2002) 295, 1219.

95 through the inactivation (only in humans) of the CMP-sialic acid hydroxylase gene. In a news report entitled "Sugar separates humans from apes", it was proposed that the loss of this enzyme might make the brain work better. *Science* (2001) 291, 2340. See also ref. 30.

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speak.⁹⁶ It has been suggested that gene expression patterns in the brain will elucidate the difference between humans and other apes.⁹⁷

Genes are necessary but not sufficient to specify our nature as people. They describe only the substrate that constitutes our *potential humanity*. Balter has said that the question, 'What makes us human?' cannot be answered by staring at a genome.⁹⁸ Another commentator has said that 'to be a human person means more than having a human genome; it means having a narrative identity of one's own'.⁹⁹ And Paabo has warned against the

insidious tendency to look to our genes for most aspects of our 'humanness', and to forget that the genome is but the internal scaffold for our existence. We need to leave behind the view that the genetic history of our species is *the* history par excellence. We must realise that our genes are but one aspect of our history, and that there are many other histories that are even more important.¹⁰⁰

He concluded that genomics in isolation can never tell us what it means to be human, and invoked the humanities as a further approach that must help define our humanness. He could have specified the events upon which theology reflects (although he did not).

Consideration of our 'exosomatic chromosomes' (culture, stories, and relationships) is required for an understanding of what it means to be human. We need to know other people to progress from an organismic potential humanity to a social *basic humanity*. The inability of (genetically normal) feral children (who grow up apart from human company) to later become integrated into society is a telling reminder that our basic humanity depends on the intangible and vulnerable requirement that we know other people. This insight is expressed in the Xhosa proverb *Umntu ngumuntu ngabantu* (a person becomes a person through persons).¹⁰¹

Spanner described how western culture has conditioned us to think of life and death as physical states of a thing-in-itself. 'The biblical understanding of life connects it with knowing – existential knowing. It thus implies entering into relationship – with God, with other persons and, to a lesser extent, with things.' Biblically, life is not a property of the thing-in-isolation, but it 'consists

96 A gene implicated in speech, *FOXP2* "may help solve the mystery of how we came to be." Balter, M. 'First gene linked to speech identified', *Science* (2001) 294, 32; Enard, W., Przeworski, M., Fischer, S.E. *et al.* 'Molecular evolution of *FOXP2*, a gene involved in speech and language', *Nature* (2002) 418, 869.

97 Enard W, Khaitovich P, Klose J *et al.* Intra- and interspecific variation in primate gene expression patterns. *Science* (2002) 296, 340. But is the difference in expression of genes in the human brain a prerequisite or a consequence of human relationality?

98 Baltimore, D. 'Our genome unveiled.' *Nature* (2001) 409, 814.

99 Mauron, S. 'Is the genome the secular equivalent of the soul?' *Science* (2001) 291, 831.

100 Paabo, S. 'The human genome and our view of ourselves', *Science* (2001) 291, 1219.

101 Villa-Vicencio, C. and de Gruchy, J.W. *Doing Ethics in Context* (Cape Town and Johannesburg: David Philip, 1994) 29.

in cognitive and responsive relationships'.¹⁰² Green also has emphasised that the Hebrew Bible does not define the human person in essentialist terms (as a thing-in-itself), but in relational terms. We are 'genuinely human and alive only within the family of humans brought into being by Yahweh, and in relation to the God who gives life-giving breath'.¹⁰³

Messer reflected helpfully in this journal on what it means to be human in the context of genomic science. He has taken his cue from the concept of the triune God, who has no being apart from communion. Therefore for us there can be no personhood prior to interpersonal relationship:

If relationship or communion is intrinsic to the being of the triune God, then human personhood, made in God's image is also inescapably relational. Human persons are not adequately described as the isolated, autonomous individuals of much modern thought, but are in some sense the products of their social relations.¹⁰⁴

A third quality that defines humanness is described by the concept of 'the image of God'. It seems that the physical (potential) and social (basic) aspects of our humanity are the necessary substrate in which God's image could be expressed. Prehistorical artefacts have documented the rise of rationality and creativity over vast time scales, but neither faculty expresses the meaning of the divine image.¹⁰⁵ To be God is to be persons in relation; so to image God is to be 'called to a life in relation', 'to be called to a relatedness-in-otherness'; 'to be called to represent God to the creation and the creation to God';¹⁰⁶ to be called 'to a unique role in God's economy';¹⁰⁷ to be called to work with God to transform the world;¹⁰⁸ to be called to reflect God and make him visible among men.¹⁰⁹ Jeeves has written recently, 'The meaning of the 'image of God' is thus to be found in the human vocation, given and enabled by God, to relate to God as God's partner in covenant, to join in companionship with the human family, and in relation to the whole cosmos in ways that reflect the covenant love of God'.¹¹⁰

102 Spanner, D. *Biblical Creation and the Theory of Evolution* (Exeter: Paternoster Press, 1987) 71.

103 Green, J.B. 'Eschatology and the nature of humans: a reconsideration of pertinent biblical evidence', *Science and Christian Belief* (2002) 14, 33. Green quotes Polkinghorne to the same effect: "The pattern that is me must include those human relationships that do so much to make me what I am, and also it must express the nature of my unique creaturely relationship with God." (p.39, note 21).

104 Messer, N.G. 'Human genetics and the image of the triune God', *Science and Christian Belief* (2001) 13, 99. Quotations are from pp.103, 105.

105 Gunton, C.E. *Christ and Creation* (Carlisle: Paternoster Press and Grand Rapids: Eerdmans, 1992) 102, 106, 120-121.

106 *ibid*, 101-102.

107 Osborn, L. *Guardians of Creation* (Leicester: Apollos, 1993) 133.

108 *ibid*, 139.

109 Konig, A. *New and Greater Things: Re-evaluating the Biblical Message on Creation* (Pretoria: UNISA, 1988) 129.

110 Jeeves, M. 'Changing portraits of human nature', *Science and Christian Belief* (2002) 14, 26.

Possession of the 'image of God' thus refers to the spiritual capacity to relate to God, and the receipt of a commission to serve him.¹¹¹ Relation and commission are aspects of 'revelation'. The Bible story of humanity starts with revelation. Prior primate evolution is but the presupposition of humanity's capacity to know and serve its creator and thereby possess his image. In knowing God, we are granted a *fulfilled humanity*. Gunton connects the three aspects of our existence:

Who we are is made known to us through the relations in which we stand. There are three forms of relation that can be abstracted from the overall network: relations with the world, with other human persons, and with God.¹¹²

But human beings have repudiated God's call by which they receive his image. In the New Testament, the words used in Genesis ('image' and 'likeness') were given new content by referring specifically to Christ (rather than humanity) as the image of God. 'He is not only the true image of God but also the source of human renewal in it.'¹¹³ The one who perfectly bears that image becomes the vehicle of the renewal of that image in all who come into relationship with him.

Jesus definitively linked the fullness of life with knowing God: 'And eternal life means knowing you, the only true God, and knowing Jesus Christ whom you sent' (Jn.17:3; see also 1 Jn.5:20). Just as our basic humanity requires knowledge of other people, so fulfilled humanity requires knowledge of God as revealed in Jesus Christ.¹¹⁴

The forms of personal knowledge that integrate us into human society and that transform us into the community of God are mediated by stories. By means of the latter,

we come to see the significance and coherence of our lives as a gift, as something not of our own heroic creation, but as something that must be told to us. ... The little story I call my life is given cosmic, eternal significance as it is caught up within God's larger account of history ... The significance of our lives is frighteningly contingent on the story of another.¹¹⁵

2.4 The scandal of particularity and the grace of God

Our genetic record implies a long history during which often numerically small populations of primates gradually acquired the features of human beings. This

111 Other theologians who juxtapose the *Imago dei* with a divine calling or commission include Ron Sider, in Berry, R.J. (ed.) *The care of Creation* (Leicester: IVP, 2000) 47-48, and Murray Rae, in Mann, L.R.B. *Science and Christianity* (Auckland: University of Auckland Centre for Continuing Education, 2001) 188,192.

112 Gunton, ref. 105, 72-73.

113 *ibid*, 100-101.

114 Hence the New Testament emphasis that God knows his people (Gal.4:9; 1 Cor.8:3), just as they know God (Phil.3:8,10; Col.3:10; 1 Jn.2:3;2:13-14).

115 Hauerwas, S. and Willimon, W.H. *Resident Aliens* (Nashville: Abingdon Press, 1989) 53-55.

seems to illuminate the question of the 'scandal of particularity'. Is it really credible that an obscure peasant carpenter could be the unique revealer of God, the divine redeemer of the world and the consummator of the universe? Is it believable that an insignificant group of tribes-people eking out an existence on the rugged hills of Palestine could be the channel by which God would redeem humankind and transform the world?

Is it feasible that a lineage of ape-like creatures progressively losing its ability to make vitamin C, its hair, and its sense of smell, and sustaining the random invasion of myriad retrotransposons, could be ancestral to *Homo divinus*? Could such inauspicious beginnings precede the creature which would reconstruct its evolutionary past, reflect on its future, and respond to its creator? It is now an empirical fact that our genetic endowment was constructed in a lineage of nondescript apes. God works through apparently insignificant and particular players to achieve unimaginably grand ends. So it is not incredible that Jesus of Nazareth should be the liberator of humankind, or that the Hebrew people should be the channel of God's dealings with the world.

Our very creation is an act of sheer grace. In an initiative of unconditioned love, God conferred his likeness upon a member of the ape family and brought into being *Homo divinus*, the ape-in-the-image-of-God, with the unique capacity to know, love and serve its creator. There is no room for hubris here. Our biological roots remind us that we are human not because of any inherent or necessary superiority to the rest of the animal kingdom, but in creaturely dependence on God's goodness. The Hebrew poet asked "What are human beings that you [God] think of them?" and then seemed to answer his own question:

... you made them inferior only to yourself,
you crowned them with glory and honour.

You appointed them rulers over everything you had made (Psa.8:5-6; GNB).

And when in selfishness we perverted every faculty that we were so generously given, God did not have to redeem us, apart from the impulse of his love and holiness. The incarnation of the eternal Son of God as one of us (an ape-in-the-image-of-God) re-established a human being as 'ruler over all things'. His self-sacrifice by which 'through God's grace he should die for everyone' (Heb.2:6-10) extends this same unconditioned grace to ever more stupendous heights.

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Glossary of technical terms

- centromere:** a constriction in a chromosome, involved in organising chromosomal movement during cell division.
- chromosome:** a DNA molecule and its associated proteins. When cells divide, the chromosomes condense into compact structures that can be observed microscopically.
- DNA:** deoxyribonucleic acid, the molecule that encodes and transmits genetic information.
- endogenous retrovirus:** A genome of the retroviral class transmitted as part of the genome of a host organism.
- genome:** the total genetic information of an organism.
- insertion site:** the exact location in a DNA molecule into which genetic elements such as retrotransposed sequences splice themselves.
- LINE:** (long interspersed nuclear element); a segment of DNA that can colonise other sites of the genome using its own reverse transcriptase enzyme.
- mitochondria:** structures within cells where energy-carrying molecules are generated. They possess a small chromosome of their own
- nucleotide:** the basic information-carrying unit of DNA or RNA.
- processed pseudogene:** a copy of a gene that has inserted into DNA via an RNA intermediate.
- provirus:** the segment of DNA representing a viral genome that has been spliced into cellular DNA
- pseudogene:** a non-functional derelict gene, generated by damage to, or partial duplication of an authentic gene
- retrotransposition:** the process by which RNA molecules are reverse transcribed into DNA, and inserted into chromosomal DNA.
- reverse transcription:** the process by which RNA is copied into DNA by enzymes ('reverse transcriptases') encoded by retroviruses or LINEs.
- RNA:** ribonucleic acid, copied from DNA, and involved in the synthesis of proteins.
- sequence:** the order of building blocks in a nucleic acid or a protein. DNA sequences consist of four different units or nucleotides (A, T, G, and C), whereas protein sequences are composed of 20 amino acids (each represented by a letter).
- SINE:** (short interspersed nuclear element): small segments of DNA

that can colonise new sites in the genome using a reverse transcriptase molecule derived from a LINE.

telomeres: the sequences at the ends of chromosomal DNA.

transcription: the process by which DNA is copied into RNA.

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