Lecture Contents

Dr Graeme Finlay delivered the lecture "Human Genetics and the Image of God" on 7th November 2006 at Queen's Lecture Theatre, Emmanuel College, Cambridge. The lecture was followed by questions from the audience and later a dinner/discussion at St Edmunds College. A transcript of the lecture follows.

Brief Biography

Dr Graeme Finlay studied for a PhD in cellular immunology, and then joined the Auckland Cancer Society Research Centre, New Zealand, where he has been working for the past 20 years. This laboratory is involved in the development of novel anti-cancer agents, and is the largest group of this nature in the southern hemisphere. Research focus has centred on DNA-binding agents that poison the DNA-organising enzyme topoisomerase II. Areas investigated have included effects on the cell division cycle, mechanisms of cell death and the activity of the tumour suppressor gene encoding p53 in cell death pathways. Since 2000 Dr Finlay has also been Senior Lecturer in General Pathology in the Department of Molecular Medicine and Pathology, University of Auckland.

Two very different currents of thought directed him into the study of comparative evolutionary genetics. The first was the explosive growth in the understanding in cancer genetics that occurred since the early 1980s. The second was the wholesale importation of American creationist ideas into New Zealand. These developments intersected in fascinating ways. They generated a writing programme designed to identify some of the extraordinary developments in genetics described in the scientific literature, and present them in terms accessible to non-biologists. The resulting booklets were all published in 2004 by Telos Books (Auckland) with the titles:

- 'Evolving Creation' 46pp. ISBN 0-476-00650-3
- 'God's Books: Genetics and Genesis' 75pp. ISBN 0-476-00651-1
- 'A Seamless Web: Science and Faith'. 59pp. ISBN 0-476-00816-6

Introduction

Some people still deny that extensive evolutionary change (macroevolution) has occurred. They deny that the existing mammalian orders or the primates (including *Homo sapiens*) could have evolved from founding progenitors. Others deny that evolutionary mechanism is compatible with the biblical assertion that God is Creator of the spectacularly diverse biosphere of which we are a part. We are told that once we understand the mechanism of our evolution, we can no longer think of ourselves as having a divinely ordained purpose. An answer to the 'how' question supposedly eliminates the 'why' question.

Such controversies are eminently resolvable. Genome science has generated accessible and compelling evidence that dispels uncertainty as to human evolutionary origins. Our genetic connectedness to (other) apes cannot call into the question the primary datum of our lives: that we are relational beings. Indeed it is our relationships with other people (and, I believe, with God) that constitute us as human. The basis of christian faith is that a personal God has revealed himself in personal terms as a person, Jesus of Nazareth.

An implication of biblical faith (that recognises the Bible as God's authoritative Word 'in all matters of faith and conduct') is a high valuation of science. The historian of science Gingerich has stated that 'the very expression "laws of nature," from the time of Boyle and Newton, derives from the concept of divine law, and it is probably not accidental that science arose in such a philosophical/theological environment'.[1] Its first practitioners had encountered God as the Redeemer who brought life out of death and therefore they recognised him as the Creator who brought order out of chaos.

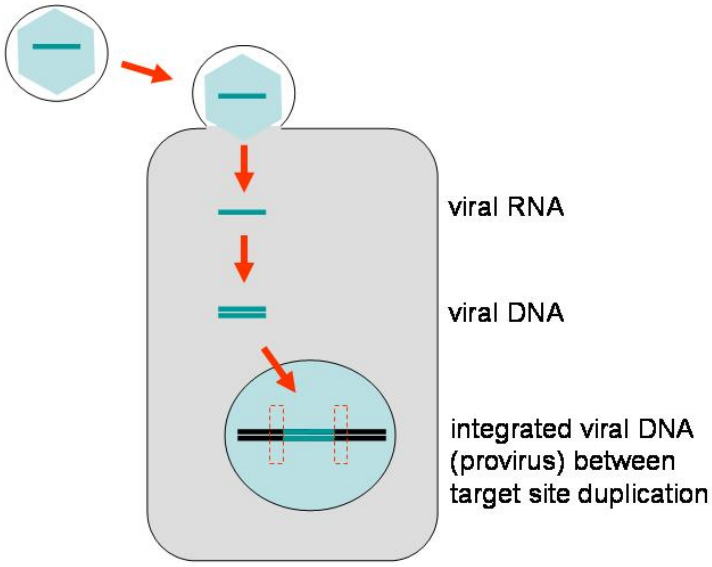
Wolpert has said that the Templeton Foundation supports courses and meetings on the topic of science and faith in 'an attempt to reconcile religious belief and modern science.'[2] I seek rather to clarify the nature of science and of christian faith, both of which are sorely misunderstood. They are different perspectives on reality. When these are understood, reconciliation can look after itself.

Our retroviral heritage

In the early 1980s, I started surveying evolutionary genetics from the vantage point of cancer cell biology. Stories about retroviruses and oncogenes were transforming our understanding of cancer. The dramatic story of the first human oncogenic retrovirus, the human T cell leukaemia virus (HTLV-1) was being told by Japanese researchers investigating an aggressive leukaemia that afflicted adults in Japan and elsewhere.[3]

Retroviruses such as HTLV-I are skilled parasites. During the infection cycle, the retroviral genome (genetic material) is copied from RNA into DNA by a viral enzyme (a 'reverse transcriptase'). The freshly made DNA is spliced into the chromosomal DNA of the infected ('host') cell. The insertion event is initiated by another viral enzyme (an 'endonuclease'), which recognizes a short sequence of bases in the DNA of the host cell, and cuts each DNA strand (so that the two cuts are separated by a few bases). This creates a gap into which the viral DNA is inserted. The loose ends are filled in and joined. The resulting retroviral DNA insert (the 'provirus') is recognized by its set of genes (*gag*, *prt*, *pol*, and *env*), its 'long terminal repeat' (LTR) sequences at each end, and flanking short 'target site duplications' (TSDs) of host DNA.

host cell DNA-TSD-[LTR-*gag-prt-pol-env*-LTR]-TSD-host cell DNA



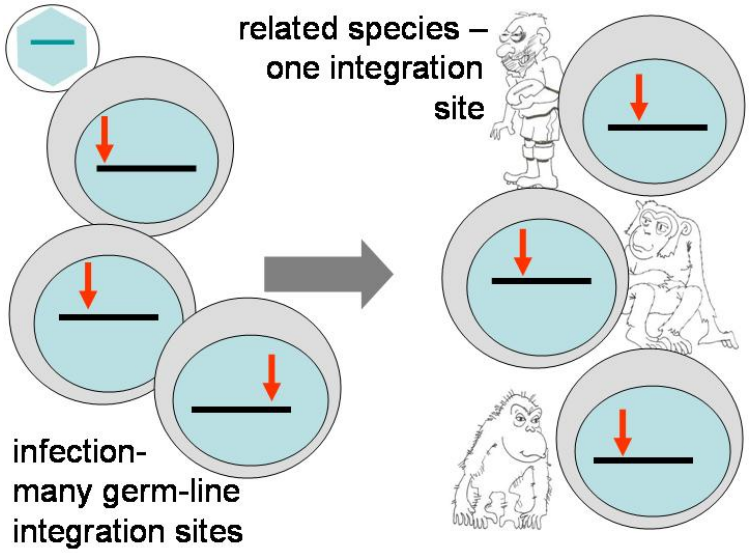
These insertional events occur randomly at sites that exist at myriad places in the host cell genome. Early in infection, many distinguishable provirus insertions are found in a cell population. Years later, when a leukaemia appears as a result of the infection, all the leukaemic cells have an HTLV-1 provirus integrated at precisely the same site.[4]

Why should all the cells in a cancer have the same inserted retrovirus? There is no way that a segment of HTLV-1 DNA could integrate faithfully into the same site of chromosomal DNA in a large population of cells. There is one conceivable explanation. The impulse to develop into a cancer was initiated in one cell harbouring one particular provirus. This cell and its offspring were driven by the provirus (and by later genetic changes) into a programme of uncontrolled multiplication, producing an expanding clone of descendents, all of which *inherited* the original provirus from the founding cell. The billions of cancer cells possess the same HTLV-1 proviral insertion because they inherited it from the one progenitor cell.[5]

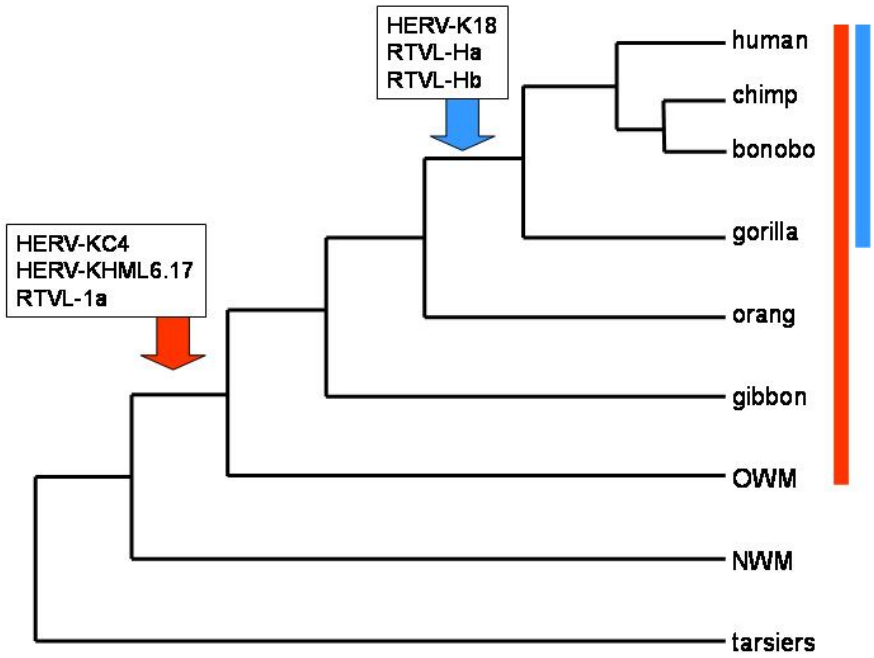
It has been found that everyone possesses retroviral proviruses in their DNA. These proviruses (or 'endogenous retroviruses', ERVs) did not enter our DNA by the familiar process of infection, but they were inherited from our parents, just as genes are. All humans have inherited the same zoo of 100,000 ERVs, classified into 80 families. If one includes related elements that possess LTRs there are 400,000 elements and 200 families constituting 8% of our DNA.[6] Regardless of our ethnicity, we are one-twelfth virus. Our DNA is a detailed historical record of past retroviral insertions into the germ-line DNA of our forbears.[7]

For all humans to possess the same set of ERVs as part of their common genetic endowment, the germ-line cells sustaining the original infections must have been ancestral to us all. When did the common ancestor(s) live? In the 1980's some reports suggested that humans and chimpanzees possessed ERVs at the same sites in their respective genomes. At that time, it was not established that the ERVs were precisely the same in the two species (same class of virus, insertion site, orientation,

TSD).[8] But it looked like it. The implications were clear. If humans and chimps did in fact possess the same ERV inserts, then both species would have inherited their collection of ERVs from a lineage of common ancestors. Human and chimps would be clonal with respect to each shared (but uniquely arising) ERV.



The fact that humans and chimps possess in common a set of ERVs was confirmed by a study of six ERVs, present in the DNA of humans and chimps, and of other primates. Three of the ERVs were found in the African great apes. They had integrated into the primate germ-line prior to the human-chimp-bonobo-gorilla radiation. The other three are present in Old World Monkeys (OWMs) and hominoids (apes including humans), but not NWMs. They entered the primate germ-line in an ape-OWM ancestor. Each ERV established that humans, chimps (and other primates that possess it) are descended from the one reproductive cell that sustained the insert.[9]



Confirmations accumulated in the literature. Representative insertions of ERVs or their LTRs are shown. In most cases, the undisturbed integration site has been characterised in species that had branched off on another evolutionary trajectory before the integration event.[10]

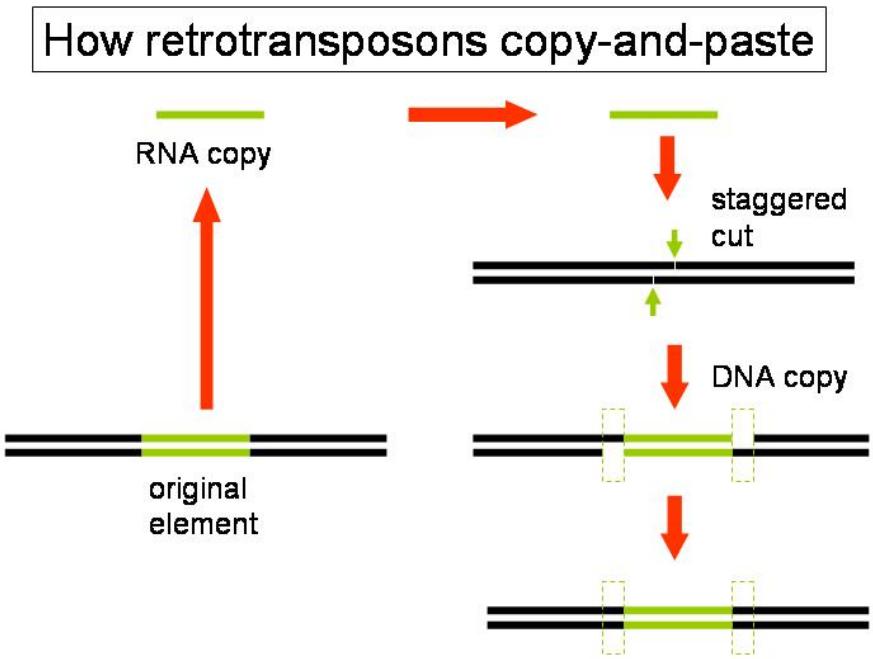
ERV	species	insertion site with target site duplication, underlined
K105	human	…CTCTGGAATTC[ERV]GAATTCTATGT…
	chimpanzee	…CTCTGGAATTC[ERV]GAATTCTATGT…
	bonobo	…CTCTGGAATTC[ERV]GAATTCTATGT…
K110	human	…GAATCTGAGAC[ERV]TGAGACAATAT…
	chimpanzee	…GAATCTGAGAC[ERV]TGAGACAATAT…
	bonobo	…GAATCTGAGAC[ERV]TGAGACAATAT…
	gorilla	…not determined…[ERV]TGAGACAGCAT…
	orangutan	…GAATCTGAGAC AATAT…
K-GC1	human	…GAATGATTAT GATGT…
	bonobo	…GAATGATTAT[ERV]ATTATGATGT…
	gorilla	…GAATGATTAT[ERV]ATTATGATGT…
	orangutan	…GAATGATTAT GATGT…
H/env59	human	…AAACAATATT[ERV]ATATTATGTT…
	chimpanzee	…AAACAATATT[ERV]ATATTATGTT…
	gorilla	…AAACAATATT[ERV]ATATDDDGTT…
	orangutan	…AAACAATATT[ERV]ATATTATGTT…
	gibbon	…AAGGAATATT ATGTT…
H/env60	human	…TCTCCAAATA[ERV]AAATATACTA…
	chimpanzee	…TCTCCAAATA[ERV]AAATATACTA…
	gorilla	…TCTCCAAATA[ERV]AAATATACTA…
	orangutan	…TCTCCAAATA[ERV]AAATATACCA…
	gibbon	…TCTCCAAATA TACTA…
H/env62	human	…GTTATCCAAC[ERV]CAAACTAAAT…
	chimpanzee	…GTTATCCAAC[ERV]CAAACTAAAT…
	gorilla	…GTTATCCAAC[ERV]CCAACTAAAT…
	orangutan	…GTTATCCAAC TAAAT…

ERVs have been instrumental in structuring our genomes.[11] Genome sequencing has shown that nearly all of the 400,000 ERV and related LTR-like sequences in the human genome are shared with chimps. There are about 100 human–specific and 300 chimp-specific ERVs. We share a long and unbroken pedigree with (other) apes.[12]

Furtive DNAzens of the genome

Our DNA is populated by many other genetic parasites (or 'transposable elements'). They do not travel between cells. Instead, they track from one generation to the next, as part of the germ-line DNA, copying-and-pasting themselves as they go.

Long interspersed elements (LINEs) are parasites of unknown origin. LINEs produce a protein that acts as an endonuclease (to initiate the insertion event), and a reverse transcriptase (to copy the RNA version of a LINE into the chromosomal DNA version).



LINE-1 ('L1') elements are the most abundant class in human DNA, with over 500,000 copies (17% of our DNA). The insertion process is haphazard, but the mechanisms by which LINEs copy-and-paste themselves are yielding to investigation.[13] Many LINE-1 segments lack TSDs, and may have arisen as repair patches at DNA breaks.[14]

Several dozen LINE-1 families are found in human DNA.

- 'L1M' elements are shared widely with other mammals, are very ancient, and have accumulated many mutations.
- Four 'L1PB' and 18 'L1PA' families are found only in primates. The oldest are present in all primates, and their sequences have diverged widely from the family type. Younger families, derived from the older families, are found in a more restricted range of species, and show less variation in sequence.
- The newest LINE-1 family is present in humans only. Many inserts are present in a proportion of individuals only. Their sequences are essentially identical.[15]
- LINEs are still actively colonising our genomes. Some 80-100 are still functional, generating new inserts in the human germ-line at a rate of one per twenty births.[16] LINEs are not an integral part of our body plan or life cycle (although some have been recruited to provide genetic functionality). They are individualistic unpredictable insertional mutagens that cause disease.[17] A family of proteins encoded by the APOBEC3 genes has the job of suppressing the

copying-and-pasting activity of LINEs and SINEs, just as they suppress the infectivity of invading retroviruses.[18]

When the insertion sites occupied by some 500 human–specific LINE-1 elements were investigated in non-human primates, in no case was an independent insertion found at the corresponding sites in those other species. The probability of two LINE-1 elements independently integrating in the same site in two different species is thus negligible.[19] If two species possess the same insert they have inherited it from the one progenitor.

Transposable elements are powerful markers for delineating lines of descent. An example is found in the centromere of the X chromosome. This LIPA7 insert is present in the great apes and OWMs, descendants of the one reproductive cell in which the insertion occurred.[20]

	left flanking sequence [L1PA7 insert] right flanking sequence
human	…AGTTCTGC[TCTAA … AAA T]GCAGACATC…
chimp	…AGTTCTGC[TCTAA … AAA T]GCAGACCTC…
gorilla	…AGTTCTGC[TCTAA … AAA T]GCAGACATC…
orang	…AGTTCTGC[TCTAA … AAAAT]CCAGACATC…
macaque (OWM	…AGTTCTGC[TCTAA … AAA D]DDDDDDATC…
baboon (OWM)	…AGTTCTGC[TCTAA … AAA D]DDDDDDATC…
vervet (OWM)	…AGTTCTGC[TCTAA … AAA D]DDDDDDATC…

Genome comparisons have shown that there are 2,000 human-specific and 2,000 chimp-specific LINE-1 sequences. These inserted after the human and chimp lineages diverged. The other half million LINEs we possess are *shared* with the chimps – a staggering weight of evidence of common ancestry.[21]

LINE-1 elements provide other cogent evidence of common ancestry. When LINE-1 RNA is being copied into DNA, the reverse transcriptase can switch from the LINE-1 RNA and start copying a bystander RNA molecule. The resulting insert will be a chimaera: part-LINE-1, part-bystander RNA, joined at a unique point. One such element contains 476 bases of L1 sequence, 40 bases copied from a nearby ERV, and another 40 bases of cellular DNA adjacent to the ERV. This unique chimaera is present in humans, chimps and bonobos. The three species that possess it acquired it by inheritance from a common ancestor.[22] Over 80 of these singular patchwork inserts reside in human DNA. They have been accumulating in primate DNA since before the origin of the simians.[23]

Short interspersed elements (SINEs) possess no genes. They co-opt the proteins made by LINEs in order to copy-and-paste themselves into new sites in the genome. The most abundant SINEs in our genome are the primate-specific ‘Alu’ elements, originally derived from a small cellular (7SL RNA) gene, and now numbering 1.1 million inserts (11% of human DNA). The LINE-1-dependent copying-and-pasting of Alu elements has been studied in cultured cells. SINEs are parasites’ parasites.[24]

Alu elements multiply through the genome largely by the activity of a few highly active ‘master’ elements. Some can lie in a quiescent state for aeons before bursting into retrotranspositional activity. Some ancient elements may still be active.[25]

- The sequenced human genome has yielded a catalogue of this Alu zoo. There are 3 major families and 213 subfamilies, arranged in an all-encompassing family tree.[26]

Major Alu families

relative age	family	extent of divergence	age, my
oldest	AluJ	15%	60
intermediate	AluS	9%	36
youngest	AluY	6%	24

- Some 7,000 individual Alu elements (mostly of the AluY group) are found in humans but not in any other species. Many have entered the human germ-line so recently that some people possess the inserted element while others retain the unoccupied target site.

Human-specific Alu subfamilies

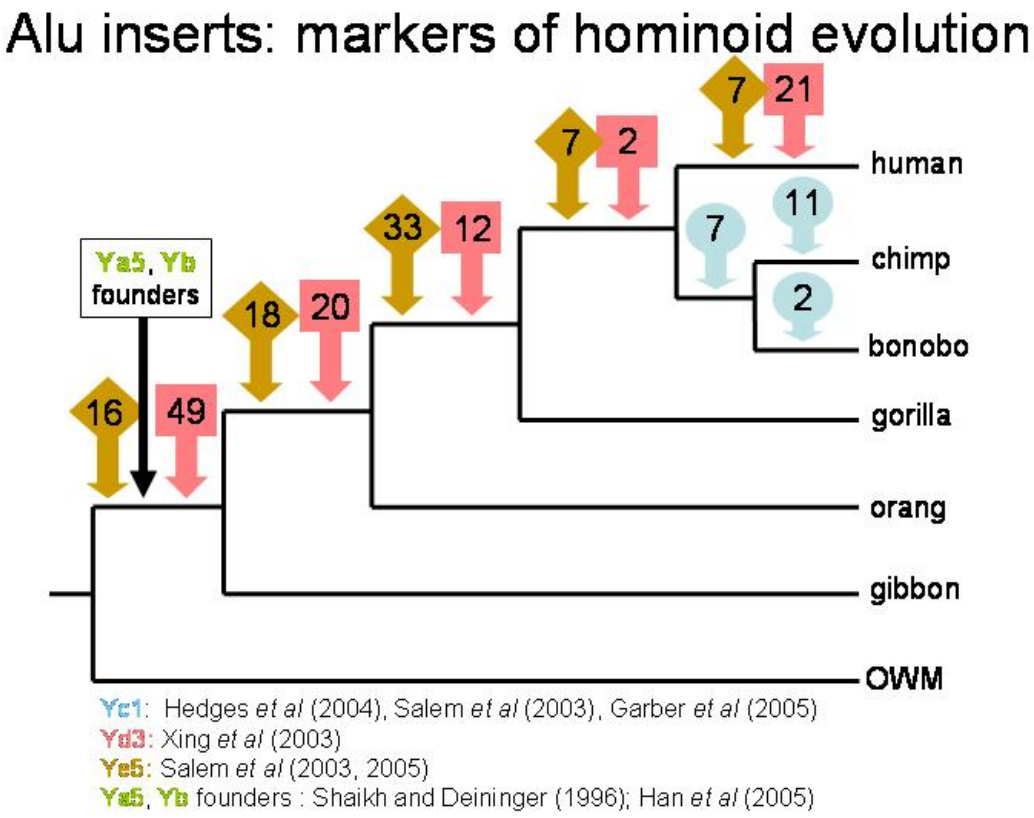
	inserts		
subfamily	total number	dimorphic, %	reference
AluYa5a2	46	68	27
AluYa8	36	31	27
AluYb9	57	23	27
AluYc1	260	21	28
AluYb8	2,200	20	29
AluYg6	176	11	30
AluYi6	136	10	30

- Alu elements are still copying-and-pasting themselves in peoples' genomes. A new Alu element is added to the human gene pool once in every 20 births.[16] New Alu inserts cause genetic disease. SINE retrotransposons are insertional mutagens just like cancer-causing retroviruses and LINEs.[17]

Nearly all (>99%) of the Alu elements in our DNA are shared with other primates. Shared elements do not arise independently: when >2500 insertions of human-specific Alu families were characterised, in no case was an insertion found in a corresponding site in a non-human species.[31] If multiple species possess a particular insert, those species are descended from the one individual in which that unique insert occurred.

The AluYa5 and AluYb families are still expanding in human genomes. They arose from Alu founder elements that inserted into hominoid (ape) ancestors.[32] Potentially active Alu elements can lie in waiting for a million generations, poised to become active when conditions become permissive.

The Yd3 and Ye5 families have been colonising ape genomes for a long time. In one study, 9 elements were shown to be present in humans and chimps but not in gorillas (pointing to a human-chimp ancestral lineage). More remotely, 45 Alu elements are shared by humans, chimps and gorillas (confirming an African great ape ancestral lineage). An additional 38 elements are shared by humans, chimps, gorillas and orangutans, and 65 by the great apes and the lesser apes (gibbons). The apes are 'monophyletic' – clonally derived from each progenitor cell that sustained the DNA insertion of one of these Alu elements.[33]



The distribution of Alu elements has outlined the phylogenetic development of the OWMs and of the New World Monkeys (NWMs). The OWMs are known to be monophylic (derived from one lineage of common ancestors) on the basis of 35 Alu elements found only in their genomes.[34] The NWMs are known to be monophyletic on the basis of 84 Alu elements shared by NWMs alone.[35]

Apes, OWMs and NWMs are simian (anthropoid) primates. More distant primate relations, the prosimians include the tarsiers, and the galago-loris-lemur group. The relationships between these groups have been controversial for a long time. The presence of four ancient Alu inserts in anthropoid primates and tarsiers but not in lorises or lemurs shows that the *Anthropoidea* and *Tarsioidea* are derived from a common lineage.[36] Alu sequences and other SINEs have elucidated the phylogenetic development of the galagos, lorises and lemurs.[37]

Genes from junk

We have co-opted genes donated by the DNAzens of the genome, as exemplified below.

(1) The *env* gene of infectious retroviruses enables the virus particles to stick to cells. The human genome possesses 16 ERVs that retain *env* genes with the capacity to produce intact proteins. These *env* genes have remained intact far longer than would be expected if they were junk.[38] These *env* proteins may function to induce the fusion of their adopted cells, as in the formation of the placental syncytiotrophoblast.

Endogenous retroviruses in our DNA that contain intact *env* genes

ERV	***time of insertion***	***name of env protein***	***ref***
ERV-FRD	simian ancestor	syncytin-2	39
ERVPb	OWM ancestor, or possibly before	-	40
ERV3	OWM-ape ancestor	-	41
ERV-WE1	OWM-ape ancestor	syncytin-1	42

The insertion site of the ERVWE1 provirus is shown below:

human	…CAATTATCTTGCAAC[ERVWE1]CAACCATG…
chimpanzee	…CAATTATCTTGCAAC[ERVWE1]CAACCATG…
gorilla	…CAATTATCTTGCAAC[ERVWE1]CAACCATG…
orang	…CAATTATCTTGCAGC[ERVWE1]CAATCATG…
gibbon	…CAATTATCTTGCAAC[ERVWE1]CAACCATG…
NWM species	…CAATTATCTTGCAAC CATG…
NWM species	…CAATTATCTTGCAAC CATG…
prosimian sp	…CCACCATCTTGCAAA CATG…
dog	…CAACCATCTTGCAAA CATG…

The expression of the ERV-WE1 *env* gene is regulated by both ERV-WE1 sequences, and by sequences of an upstream LTR-containing element of the MaLR class. ERV-WE1 has undergone a 12-base deletion that enhances its ability to induce cell fusion. This unique deletion has been shown in 8 OWM species and 6 hominoid species, and demonstrates their common ancestry.

(2) The insertion of an *Hsmar1* transposon has contributed to the assembly of a new gene. The insertion of the *Hsmar1*element (and of an Alu element), and a 27-base deletion (required for the incorporation of the *Hsmar1* sequence into a pre-existing gene), occurred in ancestors of the simian primates. The *Hsmar1* and Alu element insertions occur at exactly the same point.

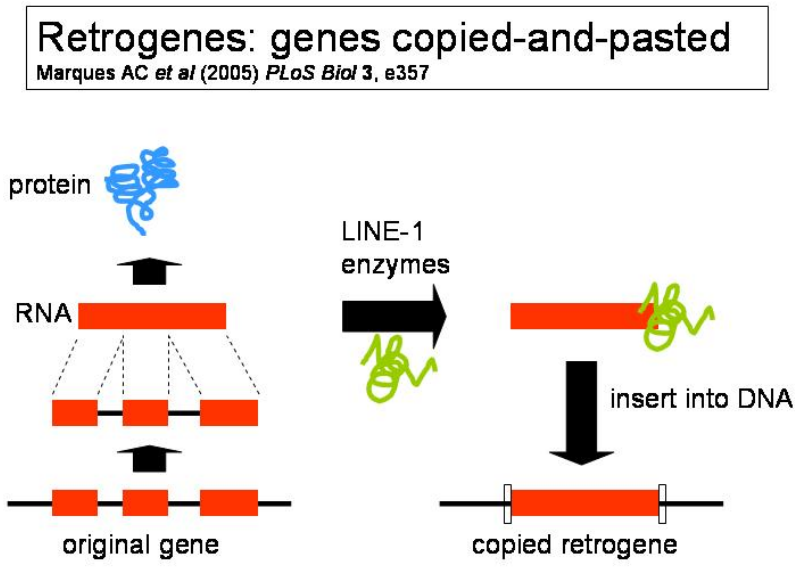
species	flank del	[Alu insert]	[hMAR insert] flank
human	…GATGG	[GGCTG…AAAAA]	[AAAAG…CCCAA]TATCT…
chimp	…GATGG	[GGCTG…AAAAA]	[AAAAG…CCCAA]TATCT…
gorilla	…GATGG	[GGCTG…AAAAA]	[GAAAG…CCCAA]TATCT…
orang	…GATGG	[GGCTG…AAAAA]	[AAAAG…CCCAA]TATCT…
siamang	…GATGG	[GGCTG…AAAAA]	[AAAAG…CCCAA]TATCT…
green mo (OWM)	…GATGG	[GGCTG…AAAAA]	[AAAAG…CCCAA]TATCT…
macaque (OWM)	…GATGG	[GGCTG…AAAAA]	[AAAAG…CCCAA]TATCT…
owl mo (NWM)	…GATGG	[GGCAC…AAAAA]	[AAAAG…CCCAA]TATCT…
tarsier (prosimian)	…AGTGGCATG		TATCT…
dog	…GGTGGCATA		TATCT…

The unique 27-base deletion is preserved in all the simian species.[43] A concatenation of random and unique events has assembled the *Hsmar1* gene.

human	…AACATCAGTT[27 base deletion]GTGGAAAT…
chimp	…AACATCAGTT[27 base deletion]GTGGACAT…
gorilla	…AACATCAGGT[27 base deletion]GTGGAAAT…
orang	…AACATCAGTT[27 base deletion]GTGGAAAT…

siamang	…ATCATCAGTT[27 base deletion]GTGGAAAT…
green mo (OWM)	…AACATCAGTT[27 base deletion]GTGGAAAT…
macaque (OWM)	…AACATCAGTT[27 base deletion]GTGGAAAT…
owl mo (NWM)	…AACATCAGTT[27 base deletion]GTGGAAAT…
tarsier (prosimian)	…AACATCAATTAGGCCGTTT…CTCAGTGGGTGGGAAT…
galago (prosimian)	…AACATCAATTAGGAAGGAA…
mouse	…GGCACCAGTTAGGAAAGGA…
rat	…GGCACCAGTTAGGAAAGGA…
dog	…AACATCAGTTAGGAGTAAA…
cow	…GACACGAGTGAGGAAGGAA…
opossum	…ACCACTCATTAAAGGACCA…

(3) The *GLUD2* gene produces an enzyme called glutamate dehydrogenase in the brain. It is a 'processed gene': a messenger RNA copy of the parent gene was inserted into primate DNA by LINE-1 enzymes.



The insert, target site duplication (underlined) and an extra CAG are identical in all the ape species. This event occurred in an ape (hominoid) ancestor. The target site in OWMs is empty.[44]

	left flanking sequence	[gene]	right flanking sequence
human	…GAAGT<u>ATAGAACAAA</u>CAG	[*GLUD2*]	<u>ATAGAACAAA</u>TAATG…
chimp	…GAAGT<u>ATAGAACAAA</u>CAG	[*GLUD2*]	<u>ATAGAACAAA</u>TAATG…
gorilla	…GAAGT<u>ATAGAACAAA</u>CAG	[*GLUD2*]	<u>ATAGAACAAA</u>TAATG…
orang	…GAAGT<u>ATAGAACAAA</u>CAG	[*GLUD2*]	<u>ATAGAACAAA</u>TAATG…
gibbon	…GAAGT<u>ATAGAACAAA</u>CAG	[*GLUD2*]	<u>ATAGAACAAA</u>TAATG…
OWM	…GAAGT<u>ATAGAACAAA</u>		TAATG…

Such irreducible complexity arising *de novo* is a recurring theme. Over 100 such 'retrogenes' have been discovered in the human genome. Complexity does arise from randomness.[45]

Genes that make us human

In summary,

- 50% of our DNA has been contributed by retroviruses and transposable elements;
- unique inserts shared by humans and other species establish common ancestry;
- an ancestral primate genome has been transformed into ours by the incremental accumulation of DNA changes, all of which reflect mechanisms that are familiar to geneticists;
- some of our genes have been contributed by the parasitic DNAzens of the genome.

The publication of the human and chimp genomes has meant that 'scientists can address anthropology's fundamental question at a new level: what are the genetic changes that make us human?'[46] Many features characterise us as human,[47] but given that 'our cognitive abilities, more than anything else', have defined our distinctive evolutionary niche, states Sikela (2006),[48] 'there is a general consensus that it is our brain and its unusual talent for complex thought that is the most significant.'[49]

The task of relating our genome to our biology is daunting. Human DNA differs from that of chimps by base substitutions (35 million), inserts and deletions (five million),[50] large duplications[51] and other rearrangements. The contribution of any one of these is not obvious. Most changes will represent random drift. Half of the changes will reflect chimp-specific alterations. The significant changes in the human lineage may have occurred in coding genes, in regulatory regions of coding genes, or in the vast expanse of non-coding 'dark matter'.[52]

It may be simplistic to search for 'the genes that made us human' in events that have occurred since our common ancestor with chimps. Goodman *et al* (2005) argue that the evolution of genes since the era of the earliest primates has contributed to our current nature.[53] 'The proposal to sequence an entire chimpanzee genome was based on the premise that this genome sequence would be needed to search for the genetic basis of being human. … it is also true that many traits used to define humanity have much deeper roots. Indeed, to identify the genetic roots of being human the comparative primate genomic data need to be enlarged and placed into a phylogenetic framework that encompasses the entire order Primates.' The sequences of multiple primate genomes are required.

Relating genetics to human biology will be a huge task. Carroll (2003) wrote:[54] 'Despite our enhanced understanding of functional genetic architecture, there remains a tendency to associate the development, function or evolution of a trait with single genes (genes 'for' speech, cancer and so on). The ghost of 'hopeful monsters' still haunts biology and is, unfortunately, a prevalent misconception in the scientific and general press ... It seems unlikely that the traits that interest us most – bipedalism, skeletal morphology, craniofacial morphology, brain size and speech – were the products of the selection of just a few genes'. It may be the interacting indivisible entirety of our genome that specifies the indivisible entirety of our biology. Carroll concludes: 'The sequencing of the chimpanzee genome will reveal no more directly about the origin of human traits than the sequence of the human genome tells us about how to construct a health baby'.[55]

Genetics are unable to describe fully what make us human. 'A complete understanding of uniquely human traits will, however, include more than DNA. Scientists may eventually circle back to those long-debated traits of sophisticated language, culture and technology, in which nurture as well as nature plays a leading

role. We're in the age of the genome, but we can still recognise that it takes much more than genes to make the human.'[46]

Explaining "humanness" is … not easily approached using the genome alone. We prefer to use the term "the human condition" to refer to the entire suite of characters that make humans different from the great apes. What it means to be human involves quantitative aspects of biochemistry, physiology and morphology as well as more qualitative arenas such as cognition, behaviour, symbolic communication, and culture.'[47]

Darwin's friend and most ardent supporter in America was the Harvard botanist Asa Gray (a devout christian). He said that man 'is as certainly and completely an animal as he is certainly something more'.[56] An American Professor of Biology Rick Colling has recently said the same thing: 'We are fully biological but also much more.'[57]

The differences in the biology of the human animal and other great apes are specified in our DNA. This whole area is open to scientific investigation. But the system may be vastly more complex than some 'genes-that-make-us-human' enthusiasts have allowed. If our minds and culture are emergent properties of matter and genetics, then genes will never tell the whole story of our humanity.

Genes for religion

Wolpert has suggested that there may be 'circuits in our brain set up by the genes that predispose us to have religious and mystical beliefs'.[58] If that were completely true, it would have no bearing on whether a transcendent being, the focus of such beliefs, exists independently of our minds. The spiritual faculty – a yearning for the transcendent – may have been of selective advantage because God is the source of the physical and moral order that makes our existence intelligible. A mental faculty that arises by natural selection need not for that reason be unconnected to an independent objective reality.

- One must presume that human rationality arose by natural selection. This cannot imply that it has no traction on reality.

- One would expect that our instinctive care for our children has arisen by natural selection. This evolutionary perspective defines parental care in consequentialist terms (it is 'good' to care for one's children). It is fully compatible with a biblical perspective that sees our care for our children in deontological terms (the moral structure of the universe, arising from the nature of God, tells me that it is inherently 'right' to care for my children).

- St Augustine said no less than Wolpert. 'Man is one of your creatures Lord and his instinct is to praise you. … The thought of you stirs him so deeply that he cannot be content unless he praises you, because you made us for yourself and our hearts find no peace until they rest in you'. Colling argues that 'the universal desire for relationship appears to extend beyond mere human interaction'. Such 'cosmic loneliness' suggests that we are 'wired for God'. Colling suggests that the 'Random Designer' created us with minds that crave for relational connections 'in order to accomplish a dual purpose – one for biological survival and the other to lead his creation to Him'.[59] If we do indeed possess an innate yearning for God, then any discovery that it is genetically encoded cannot

undermine the assertion that God ordained that it be there. The action of God is not an alternative to the molecular biological mechanisms disclosed by science.

However, we should not accept Wolpert's thesis without critical reflection. He compares the tendency to 'religious belief' (considered to be genetically encoded) with science: 'Scientific thinking is not programmed in our brains'.[60] This provides the underlying structure to his book, and the basis of the exalted status given to science. However, 'science' and 'religion' are not comparable concepts. The equivalent of 'science' is 'theology'. It is these that are systematic, rigorous, scholarly, communal activities, not genetically encoded. Science seeks understanding of natural history (such as primate evolution); Christian theology seeks understanding of God's actions in concrete human history. The basis of each intellectual discipline is the empirical world. The equivalent of 'religion' (causal beliefs regarding the spiritual world) is that set of causal beliefs that interprets the material world. The capacity to entertain such beliefs, whether spiritual or physical in nature, may well reflect genetically encoded, specifically human neural circuits. To be human is to engage in the spectrum of causal beliefs. All of our causal beliefs need to be critiqued at the bar of the appropriate discipline.

Wolpert is a developmental biologist, but he does not discuss the limits of genetics as seen in the plasticity of the brain. Genes provide the neural substrate upon which experience acts to mould our brains. With a faculty as basic even as that of sight, it is *experience* that turns potentiality into actuality. 'If babies born with cataracts fail to have them removed within their first year or so, it avails little to remove them, for the vision tuning program has shut down…'.[61] This is an instance of amblyopia, and reflects experience–dependent circuit refinement during an all-important critical period: 'the seemingly innocuous act of covering an eye can profoundly alter the physical structure of the brain'.[62] The brain develops anatomically in response to environmental inputs, experience, and training. This has been shown by quantifying morphological changes in the brains of musicians, jugglers, taxi drivers, and university students.[63]

Genes and experience

The physical structure and the function of the brain, genetics and all, is moulded early in life by the attention and love of those to provide care. Neural and behavioural abnormalities occur in young children who have suffered socio-emotional deprivation. Brain imaging (PET using 2-deoxy-2-[^{18}F]-glucose/MRI) has shown reduced metabolic activity in certain parts of the brain of children adopted from institutions where they experienced severe neglect. This is associated with structural abnormalities in the white matter tract (left uncinate fasciculus) which connects the malfunctioning regions.[64]

Perry has stated that 'Genes are designed to work in an environment ... Genes are expressed by microenvironmental cues, which in turn are influenced by the experiences of the individual.' In the just fertilised ovum, the chemical processes that drive development essentially genetically-determined. By birth, 'environmental cues mediated by the senses play a major role in determining how neurons will differentiate, sprout dendrites, form and maintain synaptic connections, and create the final neural networks that convey functionality. By adolescence, the majority of the changes that are taking place in the brain of that child are determined by experience, not genetics.'[65]

Sensory neglect in childhood leads to abnormal brain development. 'In the development of socio-emotional functioning, early life nurturing appears to be critical. If this is absent from the first three years of life, and then a child is adopted and begins to receive attention, love and nurturing, these positive experiences may not be sufficient to overcome the malorganisation of the neural system mediating socio-emotional functioning.'[66]

These 'experiments' of nature are not true experiments. All variables (alchohol exposure *in utero*, nutrition) cannot be controlled. However, experiments in non-human primates have established that boring environments make for plain-looking brains. 'On the other hand, enriched animal environments – enclosures that stimulate the complexity of a natural habitat – lead to dramatic increases in both neurogenesis and the density of neuronal dendrites, the branches that connect one neuron to another. Complex surroundings create a complex brain.' Our environments can profoundly influence the structure of our brain.[67] In the study of brain pathology, environmental enrichment has been a poor cousin to genetics and pharmacology, but exerts 'a range of dramatic effects'.[68]

'As with other brain-mediated capabilities, the capacity to form relationships results from the experience-based expression of an underlying genetic potential … The somatosensory bath – the smells sights, sounds, tastes and touch – of the loving caregiver provides the repetitive sensory cues necessary to express the genetic potential in this infant to form and maintain healthy relationships.'[69]

Anyone with an *a priori* commitment to describe humanity in exclusively physical (genetic) terms has a problem. Our brains, minds and humanity arise not only from our genes, but from non-quantifiable ('spiritual') qualities such as love, joy, peace, patience, kindness, goodness, faithfulness, gentleness, and self-control – all of which are invisible to the tools of science. That which is spiritual must be admitted as constitutive of my neural development as a human person.

Such a tangible reality as human 'life' requires such an apparently intangible thing as communication, relationship, and words. Take the words quoted by Jesus at his temptation:

> *Man shall not live by bread alone, but needs every word that God speaks.* (Matt:4:4; from Dt 8:3)

or by Peter when Jesus asked his disciples whether they would leave him:

> *You have the words that give eternal life.* (Jn.6:68)

Supremely, consider the words of St John:

> *The Word was the source of Life.* (Jn 1:4)
> *We write to you about the Word of life'* (1Jn 1:1)

Here the writer uses the concept 'logos' that would be meaningful to both Jewish and Greek readers, to refer to Christ, who as the 'Word' was God's personified self-expression to humanity. As God's Word he is life-giving.

Spiritual life is life in relation to God. This life comes from experiencing the grace of the One into whose society we are graciously included. Here is a concept of the concreteness of life arising from the apparent abstractness of personal relationship. It is a concept that the reductionistic materialist may not see. Mackay said 40 years

ago, ‘Just as we see psychological life embodied in the physical brain, so we can see spiritual life embodied in the psychological mechanisms of a person. Just as psychological life is related to the activity of nerve cells, so spiritual life is related to the scientific mechanistic structure of psychological theory.[70]

Humanity and ‘the gracious Other’

Our humanity is not guaranteed by the possession of a human genome. The development of our humanity is consequent upon such a non-material and vulnerable reality as inter-personal relationship. The Franciscan Friar Salimbene relates a story about the Emperor Frederick II of Hohenstaufen, who was intrigued about the origins of language. He ordered that some children be raised from birth in complete silence, in order to ascertain what language they would speak. Perhaps they might spontaneously speak the Language of Heaven.

Frederick’s experiment was performed by ‘bidding foster-mothers and nurses to suckle and bathe and wash the children, but in no wise to prattle or speak with them; for he would have learnt whether they would speak the Hebrew language (which had been the first), or Greek, or Latin, or Arabic, or perchance the tongue of their parents of whom they had been born. But he laboured in vain, for the children could not live without clappings of the hands, and gestures, and gladness of countenance, and blandishments.’[71]

It seems that the children never learnt to speak any language. Their genes for humanity and for religion did not kick in. They died in infancy. We live, develop and grow as human, not according to some deterministic genetic blueprint, but by being immersed in the nurture, love and encouragement of a prior human community. The action of genes in our brains is modulated by the experience of communicated care. ‘The untouched newborn may literally die.’[72]

Much may be learned from children who have spent their earliest years apart from human company, either because of severe neglect, or because they were separated from society and raised by animals. An example of this has come to light recently in the Pacific, where a boy was kept with the chickens, pecked his food from the ground, and when found, did not learn to speak or enter into society.[73]

Stories of neglect (Genie) or of separation (Amala and Kamala) may be found in the ‘Feral Children’ website.[74] When introduced into society, such children do not learn to speak, or develop a sense of ‘I’ as a human being, or become socialised. The neglected child Genie, for example, could not grasp the meaning of pronouns. She used ‘I’, ‘me’, and ‘you’ interchangeably.[75] Language is learned only in the companionship of others and may be necessary for human consciousness.[76]

When it comes to being fully human, genetics counts for nothing if an infant is separated from humanity. Our humanity is the outcome of ‘three kinds of adaptive history’: the influence of biological evolution through the genes, the evolution of neural circuits through experience, and the influence of cultural evolution. It seems that ‘culture and speech are essential for the making of the human mind’. The situation is complex, because ‘it could be that the lack of a social trigger at the right moment, meant that certain genetic programmes failed to kick in’.[77]

Steeves has said that ‘Defining “human” by means of distant hairy relatives or genetic tests capable of being run only by a few experts in our society is just as

unfulfilling as defining "human" as a creature with a chin. …Perhaps being human is best understood as being a particular character in the intertwining stories of the living world. … What I have in mind is the notion that the burgeoning consciousness of the infant will not necessarily develop into human intentionality on its own but rather requires the presence of a Significant Other who is human. This "gracious act of attention" is thus responsible for "creating" a human-person … Without a human Other to attend to the child *as human*, the child does not become human – which is not to say that feral children have no sense of Self or Other, but rather that such senses do not include "humanity" ... Humans we know are not defined genetically or anthropologically …Humanity is in some respect the result of specific treatment within one's community … Being human is being treated by humans as human.'[78]

When I studied for my BTh with the open University of South Africa, I came across and was hugely impressed by the Xhosa saying '*umuntu ngumuntu ngabantu*' or 'a person becomes a person through persons'.[79]

Our genes are absolutely necessary but completely insufficient to define our humanity. Our status as human beings arises from personal knowledge. What our genetics do is to give us the ability to receive the love of others which in fact confers upon us our humanity. This is congruent with the words of Christ:

> *And eternal live means knowing you the only true God, and knowing Jesus Christ, whom you sent* (John 17:3).

In his first letter, St John spelled out a similar concept:

> *the Son of God has come and has given us understanding, so that we know the true God. We live in union with the true God – in union with his Son Jesus Christ. This is the true God and this is eternal life* (1John 5:20).

As human beings we transcend our genes because they could never make us human. It is the love of humans who have made us human. In being known and loved we know and love. In similar manner I believe that we are socialised into the community of God only by the communication of his grace. No extra material is added to our humanity, but just as we have human life through knowing, so we have spiritual life - the fullness of life – in knowing the WORD of God, spoken in Jesus Christ.[80]

I believe that the words of St Paul, written to the christian community at Philippi, reveal the apogee of authentic humanity:

> *'All I want is to know Christ and to experience the power of his resurrection, to share in his sufferings, and become like him in his death, in the hope that I myself will be raised from death to life.'* (Phil 3:10-11)

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TGC (encodes the amino acid cysteine) → TGA (a 'stop' signal)
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55. Similarly, Lahn has said, 'If you didn't tell me that humans were special biologically, I wouldn't have predicted it looking at the human genome'; quoted by Holms R (2004). Chimp genome preview: the great invertors. *New Scientist* **21** (February), 41-43

56. Moore JR (197x). *The Post-Darwinian Controversies*. (Cambridge: CUP) p.279

57. Colling R (2004). *Random Designer*. (Bourbonnais: Browning Press), p.67

58. Wolpert, ref. 2, p.217. Other postulates include: 'brain function in relation to belief has a strong genetic basis' (p.35); 'our brain has a natural tendency to find consistent and reasonable explanations for important events, and so religious beliefs are most likely partly genetically determined' (p.137); 'religious beliefs have a genetic component' (p.138). These statements seem to boil down to the notion that the capacity to engage in religious or metaphysical beliefs (including 'reductionist materialist atheist' ones, p.x) arise from a genetically-encoded neural potentiality.

59. Colling, ref.57, p.147

60. Wolpert, p.201

61. Leiber J (1997). Nature's experiments, society's closures. *Journal for the Theory of Social Behaviour* **27**, 325

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64. Decreased metabolic activity has been demonstrated in the orbital frontal gyrus, the infralimbic prefrontal cortex, the amygdala and head of the hippocampus, the lateral temporal cortex and in the brainstem: Chugani HT, Behen ME, Muzik O *et al* (2001). Local brain functional activity following early deprivation: a study of postinstitutionalized Romanian orphans. *NeuroImage* **14**, 1290; Eluvathingal TJ, Chugani HT, Behen ME *et al* (2006). Abnormal brain connectivity in children after early severe socioemotional deprivation: a diffusion tensor imaging study. *Pediatrics* **117**, 2093; for a review, see MacLean K (2003). The impact of institutionalization on child development. *Development and Psychopathology* **15**, 853. Effects of institutionalisation included abnormal intellectual and physical development, behavioural problems (stereotyped behaviour, attention difficulties, problems relating to peers), indiscriminate friendliness, and loss of attachment.

65. Perry BD (2002). Childhood experience and the expression of genetic potential: what childhood neglect tells us about nature and nurture. *Brain and Mind* **3**, 79 (the quote is from p.86)

66. Perry, p.87

67. Lehrer J (2006). The reinvention of the self. *Seed* **2**, 58. This article discussed the work of Elizabeth Gould and Ronald Duman.

68. Nithianantharajah J and Hannan AJ (2006). Enriched environments, experience-dependent plasticity and disorders of the nervous system. *Nature Reviews Neuroscience* **7**, 697

69. Perry. p. 94-95

70. McKay DM (1965). *Christianity in a Mechanistic Universe*. (London: IVP), pp.67-69

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72. Perry, p. 89

73. 'Saving a wild boy', Extreme Close Up Productions, contactable at info@greatjourneys.org

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76. Lieber, p.335

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79. Villa-Vicencio C and de Gruchy J (1994). *Doing Ethics in Context*. (Maryknoll: Orbis Books and Capetown and Johannesburg: David Philip), p.29

80. One other point must be made about Wolpert's 'religion-is-in-the-genes' hypothesis. Nowhere did he engage the truth claims of Christianity. When were the gospels written? Did Jesus live as the gospels say he did? Did he claim to come from God? Did the first Christians really believe that Jesus was risen? The record of our evolution as inscribed in our genes reveals an epic story in all its contingent particularity. All creatures that possess a particular ERV or SINE are the descendents of the one organism in which the instance of insertion occurred. The biblical understanding of God has likewise grown as an epic story of unique events in history. The particularities of an Abraham, a Moses and an Isaiah (refugees from the all-encompassing polytheism of the magnificent civilisations of Ur, Egypt and Babylon) are sources of my awareness and understanding of God. Supremely the uniqueness of 'God's great historic act in Christ … imposes an inescapable scandal of particularity' (John Polkinghorne, *Science and Christian Belief*, p.186). It is history, not genetics, that confronts us with God – a God who is strikingly different to what we may naturally intuit. The singular, radically counter-intuitive teachings of Jesus ('happy are you who poor'; 'love your enemies') speak not of genetics but of encounter with Someone who takes us by surprise.