Seeking Adam: Questions from Genetics
David L. Wilcox
“I found a way to save a bundle on this project — we can recycle 98 percent of the chimp DNA!”
The Questions Behind My Theses!!

1. Is Adam M.I.A.???
2. Did Grandma marry a Neanderthal?
3. How do you reprogram a recycled ape brain?

This Week's Data

Just show me the data!!
Setting the Stage: Presuppositions

The earth and its data belong to the Lord – It’s His creation.

Theology has made predictions about the shape of the creation.

Recently discovered data differ from some of those predictions.

All theories are human opinions, but the data belong to God.

Thus, data can falsify theories from both science and theology.
Thesis: The genetic evidence showing that *Homo sapiens* shares a common ancestor with the chimpanzee (and other more distant living species, as well as Neanderthals) allows for no reasonable alternate explanation.

Of course, God could have made Adam with a genome that matched the chimps (and Neanderthals) down to the retrovirus insertions. But that would mean He intentionally built a fictional genetic history into our genome, which I take to be unworthy of the God of truth. That does not necessarily mean there was or was not a ‘special’ work of God at some point in the process of human origins – just that the dust God equipped as His image was a hominine.
Evolutionists’ Headaches

Headache Number One: The Very Missing Link

If the evolutionists’ theory is correct, then present-day man was formed after simple types of life had changed to more complex types throughout millions of years. We would naturally expect to be able to find hundreds, even thousands of examples of skeletons which are reptiles half changed to birds, or of animals half changed to men.

But do we find all those positive proofs that evolution is indeed the answer to the question of man’s existence on earth? Far from it!

Instead of thousands, or hundreds, or scores of examples of links between beast and man, we find not one undisputed example.
Thesis: We have anthropoid roots. The genetic evidence which shows that *Homo sapiens* shares a common ancestor with the chimpanzee (and other more distant species) allows for no reasonable alternate explanation.
In every measure made, the human to chimp distance is the minimum. This ‘falsifies’ the predictions of the special creations of kinds following common plans in God’s mind.

It supports a pattern of shared descent - people & chimps descended from common ape ancestors.

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Table 19.1 Genetic distances between humans, chimpanzees, and gorillas (Hacia, 2001)

This table gives estimates of the percentage sequence divergence between species pairs, based on examinations of 4.8–29.3 kb of sequence.
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**Humans and Apes Genetic Distances**

- **Table of Genetic Distances**
- **Tree Diagram**

- **Legend:**
  - Hsa: Homo sapiens
  - Ppa: Pan paniscus
  - Ptr: Pan troglodytes
  - Ggo: Gorilla gorilla
  - Ppy: Pongo pygmaeus
  - Hla: Hylobates lar
  - Mmu: Macaca mulatta
  - Mni: Macaca niger
  - Mne: Macaca nemestrina
  - Pcy: Presbytis cynocephalus
  - Tge: Tarsius bancanus
  - Lat: Loris tardigradus

- **Distances:**
  - OW M: Genetic distances are measured in nucleotide substitutions per site.
At insertion, 3' & 5' sequences are identical

Human Retrovirus Insertion Trees – Comparing Sequences
Neutral and Negative Mutations & Effects of Selection

13,550 genes – 5.5 mb

Nature 437, 69-87 (1 September 2005)
| doi:10.1038/nature04072; Received 21 March 2005; Accepted 20 July 2005 -- Initial sequence of the chimpanzee genome and comparison with the human genome
From report of Chimp Genome Sequence
*Nature* 437, 69-87 (1 September 2005)

Mutations in 13,355 of 21,000 protein coding genes
Relative distances between human and chimp genomes

In Exons - altered amino acid assignments – 1.5
In Exons - synonymous a. a. assignments – 6
In Introns – 8
In Intron splicing junctions – 0.5

The sequence differences are proportional to selective (functional) importance, not to relative human / chimp morphological difference. If differences driven by ‘common plan’, would expect all distances to be equivalent.
From: Wayne Frair, Kurt Weis

I'm no kin to the monkey (or Chimp)?

Expected (predicted) genetic sequence distances based on phenotypic data & / or special creation theory

Monobaramin (Species)

1960's - Pre-genetic evaluation of human / chimp differences

From: Wayne Frair, Kurt Weis
Thesis: Multiple lines of genetic evidence are incompatible with descent from a single human ancestral pair. E.G., the HLA (immune) loci retain too much diversity, and techniques such as linkage disequilibrium and retained diversity indicate a long term human population of around 10,000. An early bottleneck is possible, but not a bottleneck of two people.

If Adam and Eve are not the sole progenitors of the human race, there are a series of critically important theological issues to reconsider. Despite their importance, we cannot deny the reality of the physical evidence and claim to reach valid conclusions. Possibly the most critical issue is the theological dependence on the sin of Adam for explaining the sinfulness of the human race.
Based on population logic – small populations lose diversity (INDELS, SNPs, alleles, Microsatellites, TEs, etc), have low levels of linkage disequilibrium, etc. Ne can be estimated for various time points in the past based on the amounts of remaining genetic diversity generated at those time points. Ne’s can be calculated for mtDNA, Y chromosomes, X chromosomes and autosomes – with sometimes differing results. The math gets complex --

But in summary: African Ne’s are about 4 fold greater than Non-African Ne’s. And, there is a general consensus for our ancestral Ne of about 10,000 – see estimates below.

Recent estimates of human Ne:

<table>
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<th>Researcher</th>
<th>Year</th>
<th>Ne</th>
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<tr>
<td>Burgess</td>
<td>2008</td>
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<tr>
<td>Tenesa</td>
<td>2008</td>
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<tr>
<td>Campbell</td>
<td>2010</td>
<td>15,000</td>
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<tr>
<td>Mele</td>
<td>2011</td>
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<td>Gronau</td>
<td>2011</td>
<td>9,000</td>
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<td>14,000</td>
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<td>Huff</td>
<td>2010</td>
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<td>Hawks</td>
<td>2011</td>
<td>10,000</td>
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Huff gives additional interesting values based on haplotypes linked to ancient Alu’s (jumping genes). The value of 9300 applies to the last million years – before that, our ancestral Ne was 18,500 (and no more than 26,000). Compare that to the Chimp Ne of 21,000 and the Gorilla Ne of 25,000.

And – different scenarios of population history can predict different – or the same – results...
Calculating population size through a bottleneck of Biblical proportions:

If the root human population is holding at 10,000, and two individuals are chosen out (or newly created) to found a new human species, and if they have 10 children, as do their descendants for the next six generations, they will restore the original population size, \(2, 10, 50, 250, 1250, 6250, 10,000 \ldots\).

If one assumes such an ‘Edenic’ bottleneck occurs as part (or start) of a period of 1000 generations (about 20,000 years), the other generations being around 10,000 individuals, one can calculate \(N_e\) (effective population size) for the entire period. \(N_e\) would be 725, which means the data would indicate there were effectively less than 1000 individuals for the entire 20,000 period. But that means isolating the period.

A lumped calculation – for the entire 200,000 years - thus, 10,000 generations – with the bottleneck: Assume a real long term yearly \(N_e\) of 20,000 (chimp level). If the total diversity for the entire period is calculated with the above bottleneck at some point, and 10,000 generations with an \(N_e\) value of 22,000 - the average \(N_e\) comes out at 11,250. That sounds like the bulk of the estimates of \(N_e\), and with the simplifying assumption that there was no bottleneck, the bottleneck cannot be spotted. But there are ways to pick it out, and to measure how strong it would be.
The common ancestors (TMRCAs) of autosomal and X-linked genes are on average, respectively, 1,500,000 and 1,000,000 years. But these deep gene genealogies are consistent with the Out-of-Africa scenario if the ancestral Ne was around 14,000. A bottleneck in the Middle Pleistocene (around 150,000 years ago) possibly arising from an ancestral structured population, can reconcile the contradictory findings from mtDNA & Y chrom. with those from the autosomes and the X chromosome. Both a “multiple archaic populations” model and a sudden bottleneck, can account for the 8-fold discrepancy between TMRCAs. Both scenarios of human evolution are different versions of a bottleneck in the human lineage before the succeeding migration out of Africa.

FIG. 2. Estimates of the TMRCAs and posterior predictive distribution for the different models of human evolution. (The short vertical lines in A and B show the TMRCA estimates for individual loci. The tall ones in C are estimates for mtDNA & the Y chr.)
Figure 4 | Inference of population size change over time. The y axis specifies a number proportional to the population size $N_e$. The x axis specifies time in units of divergence per base pair (along the top in years for mutation rates of $0.5 \times 10^{-9}$ to $1.0 \times 10^{-9}$ per site per year). The analysis assumes that the
For example, Vern Poythress rejects common ancestry and (erroneously) claims that estimates of \( Ne \) are long-term averages unable to detect a bottleneck down to two individuals:

ADAM VERSUS CLAIMS FROM GENETICS

Vern S. Poythress

\textit{WTJ} 75 (2013): 65-82

Information based on correlations between nearer locations on a chromosome probes further into the past, but the analysis always results in figures that represent a rough average over many generations in the human population. Consequently, the principal figures, like 3,100 for non-African populations and 7,500 for the African population, represent average populations over many generations. They say nothing one way or the other about whether the size decreased rapidly to two individuals in the more distant past.
Global Phylogenetic Tree

- Han Chinese
- Masaai
- Sandawe
- Hadza
- Luhya
- Yoruba
- amaXhosa
- Ju/'hoan
- !Xun
- Vasekela
- Mbuti Pygmy
- Biaka Pygmy
- European

Legend:
- Ju/'hoan (n=19)
- !Xun (n=14)
- Xhose (n=15)
- Coloured (n=25)
- Baster (n=30)
**Mhc-DQB1**

phylogenetic tree

**To much diversity to have come from 2 people**

**Too many Adams??**

**HLA Histocompatibility Loci**
Reshuffling of ancient peptide binding motifs between HLA-DRB multigene family members: Old wine served in new skins

Balancing selection for functional diversity retains exon sequences despite mutation & recombination

Doxiadis 2008

Exon 2
Reshuffling of ancient peptide binding motifs between HLA-DRB multigene family members: Old wine served in new skins

Doxiadis 2008

Mixing of introns by recombination, is unconstrained by selection
Thesis: With a high degree of certainty, the genetic data shows that the modern human species, *Homo sapiens*, originated as a single small African population about 200,000 years ago.

Theological questions are raised by such human genealogical patterns. Can ‘Adam’ be moved back to the ‘origin point’ of modern humanity, about 190,000 years ago? Can a later ‘Adam’ function theologically if humanity has spread across the entire earth by 15,000 BC (and most of the earth by 40,000 BC)?
"The Dawn of Human Matrilineal Diversity."
Schematic Representation of the Human mtDNA Phylogeny within Hominini (Left) Hominini phylogeny illustrating approximate divergence times of the studied species. The positions of the RSRS and the putative Reconstructed Neanderthal Reference Sequence (RSRS) are indicated by the black star. (Right) Reconstructed mtDNA phylogeny showing the positions of the RSRS, the putative Neanderthal reference sequence, and the reconstructed Mitochondrial 'Eve' for each hominin species. The approximate divergence times are indicated by the numbers: H (Homo sapiens) c400K, N (Neanderthal) 170K, and S (Sapiens) 170K.

Behar 2012: ‘Copernican’ Reassessment of the Human Mitochondrial DNA Tree from its Root
100,000 year old South African tribal separation

Shows the ancient tribal separation of human groups in South Africa – 100 K +
Qiaomei 2013 A Revised Timescale for Human Evolution Based on Ancient Mitochondrial Genomes

mtDNA genealogy including ‘fossil’ modern sequences
Mendez 2013  An African American Paternal Lineage Adds an Extremely Ancient Root to the Human Y Chromosome Phylogenetic Tree

Debate over mutation rate

Karafet 2008
Cruciani 2011
Scozzari 2012
Mendez 2013

‘Y Chromosome Adam’
Schlebusch 2012 Genomic Variation in Seven Khoe-San Groups Reveals Adaptation and complex African History

Nuclear SNP’s

Published by AAAS
Abstract

The emergence of more refined chronologies for climate change and archaeology in prehistoric Africa, and for the evolution of human mitochondrial DNA (mtDNA), now make it feasible to test more sophisticated models of early modern human dispersals suggested by mtDNA distributions. Here we have generated 42 novel whole-mtDNA genomes belonging to haplogroup L0, the most divergent clade in the maternal line of descent, and analysed them alongside the growing database of African lineages belonging to L0’s sister clade, L1’6. We propose that the last common ancestor of modern human mtDNAs (carried by “mitochondrial Eve”) possibly arose in central Africa ~180 ka, at a time of low population size. By ~130 ka two distinct groups of anatomically modern humans co-existed in Africa: broadly, the ancestors of many modern-day Khoe and San populations in the south and a second central/eastern African group that includes the ancestors of most extant worldwide populations. Early modern human dispersals correlate with climate changes, particularly the tropical African “megadroughts” of MIS 5 (marine isotope stage 5, 135–75 ka) which paradoxically may have facilitated expansions in central and eastern Africa, ultimately triggering the dispersal out of Africa of people carrying haplogroup L3 ~60 ka. Two south to east migrations are discernible within haplogroup L0. One, between 120 and 75 ka, represents the first unambiguous long-range modern human dispersal detected by mtDNA and might have allowed the dispersal of several markers of modernity. A second one, within the last 20 ka signalled by L0d, may have been responsible for the spread of southern click consonant languages to eastern Africa, contrary to the view that these eastern examples constitute relics of an ancient, much wider distribution. Citation: Rito T, Richards MB, Fernandes V, Alshamali F, Cerny V, et al. (2013) The First Modern Human Dispersals across Africa. PLoS ONE 8(11):
Rain, Vegetation and marine sediment – Sahara Climate

Figure 4 | Inference of population size change over time. The y axis specifies a number proportional to the population size $N_e$. The x axis specifies time in units of divergence per base pair (along the top in years for mutation rates of $0.5 \times 10^{-9}$ to $1.0 \times 10^{-9}$ per site per year). The analysis assumes that the
The common ancestors (TMRCAs) of autosomal and X-linked genes are on average, respectively, 1,500,000 and 1,000,000 years. But these deep gene genealogies are consistent with the Out-of-Africa scenario if the ancestral Ne was around 14,000. A bottleneck in the Middle Pleistocene (around 150,000 years ago) possibly arising from an ancestral structured population, can reconcile the contradictory findings from mitDNA & Y, with those from the autosomes and the X chromosome. Both a “multiple archaic populations” model and a sudden bottleneck, can account for the 8-fold discrepancy between TMRCAs. Both scenarios of human evolution are different versions of a bottleneck in the human lineage before the succeeding migration out of Africa.
Thesis: The African ecosystem collapsed and rebounded 150,000 years ago – a glacial ‘winter’ followed by ‘spring’ – triggering northward expansion & cultural changes such as clothing - the first major geographical division of *Homo sapiens*.
Blome, M.W., et al., The environmental context for the origins of modern human diversity: A synthesis of regional variability in African climate 150,000 to 30,000 years ago, Journal of Human Evolution (2012),

Figure 14. Summary of the circum-Africa climate data from 150 to 30 ka including sea surface temperatures (SSTs) and each region from north to south on the continent. The terrestrial data across the continent do not vary in concert with the Marine Isotope Stages, whereas the SSTs appear to be following this more global signal.
FIG. 1. Divergence time of human head and clothing lice. The posterior distribution for the divergence of head and clothing lice (gray curve) places the median estimate for the origin of clothing lice at 170 Ka (black arrow). This estimate is substantially older than a previous estimate of 30–112 Ka from molecular data (Kittler et al. 2003) and is consistent with the relative antiquity of the first archaeological evidence for hide scrapers;780 Ka (Carbonell et al. 1999), the loss of human body hair by ;1.2 Ma (Rogers et al. 2004), and the first evidence for tailored clothing ;40 Ka (Delson et al. 2000), which are indicated by blue arrows. Furthermore, the median estimate lies within the ice age coincident with Marine Isotope Stage 6 ;130–190 Ka (EPICA Community Members 2004), indicated by the red-shaded region.

Thesis: The Earth was settled from Africa. A single population left Africa about 60,000 years ago, settling along the Indian Ocean eastward to Australia. 40,000 years ago, more tribes left the Middle East, moving north into Central Asia and Europe, and reaching the Americas around 17,000 years ago. The timing of these settlements was dependent on ice age climate cycles.

Even if the Garden of Eden is moved to Africa, it is difficult apply the geographical implications of Genesis 2 to Africa. Notably, the issues of geographical location (Africa), the long history prior to leaving Africa, and the historical events of the early chapters of Genesis. Thus, a theological issue is often raised – is Genesis primarily about Israel or all of humanity?
The earth was settled by African emigrants leaving about 65,000 years ago - The first wave moved eastward along the Indian Ocean, settling East & South Asia. A second wave left Middle East refuges around 45,000 years ago - east through Asia & north-west across Europe.
The “climate catastrophe” caused by the explosion of the Indonesian super volcano Toba 73,000 years ago shut down the Saharan ecosystem and drove its population southward, replacing local males (Y chromosomes).
Thesis: The surprisingly complete genomic data from our extinct closest relatives, the Neanderthals and Denisovans, provide important clues to human uniqueness – and raise interesting questions. They were apparently functionally different, but yet we interbred with them - slightly.

The existence of archaic human species which were in intimate contact with modern humans raises questions regarding their spiritual status, the nature of the image of God, and the time-line for the appearance of true humanity. But such an evaluation requires a significant look at how they differed, and what effects the interbreeding had on modern people.
A possible model of gene flow events in the Late Pleistocene.

The direction and estimated magnitude of inferred gene flow events are shown. Branch lengths and timing of gene flows are not drawn to scale. The dashed line indicates that it is uncertain if Denisovan gene flow into modern humans in mainland Asia occurred directly or via Oceania. D.I. denotes the introgressing Denisovan, N.I. the introgressing Neanderthal. Note that the age of the archaic genomes precludes detection of gene-flow from modern humans into the archaic hominins.
20% of the Neanderthal genome can be recovered from Asian and European populations.

- Average % is 1.5% to 2.1%
Fig. 2 Genomic distribution of surviving Neandertal lineages. (A) Neandertal lineages identified in East Asians (ASN, red) and Europeans (EUR, blue). B Vernot, and J M Akey Science 2014;343:1017-1021
### Extended Data Table 1 | Gene categories enriched or depleted in Neanderthal ancestry

<table>
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<th>Biological pathway (GO categorization)</th>
<th>Neandertal ancestry</th>
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<th>East Asian FWER</th>
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<td>&lt;0.001</td>
<td>&lt;0.001</td>
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Enrichment of Gene Ontology categories in genes depleted or enriched Neanderthal ancestry was assessed using the hypergeometric test implemented in the FUNC package. We report family-wise error rate (FWER) P values associated with each GO category (P values corrected for the testing of multiple categories).

### Extended Data Table 2 | Neanderthal-derived alleles that have been associated with phenotypes in genome-wide association studies

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<th>rs id</th>
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<td>rs75418188</td>
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<td>rs117767867</td>
<td>17:6,946,330</td>
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<td>1.85</td>
<td>11.54</td>
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</table>
Figure 2 | Phylogenetic relationships of the Altai Neanderthal. a, Bayesian tree of mitochondrial sequences of the toe phalanx, the Denisovan finger phalanx, six Neanderthals and five present-day humans. Posterior probabilities are given for branches whose support is less than one (Supplementary Information section 2b). b, Neighbour-joining tree based on autosomal transversion differences among the toe phalanx, four Neanderthals, the Denisova genome and seven present-day human individuals. Bootstrap values are shown for branches supported by less than 100% of 1,000 bootstrap replicates (Supplementary Information section 6).
Thesis: The molecular evidence indicates that a myriad of neural control sequences rather than the addition of a few major effect genes were used to mold humanity. This involved significant selection, drift and mutation (including transposons).

Much of the unique nature of humanity was apparently produced over an extended period of time by secondary causes acting upon an already complex genome. Or, does becoming human require sudden ‘injections’ of ‘new information’? Could human neurological advances be produced by altering levels of gene activity – or would they require new genes? This raises questions of divine governance, of course. Is this design or unguided happenstance? How does it affect our understanding of the image of God?
Protein coding !!

Non-coding Genes Account for Most Transcription from the Genome:

- 90% Transcriptionally active
- 1% Protein encoding
- 9% Regulatory sequences
- 20% Repetitive DNA
- 15% Unique noncoding DNA
- 14% Repetitive DNA unrelated to transposable elements
- 10% Simple sequence DNA
- 17% L1 sequences
- 5% Large-segment duplications
- 3% Simple sequence DNA

Classes of non-coding RNA:

- sncRNAs Small non-coding RNAs (~200 nt)
  - siRNAs Small interfering RNAs
  - piRNAs Piwi-interacting RNAs
  - snoRNAs Sno-derived RNAs
  - mRNAs MSY-2-associated RNAs
  - mirRNAs MicroRNAs
  - moRNAs MicroRNA-offset
  - crasiRNAs Centrosome-associated RNAs

- snRNAs Small nuclear RNAs
  - PARs Promoter-associated RNAs
  - xirRNAs X-inactivation RNAs
  - tel-iSNAs Telomere small RNAs

- IncRNAs long non-coding RNAs (~200 nt)
  - Signal IncRNA
  - Decoy IncRNA
  - Guide IncRNA
  - Scaffold IncRNA
Overview of regulatory roles of non-coding RNAs

I. Signaling
II. Decoy
III. Guides
IV. Scaffolds
ALU family only found in Primates – human ALU’s show twice as much insertion activity as chimp ALU’s – with expected higher diversity (1.7) in chimps. Humans have unique families.

The human genome carries about 1,100,000 copies of the 0.28-kb Alu retroposon, the major human SINE; spaced, on average, about 10 kb apart.

Alu (Arthrobacter luteus) restriction endonuclease
SINE RNAs control the heat shock response in mouse and human cells. A) Pol III transcribed SINE RNAs increase upon heat shock. B) During heat shock, mouse B2 RNA or human Alu RNA enters complexes at the promoters of repressed genes. TFIIF facilitates dissociation of B1 RNA from Pol II. C) Heat shock activated genes are resistant to repression by B2 RNA and Alu RNA.


OR: Jacques et al. 2013 titled “The Majority of Primate-Specific Regulatory Sequences Are Derived from Transposable Elements”.
Higher editing level of ALU transcripts in human vs. nonhuman primates.

(A) Editing levels of 75 sites in six transcripts - cerebellum - 4 humans, 2 chimps – 2 rhesus
Average editing values were normalized & colored with blue-yellow gradient.

(B) Editing level per site for three species. Human editing sites are ordered in decreasing editing levels, & nonhuman primate editing sites are aligned accordingly.

(C) Total editing levels in cerebellum tissues of eight individual primates: are plotted. The bar size is proportional to the total of the editing levels in all tested sites.
Abstract: Transposable element insertions have strongly affected human evolution

Contributed by Roy J. Britten, October 4, 2010 (sent for review June 7, 2010) PNAS

Comparison of a full collection of the transposable element (TE) sequences of vertebrates with genome sequences shows that the human genome makes 655 perfect full-length matches. The cause is that the human genome contains many active TEs that have caused TE inserts in relatively recent times. These TE inserts in the human genome are several types of young Alus (AluYa5, AluYb8, AluYc1, etc.). Work in many laboratories has shown that such inserts have many effects including changes in gene expression, increases in recombination, and unequal crossover. The time of these very effective changes in the human lineage genome extends back about 4 million years according to these data and very likely much earlier. Rapid human lineage-specific evolution, including brain size is known to have also occurred in the last few million years. Alu insertions likely underlie rapid human lineage evolution. They are known to have many effects. Examples are listed in which TE sequences have influenced human-specific genes. The proposed model is that the many TE insertions created many potentially effective changes and those selected were responsible for a part of the striking human lineage evolution. The combination of the results of these events that were selected during human lineage evolution was apparently effective in producing a successful and rapidly evolving species.
Thesis: Can the Imago Dei be viewed as a measurable biological characteristic related to cognition? A number of surprising parallels to human cognitive functions have been observed in a diverse assortment of large brained, highly social animals.

If certain animals show qualities of cognition, empathy and even moral judgment which we have traditionally considered unique human qualities, would this change their spiritual status? Are such animals “almost human” - or “nothing but animals” – or what? Does the existence of such animals alter our status as humans – and if so, how? If our special features reflect particular molding, why are so many of them reflected in the rest of creation? Is this what it means to be a ‘creature of earth’? And, how does such information impact on our responsibilities as stewards of God’s world?
Monkey See, Monkey Do

Nut Cracker

Watching Mama
Chimpanzee Cultural Diversity

Map 1: Cultural differences between three neighboring chimpanzee communities in the Tai forest.

North Group:
- Driver ants deep-dig
- Termite mound pound
- Thorotermes pound
- Day-rest
- Knuckle-knock courtship

Middle Group

South Group:
- Young pith eat
- Ant dip
- Leaf swallow
- Crack Cuda Nuts
- Decayot Strychnos

All groups
- Nature pith chew
- Driver ants surface-dig
- Fresh Strychnos
- Day-rest play start
- Day-rest courtship
- Musanga leaf swallow
- Stone-hammer choice

Brainy Bird Brains

War and Peace

Making an Escape

Memory and Self-Aware
Sense of Self and Linguistic Coordination
Thesis: Can the Imago Dei be viewed as a measurable biological characteristic? Although human cognitive functions have parallels in large brained, highly social animals, human cognitive capacity is indeed unique. The obvious central feature is recursive thinking, notably as expressed in human language, metaphor, overlapping rational maps, and theory of mind.

What produces our vaunted ability to perceive reality and to think rationally? Can we be fully human without language – i.e., does our ‘language brain’ create our categories? Does recursive thinking imply insight or confusion of categories? We have a powerful ability to ‘read’ another’s thought, but do we inappropriately deploy our perception of ‘other minds’ against an empty universe? Are spiritual perceptions mental static (conceptual synesthesia), confusion between disparate mental systems? When we created culture, did we also create God?
Homo sapiens

They looked human, But were they ‘in the image’??

Can we see the mind by artifacts??

Rule

Responsibility

Righteousness

Reason

Relationship

Language??

8

IMAGO DEI
Logicomathematical versus Physical Knowledge in Monkeys, Chimps & Humans

Physical knowledge – onset, offset & extent the same in all.

Logicomathematical Knowledge –
- In Humans, parallels development of physical knowledge.
- In monkeys, occurs after PK complete, shorter period, no overlap
- In chimps, occurs before PK complete, ends sooner, some overlap.

E.G., Classification Skills

**Extent**
- Monkeys – single categories
- Chimps – two categories
- Humans – multiple categories and hierarchies

**Onset Age**
- Humans, youngest; Chimps, intermediate; Monkeys, oldest

**Velocity**
- Humans, fastest; Chimps, intermediate; Monkeys, slowest

**Offset Age** (when classification cognition stops developing)
- Humans, oldest, Chimps, intermediate; Monkeys, youngest
H = 2.5 yr.
C = 6 yr.
O = 10 yr.

Table 1. The PCTE, including domains, scales, and tasks (26).

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<th>Task</th>
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</tr>
<tr>
<td></td>
<td></td>
<td>Object permanence (3 items, 9 trials)</td>
<td>Tracking of a reward after invisible displacement.</td>
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<tr>
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<td></td>
<td>Rotation (3 items, 9 trials)</td>
<td>Tracking of a reward after a rotation manipulation.</td>
</tr>
<tr>
<td></td>
<td></td>
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<tr>
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</tr>
<tr>
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<td></td>
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<td>Discriminating quantity with added quantities.</td>
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Social Cognition

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</table>
Copycat. A young participant needlessly wipes a blue stick along a box's edge before using it to open the lid, just as his adult instructor did.
Figure 3. Schematic of the sharing task. In the reference phase (A), the infant chose one of the two toys (only one reachable at a time) - her preferred toy. After the infant had taken one toy, the familiar experimenter gave the infant the other (non-preferred) toy (not depicted here). In the request phase (B), an unfamiliar experimenter asked for a toy while looking directly at the infant. Here, the infant shares her preferred toy ("altruistic sharing").
The Social Brain –

I feel your pain...

Your attitude wounds me.....
Mean social group size for individual primate taxa (principally, 1 species per genus) plotted against relative neocortex volume (indexed as neocortex volume divided by the volume of the rest of the brain). Simian (solid symbols) and hominoid (open symbols) taxa are shown separately. The datapoint for humans is that obtained by Dunbar (1992a).
For a supernatural-based religion to have any force in making us toe the social line, I have to believe that you suppose that there are super-natural beings who can be made to understand that you and I desire that things should happen in a particular way. This involves four levels of intentionality (marked by the italicized words). Making religion a social as opposed to individual phenomenon thus adds significantly to the cognitive load needed to underpin it. - for coordinated rituals. Dunbar
Penn Research Shows That Young Children Have Grammar and Chimpanzees Don’t

Fig. 1. Syntactic diversity in human language (A), memory-based learning model (B), and Nim Chomsky (C) (details of the data are provided in SI Text). The diagonal line denotes identity; close clustering around it indicates strong agreement. For humans and Nim, the model predictions are made on the assumption that category combinations are independent. For the memory-based learner, the model prediction is based on frequency-dependent storage and retrieval. Only human data are consistent with a productive grammar ($\rho_c = 0.977$). Both the memory-based learning model ($P < 0.002$) and Nim ($P < 0.004$) show significantly lower diversity than expected under a grammar.
New insights into differences in brain organization between Neanderthals and anatomically modern humans

Eiluned Pearce, Chris Stringer and R. I. M. Dunbar

Proc. R. Soc. B 2013 **280,** 20130168, published 13 March 2013
Clinical studies demonstrate that the tempo & mode of brain development affect the pattern of neural wiring, hence, behavior & cognition. Brain development tempo & mode also affect brain shape & size.
A uniquely modern human pattern of endocranial development. Insights from a new cranial reconstruction of the Neandertal newborn from Mezmaiskaya Gunz, et. al. 2012

**Fig. 1. Neanderthal and modern human brains grew differently.**

At birth, Neanderthals and modern humans have very similar endocranial volumes and shapes (red: Le Moustier 2; blue: modern human). (B) A principal component analysis of endocranial shape changes from birth (age group 1) to adulthood (age group 6).
“Dental evidence for ontogenetic differences between modern humans and Neanderthals” Tanya Smith 2010, PNAS

Fig. 3. Regression of predicted versus actual age for eight fossil juveniles and 36 recent (living) humans. Predicted ages are derived from human radiographic calcification standards.

Fossil H. sapiens are represented by Qafzeh 10 and Irhoud 3; Neanderthals are represented by Engis 2, Gibraltar 2, Krapina Maxilla B, Obi-Rakhmat 1, Scladina, and Le Moustier 1 (from left to right).
Figure 1. Modern human ‘globularization-phase’.

Note parietal & cerebellar enlargement

Comparison of Neanderthal and Chimpanzee developmental trajectories
SUPRAMARGINAL GYRUS – A evolutionary recent gyrus that split off from the inferior parietal lobule. The supramarginal gyrus is involved in the contemplation and execution of skilled and unskilled movements. It is unique to humans, and damage to it leads to apraxia.

ANGULAR GYRUS – A evolutionary recent gyrus that split off from the inferior parietal lobule. A brain area situated in the lower part of the parietal lobe near its junction with the occipital and temporal lobes. It is involved in high-level abstraction and abilities such as reading, writing, arithmetic, left-right discrimination, word representation, the representation of fingers, and possibly also the comprehension on metaphor and proverbs. The angular gyrus is possibly unique to humans. It is also probably rich in mirror neurons that allow you to see the world from another’s point of view spatially and and (perhaps) metaphorically – a key ingredient in morality.
Jean Decety – U. Chig. - “Individuals who are sensitive to justice and fairness do not seem to be emotionally driven. Rather, they are cognitively driven.” - The brain regions underpinning moral judgment share resources with circuits controlling other capacities such as emotional saliency, mental state understanding and decision-making.
This article examines the possible origins of modern thinking by evaluating the cognitive models of working memory, executive functions and their interrelationship. We propose that a genetic mutation affected neural networks in the prefrontal cortex approximately 60,000 to 130,000 years ago. Our review of cognitive and archaeological evidence yields two possibilities: either it was non-domain specific, affecting general working memory capacity and its executive functions, or the mutation was domain-specific, affecting phonological storage capacity. We discuss the sequelae of these possibilities for modernity, including language enhancement, greater reasoning, planning, and modelling abilities, and increases in fluid general intelligence.
Development of Working Memory Maintenance

Charles F. Geier, Krista Garver, Robert Terwilliger, Beatriz Luna

*Journal of Neurophysiology* 1/2009  **Vol. 101**, no. 84-9  DOI: 10.1152/jn.90562.2008

The developmental changes in brain mechanisms supporting Visual Spatial Working Memory across different delay periods. Forty-three healthy subjects (17 adults, 18–30 yr; 13 adolescents, 13–17 yr; 13 children, 8–12 yr) were scanned as they performed an oculomotor delayed response (ODR) task with short (2.5 s) and long (10 s) delay period trials. Results showed that all age groups recruited a common network of regions - frontal, parietal, and temporal - indicative of a needed core circuitry. Several age-related differences in the recruitment of regions, supporting short delay trials, including fronto-caudal areas, which could contribute to known differences in initial memory-guided saccade precision. Adults primarily recruited additional posterior parietal cortex (PPC), whereas children and adolescents recruited a considerably more extensive distributed circuitry.
Thesis: Is the Imago Dei due to neurologically measurable qualities which correlate / explain unique human cognitive traits? Such unique functions of human cognition are indeed due to unique neurological functions, products of very extensive genetic changes which are being gradually identified.

We rewire our children’s brains as they mature. Do we then ‘create’ the framework which defines rationality and morality? Does having neurological correlations for our spiritual perceptions mean that they are no more real than ‘phantom limb pain’? I.e., did our brain create God as a by product of other, more useful, social characteristics? If human neurological differences are due to slight changes in the expression of certain key developmental control genes, does that mean our minds are simply accidental products of ‘chance’ mutations?
What effects do the previously discussed multiple classes of genetic control alterations have on human function?

Significant unique human genetic alterations in function include thousands of agents active in cell proliferation and differentiation, tissue organization, long axonal and dendritic growth, axonal branching and connectivity, timing and amount of synaptic plasticity, astrocyte differentiation, and so on.

Humans have more neurons than chimps, but not as many as you would think. The real difference is in their neuropil – i.e., the white matter between the neurons.

Human neurons have an order of magnitude more neural connections, longer axons with more branches, increased long connectivity, increased local modularization and dramatically delayed synaptic maturation.

Humans also have unique classes of astrocytes (which are now known to modulate synaptic activity), with ten times more processes and faster calcium waves.

The human neural system also retains a unique genetic plasticity which extends throughout the life span.
RE: Human Neural Genetic Change – Low Hanging Fruit Reference List

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Hu, et. al., 2012 Evolution of the human-specific microRNA miR-941 Nature Communications 3, 1145

Chein, et. al., 2013 Targeted Disruption in Mice of a Neural Stem Cell-Maintaining KRAB-Zn Finger-Encoding Gene That Has Rapidly Evolved in the Human Lineage PLOS One 7;10, e47481

Figure 6. Origination of new genes up-regulated in PFC relative to non-neocortical regions after primate split. Branches 9~12 follows.
Developmental trajectory of MFLD. Graphs show best-fit curves for MFLD data in humans (A; n = 24) and chimpanzees (B; n = 20) arranged by age in years.

Signature of recent positive expression upstream of MEF2A gene (synaptic differentiation)

A) The phylogenetic relationship of human, Neanderthal, chimpanzee, and rhesus macaque species – divergence MYA. (B) Proportion of human-derived SNPs measured using a 50-kb sliding window in the MEF2A gene region (C) Distribution of the proportion of human-derived SNPs for all windows across the human genome. (Red arrow)

Time-shift in expression of module 1 (synaptic timing) genes among species.
Unique modern genes from the initial Denisovan study – Meyer, et. al. 2012

They were examining protein coding sites highly conserved in primates – but changed in the modern human lineage after separation from the Denisovans.

Of the 23 most conserved positions with significant amino acid changes.

8 affect nervous system genes (function or development)
(NOVA1, SLITRK1, KATNA1, LUZP1, ARHGAP32, ADSL, HTR2B, and CNTNAP2).

SLITRK1 and KATNA1 – axonal and dendritic growth
ARHGAP32 and HTR2B - synaptic transmission
ADSL and CNTNAP2 are implicated in autism
CNTNAP2 is regulated by FOXP2 & is associated with speech problems

Also, 4 newly changed loci affect the skin, and 6 of them affect the eye.

Recent substitutions IN FOXP2 locus that are fixed or at high frequency in present-day humans.

A Recent Evolutionary Change Affects a Regulatory Element in the Human FOXP2 Gene. Maricic, et. al., 2013
Thesis: If the Imago Dei is a neurological matter with measurable implications, it should be possible to identify a pattern of change in the fossil and archaeological records. However, the appearance of modern skulls around 200,000 years ago, and the archaeological expression of modern cognition such as symbolism are not necessarily synchronous.

The spiritual status of both the earliest anatomically modern people and the later archaic 'people' such as the Neanderthals remains problematic. The modern skull has unique qualities, but the large Neanderthal brains place their owners into a theologically undefined category. The culture of the first anatomically modern people seems to be much the same as that of archaic hominines. Also, the archaic hominines had abilities greater than any living animal species, raising the issue of their spiritual status. The ongoing debate over whether modern and archaic populations are truly different shows the power exercised by paradigms in the interpretation of data – and the power of ideologies in choosing paradigms.
Thinking ahead – tools, art and cognition – Europe 40,000 BP
Pinnacle Point, South Africa. 165KYA – heat treated silicate blades
Matched Beads and Bone Spear Points –

Blombos Cave
South Africa
85,000 BP

Skhul Cave, Mt. Carmel, 125,000 BP
Stone Age jottings

French caves are known for their prehistoric rock art. But also marked on the walls around the paintings are 26 symbols that have appeared again and again at French sites across 25,000 years of prehistory. Early signs suggest that many of these symbols crop up in other parts of the world too, leading some to wonder if symbolic communication arose with early humans.
Thesis: Although they raise theological issues, non-traditional theological models for Adam which more easily fit the physical evidences have been proposed.
Alternate Paradigms about Adam

**Theory:** Adam was made directly from the clay by God’s direct act. The silicon of the clay was transformed into carbon, etc. in order to make the proteins, DNA, etc. of his body. There is no biological connections to any other form of life.

**Theory:** God created the human body by evolution, and then breathed into one of them a living soul. He became Adam. We are all descended from Adam, and we all sinned with him.

**Theory:** God created the modern human body from an archaic hominid lineage by a causing a sudden “macro-mutation” (big change) in the genes of a developing embryo. That baby was Adam, and God taught him to talk (and walk) in the garden of Eden. (So genealogies called Adam “the son of God”). Adam was biologically separated from his ancestors, and we are all his descendants.

**Theory:** There were many true humans scattered across earth (God made them through evolution), but none of them knew there was a moral law. God picked out Adam as representative of the race, put him in the Garden, put him to the test. Adam blew it. Because of this, death passed upon all men. In Adam’s fall within the law, their sin was condemned without the law. The lot of us became rebels, subject to death.

**Theory:** “Adam” is a metaphor for a small band of early humans that God “put to the test”. They failed it, and we are all sinners because we are descended from them. These humans had evolved (with God’s guidance) from more primitive types.

**Theory:** Adam is a metaphor for the human dilemma. We are all “Adam” and “Eve”. We all “fall” and become sinners – maybe due to our environment, maybe due to our genes. After all, what can you expect of an evolving ape in trousers? But God is not yet finished creating us. Someday we’ll be fully developed – into angels.
Adam and the Sin Problem

**Generic Head** – Sin originated with Adam, and has been passed along to all his descendents (which is everybody) like a genetic inheritance.  (? Does this mean Adam was the only ancestor for the race – or just a particular man who is in all our genealogies? – AKA, Y chromosome Adam)).

**Federal Head** – Sin originated with Adam.  He was not the only man living, but God appointed him as representative and put him to the test.  When he sinned, sin passed on to all men everywhere (and when) by divine fiat.  I.E., there was a sudden transformation of human life.

**Tribal Head** – Adam was the “head man” of a small tribe put in the garden.  The tribe was put to the test, and they all followed Adam’s lead into sin.  We are all descended from that tribe (alone?) and have inherited their sinful nature.

**Cultural Head** – Adam was the appointed race representative in the garden.  He sinned.  Sin passed on from Adam to all other people then (and now) alive by communication between people – especially in families.  Human society suffered a gradual transformation as sin spread like an infectious disease.

**Experimental Head** – Sin was already there, but we don’t know how – that’s why the garden was needed, the perfect environment.  Adam was the experimental proof of the human condition – he showed we humans are all sinners by nature – that it is not environmental.

**Symbolic Head** – Adam was a character in a story told to illustrate the human dilemma – we are sinners for some reason or other.  But the story does not represent the origin of that state, only it’s nature as rebellion against God.
Thesis: It is not possible (or necessary) to exclude the hand of God from the origin of humanity (or from the origin and direction of anything else) by describing its origins through natural causes, no matter how good that description is. That applies to the arguments of both Naturalists and Creationists – which in this case are much alike.

Psalm 104: All creatures look to you to give them their food at the proper time. 28 When you give it to them, they gather it up; when you open your hand, they are satisfied with good things. 29 When you hide your face, they are terrified; when you take away their breath, they die and return to the dust. 30 When you send your Spirit, they are created, and you renew the face of the ground.
When God speaks from Eternity, which part of space and time does not respond in obedience?
Case Study - B. B. Warfield (1851-1921)

Systematic Theologian at “old” Princeton Seminary -- Formulated concursus argument for inspiration of Scripture, wrote for Fundamentalist involved in founding Fundamentalism (not dispensational).

from:"On The Antiquity and Unity of the Human Race" (1911)

"The fundamental assertion of the Biblical doctrine of the origin of man is that he owes his being to a creative act of God. Subsidiary questions growing out of this fundamental assertion, however, have been thrown from time to time into great prominence, as the changing forms of current anthropological speculation have seemed to press on this or that element in, or corollary from, the Biblical teaching. The most important of these subsidiary questions has concerned the method of the divine procedure in creating man. Discussion of this question became acute on the publication of Charles Darwin's treatise on the "Origin of Species" in 1859, and can never sink again into rest until it's thoroughly understood in all quarters that "evolution" cannot act as a substitute for creation, but at best can supply only a theory of the method of the divine providence...It is to theology...a matter of entire indifference how long man has existed on earth
As the Bible is of God, it is certain that there can be no conflict between the teachings of the Scriptures and the facts of science. It is not with Facts, but with theories, believers have to contend.

Many such theories have, from time to time, been presented, apparently or really inconsistent with the Bible. But these theories have either proved to be false, or to harmonize with the Word of God, properly interpreted.

The Church has been forced more than once to alter her interpretation of the Bible to accommodate the discoveries of science. But this has been done without doing any violence to the Scriptures or in any degree impairing their authority.

Such change, however, cannot be effected without a struggle. It is impossible that our mode of understanding the Bible should not be determined by our views of the subjects of which it treats.
Real World

Theoretical side – Shaping Principles

- Theories
- Paradigms
- Epistemes
- World-View

Evaluation of ideas done by Human Investigator

- Satisfaction^T
- Satisfaction^P
- Satisfaction^E
- Satisfaction^W

Faith

COHERENCE POINT

Experimental side – Reality Testing

God’s Creation

God’s Word

Wrestling with the Angel
Science is the effort to explain the patterns we see in the natural order.

It is considered important in science to not formulate complex conclusions until enough physical data is collected to reveal statistically verifiable patterns.

Scientific theories are explanations of demonstrated patterns of physical data.

Good theory is expected to have the power to predict the shape of future physical data.

Continued acceptance of a theory in science is not supposed to be because of its source or its history, but rather because of its power to continue to predict and explain new observed patterns of real world data.

Historically, this attitude of science – the dependence on empirical testing – derives from the belief that God chose to make His creation according to His own free will.

Science progresses / changes, in part, as a function of advances in technology – note - telescopes, microscopes, chemical and genetic techniques, etc. = new data
1. The earth and its fullness belongs to the Lord - it is His creation. Expectations (predictions) about the earth which are drawn from the Biblical narratives are thus verifiable or falsifiable by valid data from God’s creation.

2. This includes theological statements which make physical world predictions. Creation’s data cannot be simply rejected, but requires theological reconciliation.

3. But traditional understandings predict (expect or state) patterns of data far different than those of modern investigation, producing a serious dilemma.

4. All theories are human formulations, but the data they explain are not human creations, but discoveries of God’s truth. Theology may reject a theory, but it cannot reject data – and that means supplying a rational explanation for them.

5. My intent is to survey some of the recent genetic data related to the nature origin and early prehistory of the human species. They raise issues which need to be faced and worked out - by theologians and scientists working together.
Meeting the challenge of physical knowledge

The flow of logic

State a **Question** to be answered by both disciplines

Give the Traditional Theological **Answer**

Give the Paleo-anthropological **Answer**

**Explain** the science (understand the nature of the data)

**Predict** the shape of the data – from Theology’s view

**Predict** the shape of the data – from Anthropology’s view

Review the presently known physical **Data**

Summarize the shape of the data as a **Thesis**

**Compare** the data to Theology’s predictions

**Compare** the data to Anthropology’s predictions

Point out **Problems** that need to be resolved
1. Thesis: The genetic evidence showing that Homo sapiens shares a common ancestor with the chimpanzee (and other more distant living species, as well as Neanderthals) allows for no reasonable alternate explanation.

2. Thesis: Multiple lines of genetic evidence are incompatible with descent from a single human ancestral pair. E.G., the HLA (immune) loci retain too much diversity, and techniques such as linkage disequilibrium and retained diversity indicate a long term human population of around 10,000. An early bottleneck is possible, but not of two people.

3. Thesis: With a high degree of certainty, the genetic data shows that the modern human species, Homo sapiens, originated as a single small African population about 200,000 years ago.

4. Thesis: The Earth was settled from Africa. A single population left Africa about 60,000 years ago, settling along the Indian Ocean eastward to Australia. 40,000 years ago, more tribes left the Middle East, moving north into Central Asia and Europe, and reaching the Americas around 17,000 years ago. The timing of these settlements was dependent on ice age climate cycles.

5. Thesis: The surprisingly complete genomic data from our extinct closest relatives, the Neanderthals and the Denisovans, provide important clues to human uniqueness – and raise interesting questions. They were apparently functionally different, but yet we interbred with them - slightly.

6. Thesis: The molecular evidence indicates that selection, drift and mutation (including transposons) were used to mold humanity. This involved significant changes to a myriad of neural control sequences rather than the addition of a few major effect genes.
7. Thesis: Can the Imago Dei be viewed as a measurable biological characteristic related to cognition? A number of surprising parallels to human cognitive functions have been observed in a diverse assortment of large brained, highly social animals.

8. Thesis: Can the Imago Dei be viewed as a measurable biological characteristic? Although human cognitive functions have parallels in large brained, highly social animals, human cognitive capacity is indeed unique. The obvious central feature is recursive thinking, notably as expressed in human language, metaphor, overlapping rational maps, and theory of mind.

9. Thesis: Is the Imago Dei due to neurologically measurable qualities which correlate / explain unique human cognitive traits? Such unique functions of human cognition are indeed due to unique neurological functions, products of very extensive genetic changes which are being gradually identified.

10. Thesis: If the Imago Dei is a neurological matter with measurable implications, it should be possible to identify a pattern of change in the fossil and archaeological records. However, the appearance of modern skulls around 200,000 years ago, and the archaeological expression of modern cognition such as symbolism are not necessarily synchronous.

11. Thesis: Although they raise theological issues, non-traditional theological models for Adam which more easily fit the physical evidences have been proposed.

12. Thesis: It is not possible (or necessary) to exclude the hand of God from the origin of humanity (or from the origin and direction of anything else) by describing its origins through natural causes, no matter how good that description is. That applies to the arguments of both Naturalists and Creationists – which in this case are much alike.