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THE FLORES SKELETON AND HUMAN
BARAMINOLOGY

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The Flores Skeleton and Human Baraminology

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Abstract. The morphology, age, and stratigraphic relations of the recently described *Homo floresiensis* skeleton suggests it might represent a distinct post-Babel human population with an extreme morphology. Combined with the morphologies and relative ages of other post-Babel humans (e.g. *H. erectus*, *H. neanderthalensis*), *H. floresiensis* suggests a high post-Flood intrabaraminic diversification rate decreasing to the present. This coincides in time with a similar pattern in non-humans, suggesting the mechanism of intrabaraminic diversification operated across all living organisms. The fact that many of the differences in fossil human morphologies can be achieved by differential development and the changes seem to be isochronous with the Biblically-evidenced decrease in human longevity suggests that human diversification may have been due to changes in development. These changes in humans probably followed pre-programmed trajectories through biological character space, the specific course of which may have been largely effected by founder effect and genetic drift in small populations following Babel.

An unusual skeleton was discovered in September of 2003 (Brown, *et al.* 2004, p. 1055) in the river-breached limestone Liang Bua Cave on the island of Flores, in the Lesser Sunda Island chain of the Wallacea Islands, Indonesia (Morwood, *et al.* 2004, p. 1087). The new fossil was given a field designation of “LB 1” for specimen number 1 from Liang Bua. It seems to be from an adult woman (age inferred from tooth wear; gender inferred from pelvis morphology) and is described as a new species of *Homo*. The Flores skeleton promises to provide insight into human baraminological studies. This note is intended to initiate discussion and encourage further research into the fascinating field of human baraminology.

THE NATURE OF THE SPECIMENS

Aside from its fragile state (the damp cave conditions reportedly left the skeleton with the consistency described as ‘mashed potatoes’ or ‘wet blotting paper’: Dalton 2004), the Flores skeleton is in fairly good condition for study. For example, the skeleton is original bone, partially articulated, fairly complete (the mandible, most of the skull, the long bones of the legs, the pelvis, as well as fragments of the sacrum, vertebrae, scapulae, clavicles, ribs, and hands and feet), and found within a small area (500 cm²:

Brown, *et al.* 2004). Furthermore, the stratigraphy of the cave sediments seems to be carefully worked out, and the excavation methods seem to be fairly well controlled (Morwood, *et al.* 2004). It thus appears that most of the objections creationists raise in regard to paleoanthropological fossils (e.g. insufficient material, multiple provenances, poor preservation) do not apply to this specimen.

There is reason for caution, however. First, both the initial description of the skeleton (Brown, *et al.* 2004) and the report on the site’s stratigraphy and the associated fossils and artifacts (Morwood, *et al.* 2004) must be considered early, preliminary reports. This is because excavations in the cave are on-going. In fact, there is even an expectation on the part of the specimen’s describers to find more of the skeleton in future field seasons (Brown, *et al.* 2004, p. 1055). Second (possibly because more material is expected), only a couple post-cranial measurements were provided in the skeleton’s description, making comparative post-cranial studies not yet possible. Third, most of the bones belong to a single individual. Although portions of at least seven other individuals were discovered (Dalton 2004, 2005a, 2005b), other than bones from LB 1, only two osteological specimens from the excavation were officially remarked upon —

a premolar and a radius shaft. As for the premolar, the official species description suggests that the premolars of LB 1 may not be distinctive enough to assign the isolated tooth to the new species. The radius provides more cause for concern. Only a portion of the shaft is preserved, so the length must be estimated. Though Brown, *et al.* (2004, p. 1060) claim "...the dimensions of the radius are compatible with a hominin of LB1 proportions", the inferred length they report (210 mm) is not as diminutive as is claimed for the specimen and pictured for the pelvis and leg bones. This indicates something is amiss (the radius is not diminutive and Brown, *et al.*'s claim to that effect is in error; or the radius length is in error; or the scales on the photographs and diminutive claims for the Flores skeleton are in error, *etc.*). Thus, the morphology represented by this specimen has not yet been demonstrated to extend beyond a single individual or, at best, a single family. It is thus not yet certain that the skeleton actually represents a true population, race or species.

THE DATE OF THE FOSSILS

The date of the specimen was determined by C-14 accelerator mass spectrometry on charcoal from the same stratum as LB 1 (18.3 ± 0.4 ka. and 17.8 ± 0.4 ka.), infrared stimulated luminescence on K-feldspars from the enclosing sediment ($< 14 \pm 2$ ka. and $\sim 6.8 \pm 0.8$ ka., with anomalous fading which suggests the dates are too young), and light-sensitive red thermoluminescence of quartz grains from the enclosing sediment ($< 38 \pm 8$ ka. and $\sim 34 \pm 4$ ka.) (Morwood, *et al.* 2004). A radiocarbon age of approximately 18,000 years for LB 1 is thus consistent with the data available. The date of the isolated premolar was bracketed above by thermal ionization mass spectrometry (TIMS) uranium series age on an overlying flowstone layer (37.7 ± 0.2 ka.) and below by a coupled ESR/uranium series age for a *Stegodon* molar from an underlying layer ($74 +14/-12$ ka.) (Morwood, *et al.* 2004). The date of the isolated radial shaft was bracketed above by the same *Stegodon* molar and below by optical thermoluminescent dating of an underlying layer (95 ± 13 ka.) (Morwood, *et al.* 2004). A minimum age for the oldest stone artifacts in the cave was determined by TIMS uranium-series dating on an overlying flowstone at 102.4 ± 0.6 ka. (Morwood, *et al.* 2004). Stone tools found at Mata Menge, another location on Flores Island, were

found in sediments overlying a reverse-to-normal paleomagnetic transition and constrained by fission-track dating of zircons in tuffs above and below the artifacts at 0.88 ± 0.07 and 0.80 ± 0.07 ma. (Morwood, *et al.* 1998). This places all reported Flores specimens – both osteological and artifactual – from Upper Pleistocene sediments.

In lieu of a broadly accepted creationist chronology, we may place these dates in a biblical chronology as follows. *H. erectus* ranges geographically across most of the Old World and stratigraphically from Lower to Upper Pleistocene. Although creationists are not in agreement about the location of the Flood/post-Flood boundary, most would place the boundary below the lowest *H. erectus*. And, if *H. erectus* is accepted as human (Lubenow 1992, 2004; Wise 2002, p. 238; Wieland 2004), this means *H. erectus* is a post-Flood human morphology with a distribution across at least three continents. Since post-Flood trans-continental distribution of humans did not occur until after Babel, we can deduce that *H. erectus* represents an early post-Babel morphology and we then deduce that both Lower and Upper Pleistocene sediments are post-Babel in age. Given that the Flores skeleton was found in Upper Pleistocene sediments, it follows that it would date from slightly later post-Flood (and post-Babel) times. The C-14 dates associated with the Flores skeleton (*ca.* 18 ka.) are substantially younger than the C-14 dates of Flood carbon (40-60 ka.: Giam 2001; Baumgardner, *et al.* 2003) but older than C-14 dates which actually correspond with dendrochronological dates on Bristlecone Pines (2-3 ka.) (*e.g.* Aardsma, 1992. Figure 3.2). Lying between the Flood and *ca.* 1000 B.C. (the time of David), the C-14 dates of LB 1 are consistent with a post-Babel date for the specimen. Thus although young-age creationists have not yet reinterpreted most of the absolute dating technologies employed for dating the Flores skeleton, a post-Babel patriarchal date is a very likely one.

IS THE SKELETON HUMAN?

The same cave deposits which preserved the Flores skeleton also yielded stone artifacts (Morwood, *et al.* 2004, p. 1089) — some of which exhibit a sophistication otherwise found only with *H. sapiens* (as opposed to even *H. erectus*) (Lahr & Foley 2004). The same deposits produced charred animal bones. The nature of the charring is unlikely to have occurred

in any way other than by the animals having been cooked on a controlled fire (Morwood, *et al.* 2004, p. 1089). The frequency of dwarf elephant bones and the very high proportion of juveniles among the charred remains, suggests preferential hunting of young *Stegodon* (Morwood, *et al.* 2004). With the *Stegodon* bones were also found a very high concentration of stone tools which in design can be used to hunt and prepare big game (Morwood, *et al.* 2004). The associated fossils and artifacts therefore suggest that someone made tools, then used those tools to hunt and kill elephants for food and then process the carcasses, and finally cooked that food. Also of interest in inferring the technological sophistication of the Flores people is the location of Flores Island. Very deep water separates Flores from both the Asian and the Australian mainlands. Thus, even during proposed maximum glacial lowstand (maximum continental glaciation), there are two islands and 19 kilometers of ocean between the Island of Flores and Asia, the closest continent (Morwood, *et al.* 1998). At high stand (no continental glaciers) there may have been hundreds of kilometers of ocean to cross. Additionally, Flores is east of Wallace's line, meaning that the floral and faunal associations of Flores actually connect it with Australia, not Southeast Asia¹. Whomever the fire-using toolmakers were, they either immigrated from Southeast Asia across at least 19 kilometers of ocean (apparently against the currents which brought in animals and plants from Australia), or a much greater stretch of ocean from the direction of Australia or elsewhere. This and other data suggests that they did this by constructing boats (Bednarik 2002). The tools and processed *Stegodon* bones found with LB 1 and in older sediments suggest fire-controlling, tool-making, and sea-faring capabilities only consistent with humans.

So far, the only osteological evidence on Flores Island of anything even similar to humans are the Flores skeleton and associated bones – all found in the same sediments with the tools and *Stegodon* bones. Morphologically, the Flores skeleton exhibits multiple characters in common with australopithecines (*e.g.* body size and relative brain size), *Homo erectus* (*e.g.* broad and thick cranial vault), and modern *H. sapiens* (*e.g.* masticatory apparatus and overall femur anatomy) (Brown *et al.* 2004). The fact that the Flores skeleton post-dates *H. erectus* and contains

characters similar to unique erectine morphologies of Indonesia (*e.g.* the double mental foramina in the mandible: Brown, *et al.* 2004, p. 1058) suggests the Flores skeleton might be a descendant of *H. erectus*. Since *Homo erectus* is considered human by a number of creationists (*e.g.* Lubenow 1992, 2004; Wise 2002, p. 238; Wieland 2004), it is most likely that the Flores skeleton is human. I would like to suggest, with Brown *et al.* (2004) and Morewood *et al.* (2004) that the Flores skeleton is from a human population which created the stone artifacts on Flores. Although all the evidence is circumstantial and the data are not all in, consistency of inductions from the data (date, skeletal morphology, sea-faring capability, hunting ability, tool construction, tool use, and controlled use of fire) seems to suggest that the Flores skeleton is from a member of a post-Babel human population on Flores Island.

HUMAN VARIATION

The most unusual (and controversial) characters of the Flores skeleton, of course, are its stature and brain size. Available evidence indicates it was a healthy adult (lacking known human pathologies, *e.g.* it is not suffering from microcephaly or dwarfism – see Falk, *et al.* 2005). Yet, standing up it was only about 1 meter tall (Brown, *et al.* 2004) – smaller than the smallest non-pathological human on record. Its morphology is also not consistent with any modern humans of small stature (dwarfs or pygmies) (Brown, *et al.* 2004; Lahr & Foley 2004), and relative bone metrics indicate allometric relationships unknown among modern humans (Brown, *et al.* 2004). Most unusual among the unique allometries is a very small brain size — even considering body size. By all measures brain size is well outside the range of modern humans, and even *H. erectus* and *H. habilis*. In fact by most measures (*e.g.* ratio of endocranial volume to femur length) the relative brain size is even smaller than that of australopithecines (Brown, *et al.* 2004). The increase in disparity of known human morphology generated by this specimen came as a surprise to everyone (*e.g.* Brown, *et al.* 2004). Developmentally, the Flores skeletal morphology probably calls for termination of fetal brain growth rates much earlier after birth than is known in any modern human and even in juvenile *H. erectus* (Coqueugniot, *et al.* 2004). Because evidence of pathology is absent, this means that the normal developmental program of the Flores skeleton

	Masoretic	Samaritan	LXX
	Adam-Lamech	Adam-Lamech	Adam-Lamech
PreFlood	118.00 ± 50.76	78.56 ± 24.95	182.44 ± 23.13
PostFlood	36.25 ± 13.80	117.50 ± 26.72	130.00 ± 27.49
	Arphaxad-Terah	Arphaxad-Terah	Arphaxad-Terah

Table 1. Mean Paternity Ages (from Genesis 5 & 11 ± 1 standard deviation). Noah and Shem are omitted from this calculation because they both lived in both pre-Flood and post-Flood times.

was well outside the range of modern humans. The Flores skeleton arguably represents the most extreme non-pathological human morphology known (Lahr & Foley 2004).

INFERRED LINEAGE

If we accept erectine and younger morphologies as human, the fossil record presents us with at least four distinct human morphologies – *H. erectus*, *H. neanderthalensis*, *H. floresiensis* (the species name given to LB 1 as the type specimen), and *H. sapiens*. Not only is the stratigraphic range of *H. erectus* a long one, it also entirely predates each of the other three morphologies. As reasoned above, the stratigraphic position (Pleistocene) and the trans-old-world geographic distribution suggests all the erectines are post-Babel (which must also be true for the other three morphologies as well, because they are stratigraphically younger). This in turn suggests that erectines may have been some of the earliest migrators from Babel and possibly the first cohort of humans to die after Babel. Since other human morphologies have not been found in these (Lower Pleistocene) sediments, it would seem that the dominant human morphology at the time of Babel was erectine and not sapiens². Furthermore, with the exception of very recent (post-Pleistocene) New World *H. sapiens*, the geographic ranges of all non-erectine humans (*H. neanderthalensis*, *H. floresiensis*, and *H. sapiens*) were previously occupied by *H. erectus* populations. All this would suggest that the other three human morphologies are somehow descendent from the erectines.

NATURE OF CHANGE

Regardless of what text is consulted, paternity ages listed in Genesis 5 and 11 show a change from antediluvian to postdiluvian times (compare pre-Flood and post-Flood values in Table 1). If these

are paternal ages at the birth of first-born sons (or consistently proportional to such ages throughout Genesis 5 and 11), the change in paternity ages from pre-Flood to Flood times may evidence a change in age of sexual maturation in the promised line. If they are characteristic of all humans contemporaneous with the listed patriarchs then the biblical text may evidence a change in age of sexual maturation (and thus rate of sexual development) in all humans from pre-Flood to post-Flood times. Given the hard-wired nature of development, this may also be consistent with the change in total longevity being due to a change in genetic programming, rather than a response to the environment.

Although the Masoretic, Samaritan, and Septuagint texts agree that paternal ages changed from pre-Flood to post-Flood times, they do not agree on either the degree or polarity of that change (Table 1). Samaritan Pentateuch ages increase by almost 50%; Septuagint ages decrease by nearly 30%; and Masoretic ages decrease by almost 70%. Therefore, whereas a change in paternal ages at the time of the Flood is consistently evidenced, until we understand more about the meaning of the differences among texts, neither the magnitude nor polarity of that change is known at present. No matter which text is used, however, paternal ages seem to be higher in the Flood-to-Abram period than they are at *present* (see Table 1), suggesting the rate of human sexual development has changed since the time of Abraham. More specifically, the mean rate of human sexual development has decreased since the time of Abraham. This in turn might be consistent with evidence in the more recent past for a decreasing age of menarche (first menstruation) (McCauley and Salter 1995; see also the data reviewed by Cuozzo 1998, pp. 191-8)³, and it would suggest that the change may be on-going. A 13 year-old body from the eighteenth century with delayed tooth eruption (Cuozzo 1998, pp. 199-200) might suggest a recent

decrease in tooth eruption times, further evidence of different developmental rates – this time in non-reproductive systems. Taken as a whole, biblical and historical data seem to suggest that developmental rates have varied in different human systems – *i.e.* the human baramin has experienced heterochrony.

Similarly, several studies have suggested differences in developmental rates between fossil and modern humans. Coqueugniot, *et al.* (2004) suggest the *H. erectus* braincase grew faster in the first year of development than is the case in modern humans. Dean, *et al.* (2001) suggest the dentition of *H. erectus* developed faster than in modern humans. Williams and Krovitz (2004) suggest that early childhood growth was more rapid in certain portions of the Neanderthal cranium than is the case in modern humans. Even though each of these involve *increased* growth rates in the past (rather than the decreased growth rates over the longer time range, as suggested by the biblical account), these studies and others do evidence heterochrony in human history (see also Minugh-Purvis and McNamara 2002), something which *is* evidenced in both biblical and historical data. The unique developmental program of *Homo floresiensis* would represent yet another example of heterochrony in human history. I propose that most of the major changes in human morphology are actually due to heterochrony. This includes changes in morphology as evidenced by osteological material, in sexual maturation as evidenced by biblical and recent historical data, and in longevity as evidenced from the biblical account.

As argued above, *H. erectus* represents the oldest post-Babel morphology. I suggest that slight differences in *H. erectus* populations at different locations around the world are due to the founder effect (*i.e.* small samples from a larger population are likely to have slightly different average morphologies, so each post-Babel population should have a slightly different average initial morphology from every other post-Babel population). Furthermore, if *H. floresiensis* is not only a descendant of the erectines (probably the Indonesian erectines: Brown, *et al.* 2004, p. 1058) but also occupied a narrow geographical area (the Island of Flores), the Flores skeleton probably represents a more recent morphology of one lineage that dispersed from Babel. *H. neanderthalensis* is another fossil morphology younger than *H. erectus*

which also occupies a narrower geographic range (Europe). Neanderthals may thus represent the more recent morphology of another lineage which dispersed from Babel – in this case in the direction of Europe. From this I infer that at least two post-Babel human populations followed distinct trajectories in developmental morphology. These rapid changes in morphology may have been facilitated by genetic drift in small, geographically and genetically isolated populations (Wise 2002, pp. 231-4). If so, then other lineages are likely to have followed other trajectories in developmental morphology. Although at this time we only have evidence from two post-Babel, pre-modern lineages, I propose that the developmental programs of many of the Babel lineages changed rapidly in post-Babel times, creating a number of unique morphologies around the world.

The Bible indicates that all humans are derived from a man and a woman who lived less than 10,000 years ago. Then, less than two millennia later (at the time of the Flood) the human population went through a population bottleneck of 8 people. Although the calculations have not been re-evaluated by creationists, these facts are probably consistent with the diversity of modern human mitochondrial DNA being derived very recently from one woman (Cann *et al.* 1987; Gibbons, 1993) and modern human Y-chromosome DNA being derived very recently from one man (Dorit, *et al.* 1995). The Bible indicates that modern humans were derived from multiple lineages that diverged from Babel within a few centuries of the Flood. This would be evidenced by morphological characters unique to a particular region being found in a complete fossil sequence from some ancestral morphology to the modern human morphology. If the initial human morphology at the time of Babel was *H. erectus* (as argued above) and conventional dates from Tertiary/Quaternary boundary to the Pleistocene/Holocene boundary should be collapsed to the period of post-Babel diversification (as also argued above), then those sequences should be found throughout Pleistocene sediments. And, that is exactly the data Wolpoff (1989; Wolpoff and Caspari 1997) uses to argue for the multi-regional origin of *H. sapiens*. In fact, the revision of the time scale demanded by Scripture may resolve the on-going (and seemingly otherwise unresolvable) controversy between the Eve and Multiregional hypotheses for the origin of modern

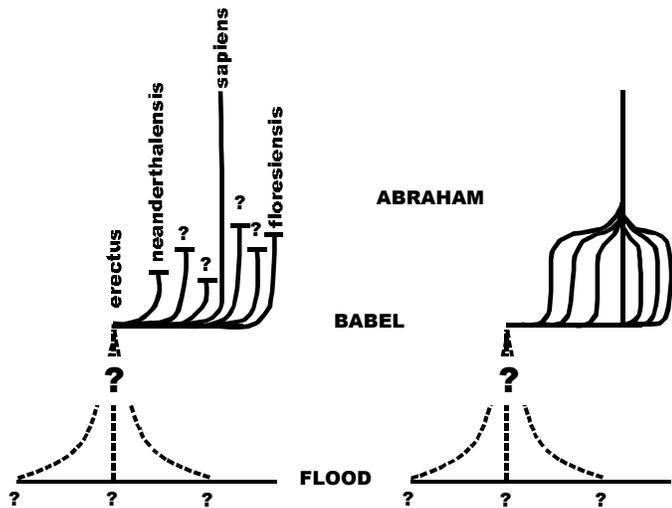


Figure 1. Tree of human diversification. On the left is a hypothesis of extinction of non-sapiens morphologies. On the right is a hypothesis of convergence of multiple post-Babel morphologies on the sapiens morphology.

H. sapiens.

On the other hand, if modern humans are derived from multiple post-Babel lineages as the Bible indicates and each lineage followed a unique trajectory of developmental change, then it would seem most extraordinary that human morphology ended up in as narrow a range as it did (with racial differences in the present far smaller than differences evidenced in human fossils). One possible explanation is that some of the Babel lineages – namely all the divergent morphologies (*e.g.* Neanderthals, the Flores people) – went extinct, leaving no descendants among modern humans (Figure 1, left diagram). This has actually been suggested for the Neanderthals based upon differences in DNA between three Neanderthal specimens and modern humans (Krings, *et al.* 1997, 1999; Ovchinnikov, *et al.* 2000). However, this hypothesis would suggest that the only Babel lineages we happen to have physical evidence for (*i.e.* Upper Pleistocene humans) are those which went extinct, never having sampled from the (presumably greater number of?) Babel lineages which did *not* go extinct. This seems improbable. Another possibility is that the various morphologies of Babel lineages actually converged in the course of time on the modern human morphology (Figure 2, right diagram). Wolpoff (1989; Wolpoff and Caspari 1997) argues that this occurs because of extensive inter-regional breeding among human populations, but the biblical account suggests

that the post-Babel lineages did NOT interbreed – at least for some time after Babel. Such a multiple convergence would be too improbable to be due to random changes in small populations (*i.e.* chance convergence by genetic drift). For it to happen it would seem necessary for the present human morphology to have been programmed into the system from before the beginning of the divergence. This in turn would also suggest that the erectine morphology (expressed at the time of Babel), the various heterochronic morphologies derived from it, as well as the present human morphology were all somehow programmed into humans at the creation. This suggests that human history may have proceeded from a time characterized by a single narrow human morphology (at Babel) to a period characterized by an explosion of human morphologies to a period characterized by another narrow human morphology (the present) (Figure 1, right diagram). This single morphology diverging to multiple morphologies before it returns again to a single morphology is somewhat reminiscent of (analogous to) the narrowness of adult morphology even with divergent developmental trajectories observed in the ontogeny of a variety of organisms (*e.g.* frogs). The latter is likely due to some sort of complexly designed ontogeny which yields the adult morphology in spite of a variety of ontogenetic trajectories — what I would call ontogenetic redundancy (an example of pre-programmed variability, or “mediated design” as defined by Wood 2003). I suggest that the narrowness of modern human variation and the variety of fossil human morphologies are due to an even more complexly designed human ontogeny which allows ultimate phylogenetic convergence on a final morphology even after generations of divergent heterochronic paths (what I would call ‘phylogenetic redundancy’).

Advantages of ontogenetic redundancy for an organism include survival to adulthood even though the usual developmental pathway is blocked as well as greater ecological diversity in development (*i.e.* providing an organism the capacity to generate the developmental morphology which best thrives in a particular environment). Similarly, phylogenetic redundancy in humans may have facilitated the survival of multiple lineages in an unstable world suffering from residual catastrophism following the Noachic Flood.

INTRABARAMINIC DIVERSIFICATION

There are several interesting similarities between the changes in post-Flood humans and changes in post-Flood animals and plants.

Various creationist arguments and studies (e.g. Jones 1972; Wood and Murray 2003, pp. 71-2; Wood 2005) suggest that the created kind may be roughly approximated by the taxonomic level of the family. Since terrestrial baramins were restricted to 2-14 ark representatives through the Flood and non-terrestrial baramins were likely substantially decimated by the Flood, the large number of speciose families in the present suggests there has been substantial speciation within baramins after the Flood (called 'intrabaraminic diversification' by Wise 1994). Early post-Flood records (e.g. in Job and Genesis) of specialized taxa (e.g. camels, lions) suggest that intrabaraminic diversification was extremely rapid (within a few centuries of the Flood). This conclusion in turn seems to be confirmed by the fossil record. Many creationists who accept the stratigraphic column (e.g. Snelling, *et al.* 1996) place the Flood/post-Flood boundary as low as the beginning of the Tertiary or lower (e.g. Austin, *et al.* 1994; Robinson 1996; Scheven 1996, Tyler 1996). Since multiple baramins (e.g. the equids: Cavanaugh, *et al.* 2003) in Tertiary and Quaternary sediments show a time sequence of a large number of distinct morphologies, it would appear that substantial speciation occurred between the Flood and the present. If *H. erectus* fossils actually represent early post-Babel humans (as argued above), then Quaternary sediments were deposited in post-Babel times, and Babel may date very close to the Tertiary/Quaternary boundary. Although evidence of speciation is found throughout post-Flood sediments, if the Flood/post-Flood boundary is close to the base of the Tertiary, most of the speciation is documented in Tertiary sediments. This means that most of the intrabaraminic diversification of non-humans occurred in the centuries between the Flood and Babel – during the time when animals and plants were obeying God's command to disperse and humans are refusing to leave Babel. For both non-humans and humans, divergence of populations occurs after geographic dispersion, suggesting geographic dispersion may play some sort of role in intrabaraminic diversification – either directly or indirectly.

Since early post-Flood intrabaraminic

diversification had to be very rapid and intrabaraminic diversification in the present seems to be slow to non-existent, Wood and Murray (2003, pp. 170-6, 196-7) and Wise and Croxton (2003) have implied that the rate of intrabaraminic diversification may have decreased in the centuries following the Flood. This change in rate may have included both a decrease in the number of new species (diversity) and a decrease in the magnitude of individual changes (disparity). This would mean that there was a decreasing increase in both diversity and disparity late in the diversification process. Human fossils show diversification at the same time that diversification is evidenced in non-human fossils, but human change is restricted to only the very end (Quaternary) of the diversification evidenced in non-humans (at least the Tertiary and Quaternary). Not beginning until late in the period of diversification might explain why the human baramin generated a lower diversity and disparity of form as compared to the diversity and disparity of non-humans after the Flood. If this is so, then some sort of clock may be controlling the diversification (e.g. occurring while certain environmental conditions persisted and/or for a prescribed number of generations following the Flood or some Flood-related environmental trigger).

Preliminary baraminological studies on non-human groups preserved in post-Flood sediments suggest that a confusing array of distinct species morphologies were generated in early post-Flood times (e.g. among non-human hominoids: Wise 1994, 1995). Rather than following simple tree-like branching patterns, these intrabaraminic diversifications seem to rapidly generate a plethora of parallel lineages making resolution of branching order virtually impossible. Some paleontologists preferred to describe these patterns as 'bushes' rather than 'trees' (e.g. Gould 1977), and Wood and Murray (2003, pp. 173-6) likened this pattern to starbursts in fireworks displays. Although on a smaller scale, a rapidly-generated unique morphology for each Babel lineage may make human diversification very similar in branching pattern to that of non-human intrabaraminic diversification.

Two other patterns which are repeated in the intrabaraminic diversification of several non-human groups of large body size (and bear further study for that reason) are the generation of confusing mosaic morphologies (e.g. non-human hominoids: Wise 1994, 1995; horses: Cavanaugh *et al.* 2003) followed by a

narrowing of diversity towards the present (*e.g.* horses, camels, elephants, and hominoids). Consistent with these patterns, the Flores skeleton displays a mosaic of characters (Brown, *et al.* 2004). *H. floresiensis* also contributes to a greater inter-specific human morphology than is seen in the present. Similarly, Powell and Neves (1999) suggest that the intra-specific variation in early New World *H. sapiens* populations was much greater than the diversity of historic native American populations. Even the parallel evolution in multiple lineages, suggested by multiple independent derivation of *H. sapiens* morphology, may be similar to the larger-scale parallel evolution indicated in non-humans (*e.g.* sabertooth morphology derived at slightly different times in Australian marsupials, South American mammals, and in at least two different cat lineages in North America), for the latter is almost certainly due to expression of common designs built into the different groups by the Creator.

The multiple similarities between intrabaraminic diversification in non-humans and diversification of post-Babel humans (timing with dispersal; stratigraphic position of fossils; magnitude of change, mosaic modification of characters; narrowing of diversity; parallelism) suggest that whatever is stimulating intrabaraminic diversification in animals may also be simultaneously stimulating morphological diversification in humans. Organismal change does not seem to be mentioned in the biblical text. However, paleoanthropological evidence suggests that the change in longevity of humans – which is evidenced in the biblical text – is coincident in both time and possibly even cause with intrabaraminic diversification in animals, plants, and even humans.

UNLIKELY MECHANISM OF CHANGE

As for the mode of this change, this writer disagrees with evolutionists (*e.g.* Brown, *et al.* 2004, p. 1060; Lahr & Foley 2004) and creationists (*e.g.* Wieland 2004) who claim that natural selection acting on mutations is the mechanism by which the Flores skeleton morphology was derived⁴. Natural selection acts on observed variation, but the neanderthal, flores, and sapiens developmental programs do not seem to have been part of any erectine population variation. And, given the highly infrequent and usually detrimental nature of phenotypically expressed mutations, as well as the complex nature of developmental programs, it

is unlikely that any of these morphologies arose by mutation. Furthermore, as Haldane (1957) suggested — in what is known as Haldane’s Dilemma — natural selection acts much too slowly to explain substantial human variation, especially if it occurred entirely within a few centuries of the Flood (see also the arguments of Wood 2002; Wood & Murray 2003, p. 178). In fact, generalizing these observations to all organisms, natural selection acting on mutations is an unlikely mechanism for the origin of biological form throughout the young-age creation model (see Wood 2005, for examples in the Galápagos Islands). The intrabaraminic changes which are evidenced in the fossil record (*e.g.* for the horses: Cavanaugh, *et al.* 2003) – and suggested by interspecific hybridization – involve morphologies very, very far outside the range of variation observed in modern organisms (as the morphologies of modern organisms are outside the range of variation observed in the older fossil organisms). And, given the highly infrequent and usually detrimental nature of phenotypically expressed mutations, as well as the complex nature of many of these past morphological characters, it is unlikely that any of these morphologies arose by mutation. Finally, even if the morphology were to arise in one member of the population, natural selection fixes that morphology only by differential death. This incurs a death load on the population, making it impossible to fix such a trait very rapidly (Haldane’s dilemma). Especially in the light of the abbreviated time scale of the young-age creation model, Haldane’s dilemma makes it unlikely to impossible that natural selection is responsible for fixing much or most of the realized biological forms in earth history. It is more likely that the only substantial role natural selection plays is the elimination of deleterious mutations (*i.e.* minimizing mutation’s damage in a fallen world).

Wise (2002, pp. 233-4) has suggested that rather than people adapting to their respective destinations (as Wieland 2004, suggests for the Flores skeleton), human morphologies may have been developed before they arrived at their final destinations (as Wood 2002, has suggested for non-humans, and Wood 2005 has suggested for some animal groups on the Galápagos Islands). *Then* people moved to locations where they felt most comfortable. So, for example, in the case of the people with the Flores skeleton morphology, their small body volume (and thus limited heat production)

and relatively high surface area / volume ratios (and thus high heat exchange rates with the environment) would likely cause them to be most comfortable only in warm (low latitude) regions. So, once the morphology is achieved, those with the diminutive morphology headed for low-latitude locales (or chose to move towards the Equator whenever they were able). If this is true, not only is natural selection not responsible for the changes in the first place, but the morphological changes in humans may have been non-adaptive. This would be consistent with what seems to be true in non-human lineages (*e.g.* weevils, tortoises, and lava lizards in the Galápagos: Wood 2005, pp. 187-197).

As one particularly interesting example among non-humans, Wood and Murray (2003, pp. 200-201; Wood 2005, pp. 174-5) utilize a non-adaptive explanation for giant tortoises (*Geochelone*) on small islands. They suggest that in Wise and Croxton's (2003) post-Flood biogeography model, the larger members of the frequency distribution of body size in tortoises might possess a more raftable morphology than the smaller members (Wood & Murray 2003, pp. 200-201; Wood 2005, pp. 174-5). For similar reasons, for elephants it would be the *smaller* members of the frequency distribution of body size that are most raftable (Wood 2005, pp. 174-5). Thus *if* tortoises and/or elephants made it to oceanic islands via rafting, the tortoises would most likely be giants and the elephants dwarfs. Wood's proposed explanation for insular gigantism and dwarfism has not yet been tested and needs to be. Interestingly enough, however, the Flores Island sediments slightly older than the Flores skeleton contain fossils of giant tortoises (*Geochelone*) and dwarf elephants (*Stegodon*) (Morwood, *et al.* 1998), as expected in Wood's proposal. In fact, with regards to *Geochelone*, Flores Island is on the path of ocean currents which leave the South American continent, flow past the Galápagos Islands, then on past Australia and Flores Island to the island of Aldabra in the Indian Ocean. In Wood's extension of Wise and Croxton's (2003) model, the fossil *Geochelone* of Flores Island should be related to and perhaps intermediate in the sequence of the modern *Geochelone* of South America, the Galápagos, and Aldabra. A non-adaptive model of change would also be consistent with the ubiquity of species decimation in the fossil record and massive species extinction in the present.

It was argued above that divergent human morphology may have converged on the narrow morphology of the present because of developmental programs pre-programmed into humans by the Creator. Laid out in biological character space, these programs may actually map out biological trajectories (as defined by Wood & Cavanaugh 2003) — perhaps multiple biological trajectories, so that getting kicked off any particular trajectory can lead an organism along another one. This sort of design of character space might be called trajectory redundancy. With this design, human morphology itself might have followed biological trajectories (*e.g.* the *H. erectus* to *H. sapiens* sequence with its associated changing size of encephalization quotient). And, if human morphology followed pre-designed trajectories, there is no need to postulate any sort of loss of information — even if some morphologies are entirely “lost” (no longer morphologically realized). Along with Wood and Murray (2003, p. 179) this author doubts that the common creationist claim of diversification via loss of information (what Wood 2002, calls ‘heterozygous fractionation’) plays a substantial role in intrabaraminic diversification at all. This author specifically rejects Wieland's (2004) claim that such a loss of information had something to do with the derivation of the Flores skeleton morphology.

SUMMARY AND CREATION MODEL DISCUSSION

More excavation is required to confirm the population status of the Flores skeleton morphology. Even without that confirmation, however, the morphological variation seen in fossil humans suggests that the post-Flood world involved very high rates of intrabaraminic diversification in all organisms — *including* humans. The rapidity of the transitions suggests that the variation potential was built into all organisms by the Creator and that the changes were neither chosen by natural selection nor even adaptive. It is likely that the diminutive morphology represented by the Flores skeleton was generated by a process of genetic drift operating on a small post-Babel population slightly divergent from other such populations by founder effect. Once they had assumed the small body size, or were well on their way to getting there, the family group made their way to the Island of Flores — ultimately by boats on the

sea.

The date of the Flores skeleton suggests it and its people lived on Flores not long after Babel. The size of Flores Island, however, seems rather small for a people group soon after Babel. It would seem that the whole earth was at their disposal and that a better (at least a larger land area) choice could have been made. We have older evidences of humans in both directions from Flores (*e.g.* Australia and Java: Lahr & Foley 2004). It's possible that the Flores people were driven from more desirable areas by other Babel lineages. Racism in the present is vicious even though morphological differences among races are only a very small percent of the morphological divergence in the days of the Flores human. Considering the universal depravity of man, it would not be surprising to discover that extreme racism was active in post-Babel days. Perhaps the Flores culture was forced to live where they did. To survive they may have had to make forays to larger land areas to bring in animals to eat. The extermination of the endemic animals found stratigraphically below the human evidences and the introduction of new animals in the sediments above would be explained by this behavior (Morwood, *et al.* 1998). A proper understanding of post-Babel times may have to include substantial violence among post-Babel lineages. It may be that post-Babel racism was more extreme than it is today — so much so as to lead to the extermination of multiple people groups. Such racial selection⁵ introduces another possible mechanism for the narrowing of human morphology in post-Flood times.

The possibility of divergent biological trajectories from *H. erectus* to *H. sapiens* introduces another caution into creationist paleoanthropology. If the trajectories of human form were divergent, it is at least as likely that the trajectories of human technology were also divergent in different Babel lineages. If so, then a particular tool technology may not be associated with a singular age across the planet (Wise 2002, p. 236). This archaeochronometer — commonly used in traditional paleoanthropology — needs re-evaluation in the creation model.

The Flores skeleton's unusual stature may also provide some insight into other unusual human statures. The Flores skeleton is unlike any modern humans of small stature and seems to have that small stature for non-pathological reasons. Analogously,

it might turn out that the giants of the post-Flood world (*e.g.* the Anakim; Goliath) were also unlike any modern humans of large stature and may have had that large stature due to non-pathological development.

TESTS

In conclusion, the Flores skeleton find is an exciting one, and will undoubtedly stimulate searches for similar divergent fossil human morphologies around the world. What follows are expectations and tests of this paper's claims:

1. Claim: *Homo erectus* is the dominant human morphology of those dispersing from Babel. Tests: First, as a creationist time scale is developed the Babel event will not long precede the oldest *H. erectus* specimen and correspond stratigraphically to the Tertiary/Quaternary boundary. Second, as more specimens are found, the *H. erectus* morphology will continue to be the exclusive human morphology from Lower Pleistocene sediments. Third, *H. erectus* morphological characters found only in particular *H. erectus* populations will otherwise only be found in younger human morphologies found in the same region.
2. Claim: Major changes in humans (including the change in longevity from pre-Flood to post-Flood times) are largely due to developmental heterochrony. Tests: First, textual data (Scripture and cultural myths), historical data (archaeological and historical records), and current biological data (medical records and observed modern variation) will consistently evidence heterochronic changes. Second, aging studies will demonstrate that changes in developmental rates can generate changes in longevity.
3. Claim: Founder effect and genetic drift led to independent changes in many post-Babel lineages. Tests: First (confirming founder effect), differences in *H. erectus* populations will turn out to be geographically specific and small (collectively generating a range of variation within the expected coefficient of variation of a human population). Second (confirming genetic drift), the creationist time scale applied to the Upper Pleistocene will demonstrate that the morphological changes in human populations occur about as fast as might be expected by genetic drift but not by any other

microevolutionary mechanism. Third, human morphologies in the Upper Pleistocene will be found to be regionally specific and (when specimens in a particular region are found in multiple stratigraphic levels) follow biological trajectories from a unique erectine morphology. Fourth, as more human specimens are found in Upper Pleistocene sediments other human morphologies will be found, each showing a confusing mosaic of characters. Fifth, increased geographic and stratigraphic information should show that the morphologies pre-date the final habitation sites (thus indicating the morphological changes are non- or pre-adaptive).

4. Claim: Divergence of human morphologies was caused by the same mechanism which generated intra-baraminic diversification in non-humans. Tests: First, the magnitude of degree of divergence among human morphologies in the Upper Pleistocene will be found to be comparable to the magnitude of degree of divergence among non-human morphologies in Upper Pleistocene sediments (less than the magnitude found in Tertiary sediments; greater than the magnitude in Holocene sediments). Second, as more Upper Pleistocene humans are found, parallel changes and mosaic characters will be identified and they will be of the same nature as the same things observed in non-human lineages (except, as indicated on the first test, on the scale evidenced in Upper Pleistocene sediments).
5. Claim: The modern human morphology was derived independently in many different post-Babel lineages (phylogenetic redundancy). Test: Comparative DNA studies on modern and divergent Upper Pleistocene morphologies will demonstrate that the ancient populations are ancestral to at least some modern humans.

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ENDNOTES

¹*Stegedon* is an exception (being from Asia), but elephants are very good long-distance swimmers – the dozens of kilometers of water between Java and various of the Lesser Sunda Islands being no significant barrier to them (Johnson 1980). Primates and humans, however, are not long-distance swimmers, so it is likely Wallace Line represents a real barrier to them, as it does to so many other quadrupeds and birds.

²Although the short time period between the Flood and Babel, the concentration of humans in a single geographic location, and the fact that Noah and Shem were still alive at Babel, collectively might suggest that the erectine morphology was also the morphology of Noah's family, this is not necessarily true. If Babel occurred during the lifetime of Peleg (as suggested by Genesis 10:25) then just about as many generations separate the Flood from Babel as separate Babel from Abraham. It could then be that as much morphological change occurred between the Flood and Babel as occurred between Babel and the present. This means Noah's morphology is likely to be at least as different from *H. erectus* as erectine morphology is different from sapiens morphology. And, since the rate of morphological change has probably decreased through time, Noah could well be even more different from *H. erectus* as erectines are different from sapiens.

³Although there is general consensus that menarche age is decreasing, the cross-cultural and historical data is confusing (see Cuozzo 1998:191-8) and the true trends need careful re-evaluation by creationists. Furthermore, although better nutrition is the most popular explanation for any trend of decreasing menarche age (see, for example, McCauley and Salter 1995), the real cause is unknown, as decreasing menarche age has been documented in populations without improved nutrition (see Cuozzo 1998:191-8).

⁴I am arguing that natural selection played no substantial role in the *origin* or modification of any of these morphologies. I do not exclude the possibility that once the morphologies had been established, selection (including natural selection) may have determined which morphologies became extinct and which did not.

⁵'Racial Selection' is to be understood to be analogous to but distinct from 'Natural Selection'. Thanks to Scott Mahathey for the suggestion of this term.