

The Genetics of Kinds - Ravens, Owls, and Doves

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1.0 Abstract

Cytochrome b (cytb), one of the most widely used and accepted genes for phylogenetic studies, was employed to evaluate the genetic diversity, from a creationist standpoint, within and between species of ravens, species of owls, and species of doves. These species were chosen since they are known to have existed shortly after the flood, some documented within 400 years of the flood. It was found that within these species, cytb varied by approximately 1 percent or less and between species, the cytb varied between 4.1% and 25.3%; for example, the Barn Owl and the Spotted Eagle Owl differed in cytb by 25.3%. This variation is more than the cytb variance between a mouse and a pig, or a horse and a cow and nearly as much as the variation between a cow and a zebra fish (29%). This study concludes that all the subject species of ravens, species of owls, and species of doves were on the Ark. The alternative theory, which is now accepted by some creation scientists, is that speciation occurred after disembarkation from the Ark; this theory requires accepting full blown evolutionary processes (speciation through natural selection etc.) functioning at speeds on the order of 60,000 times that of published evolutionary literature.

Based on this analysis of ravens, owls and doves, two hypotheses are submitted which are in tune with both the Bible and the DNA genetics, and are not dependent on any evolutionary processes.

2.0 Background/Discussion

Creationist have long maintained that the kinds, or species observed today are distinct and there are no intermediate forms (Morris, H. M., 1974) and this research and paper supports that theme.

The following discussion provides background for this research and supporting evidence for the following two hypotheses: (1) the "genetic reset" theory and (2) the "deep sleep" theory, both of which are sound Biblically and not dependent on any precept of the evolutionary hypothesis.

2.1 The Basic Dilemma

The basic dilemma concerning the voyage of Noah's Ark is: how did Noah keep so many kinds of animals alive on the Ark for a year? Since there are so many birds species presently living on earth (Sibley, Charles G., and Monroe, Burt L.), the tendency for creationists is to speculate that the Biblical kinds were only a portion of the present-day species, and that the Ark contained possibly only the "genus," "family," or "order." The problem with this speculation is that it is in conflict with the Biblical, fossil, and DNA evidence. The Bible clearly states that every kind and sort of bird was taken on the Ark (Genesis 6:19, Genesis 7:14); and, the fossil record shows that before the flood there were multiple species of each genus, family, and order. Then, the most daunting task encountered by this speculation is explaining how the reduced number of kinds expanded into the numerous species living today. This dilemma has placed creationists in the position of having to decide between the Bible and evolution. Many have chosen a euphemistic version of evolution and used terms such as microevolution, natural selection, speciation, etc.. However, it is still evolution. For those of us who believe the Biblical timeframe of creation, it would require the evolutionary processes to produce new species in just 378 years; this is the time when

Abraham sacrificed a turtle dove and the young pigeon (Genesis 15:9) which were different than the dove that Noah released from the Ark (Genesis 8:8). This means that if evolution could produce these species in such a short time, there would be much available proof of evolution; however, this is not the case and evolution is not observable; the only reason evolutionary theory has survived is by expanding the time frame to millions of years and by adding the multiple, fictitious common ancestors.

John Woodmorappe addressed these problems of lodging large numbers of animals in a book called "Noah's Ark: a Feasibility Study" (Woodmorappe, John. 1996). He went into great detail in discussing the problems of space, feeding, cleanliness, ventilation, air quality and all the other problems associated with the Ark. His feasibility study resulted in the conclusion that if only a portion of the present-day species (fewer than 16,000) were onboard, it would be possible, although difficult, to keep them alive on the Ark for approximately one year. This book did a very good job of defining the problems involved with lodging so many animal and keeping them alive; however, in all practicality, it would take a miracle to survive the work, the environment and the predator/prey instincts. Anyone who has kept one horse in a stall knows what a Herculean task it would be to keep thousands of animals on the Ark.

The Bible mentions only one window on the Ark, and that window was only 18 inches by 18 inches (Genesis 6:16); and, although it is not clear, there was probably very limited ventilation, especially to the lower levels. Noah's Ark would be a very bad design to keep tens or hundreds of thousands of animals alive with their metabolisms performing at full capacity. But, God did not make a mistake; He is the master designer and the design of the Ark was perfect, perfect for preserving those creatures that possessed the "breath of life." Also, it appears that not one species was lost (Genesis 8:1 and 19).

2.2 Biblical Basis and Assumptions

2.2.1 Genetic Reset History

Genetic resets are documented in the Bible at least four times:

- **The First Genetic Reset** As a result of the original sin, God reset the creation genetics. The DNA was necessarily changed in humans in that they became mortal and women's pain was multiplied in childbirth (Genesis 3:16). Other DNA changes included the serpent who lost his legs (Genesis 3:14); and, all of the livestock and beasts of the field were cursed (Genesis 3:14), "but not as much as the serpent." This implies a DNA changed in all the livestock and beasts of the field. Concerning plants, the earth brought forth "thistles" and "thorns" (Genesis 3:18) implying new and different DNA and a new ecosystem to accommodate the new genetics.
- **The Second Genetic Reset** The second DNA reset occurred at the time of the flood. Man's life span was greatly reduced from 900 plus years (Genesis chapter 11) implying a DNA change; the concept of clean and unclean animals appeared in the scriptures (Genesis 7:2); and, the authorization of eating meat was introduced (Genesis 9:3). The flood changed the entire ecosystem implying significant DNA changes to all life forms. The fossil record bears out that the ecosystem was very different before the flood, e.g. massive dinosaurs with small nostrils, dragonflies with 2 foot wingspans, and tropical vegetation near the poles.
- **The Third and Fourth Genetic Resets** According to the Bible, there will be at least two more genetic resets: the third reset will occur when we change in a "twinkling of an eye" (I Corinthians

15:52), just before the millennium; and the fourth, when we enter eternity (I Corinthians 15:40 , Revelation 21).

2.2.2 Voice Control

This is God's creation and He uses His voice to control it. The entire Bible is full of voice control occurrences. Through voice control, God created all things, calmed the wind, healed the sick, raised the dead, cast out demons, conquered death, and healed the brokenhearted. Also, there is proof that the creation is responsive to voice control, even if it is not the voice of God. We are told, by Jesus Himself, that if we believe, we can say to a mountain "be cast into the sea," and it will happen (Mark 11:23).

Twice, God gave the command to "be fruitful and multiply and fill the earth". The first occasion was in the beginning on day six when the creation was completed (Genesis 1:28). The second occasion was after the departure from the Ark (Genesis 8:17,9:1). So, it is evident that His purpose did not change in the new ecosystem; He wanted the new world to be filled; this required man and animals to be equipped for survival and reproduction in the new world, including its new ecosystem. There was no time for natural processes (i.e., multiple accidents and accidental selection of accidents) to prepare the creation for the new world; knowing the complexity of ecosystems, it had to be done by the creator who understands these complexities.

2.2.3. Possible Voice Control Mechanism -Transmission of mtDNA Generation to Generation

It is evident that God reduced lifespan immediately after the flood down to approximately 120 years at the time of Moses (Deuteronomy 34:7) and 70 years at the time of David (Samuel 5:4, 1 Kings 2: 10-12). This is a transition that is probably coincident with the ice age which was initiated by the flood and lasted approximately 700 years (Oard, M., 2007). And, the entire ecosystem was changing to what we have today. These facts render the question, "what mechanism did God use to accomplish this?" DNA is a language (Collins, 2006) and God possibly spoke the genetic reset into those who were in a deep sleep on the Ark, and it appears that mitochondrial heteroplasmy is a possible tools that he used for this task.

In human reproduction, the mature oocyte contains 100,000 to 750,000 mitochondrial DNA (mtDNA) copies and is fertilized by the sperm which generates a blastocyst containing approximately 483,000 copies of the mtDNA in the Inner Cell Membrane (ICM); which in turn develops and harbors the Primordial Germ Cells (PGM) each of which contains approximately 200 copies of the mtDNA (St. John, Justin C., 2010); and each of the embryonic stem cells used in this construction contain approximately 20 copies of mtDNA (Rivolta MN, 2002). The processes involved with replication and inheritance of mtDNA are not well understood, but show what varied genetic information is available for transmission of mitochondrial DNA from generation to generation.

This transmission of mtDNA is quite different than nuclear DNA in that with nuclear DNA, only one copy is transferred to the next generation. It is a shuffled mixture of ovum haploid and sperm haploid DNA, but once it is determined the resulting embryo is defined by only one nuclear DNA.

This method of transmission of mtDNA is of great interest concerning the inheritance and possible prevention of mitochondrial diseases, but also of interest from a genealogy standpoint. It has been found that it is common to have mitochondria that are heteroplasmic, meaning that it contains more than one mitochondrial genome. From a creationist standpoint, this is very interesting in that this heteroplasmic mitochondria could explain why the genetic reset took several generations to establish as documented in Genesis chapter 11. If there are only a few copies of a certain variation of mtDNA in the oocyte, they can be latent for several, or even many generations.

Mitochondrial heteroplasmy is somewhat common in humans. The American Journal of Human Genetics reported in 2010 that 37 heteroplasmies at 10% frequencies or higher at 34 sites were found in 32 individuals (Li, M., et. al. 2010).

It would be tempting to use this heteroplasmic attribute coupled with a stochastic modeling to explain speciation after the flood; but, it wouldn't fit the general theme of the Bible. There is a difference between natural variation which gives us our uniqueness and mutations which have developed due to the original sin. Mutations result in disease and shorter life span. Heteroplasmy, is most probably a result of sin.

This is a fascinating branch of research and creationists, Genesis and Genetics included, should exploit it.

2.2.4 Genetic Space Between Species

The subject species examined in this paper are genetically distinct, meaning the species do not have a genetic overlap, but all demonstrated a genetic void between species. The data show that within species the natural variation, genetic distance, is approximately one percent of cytb and between species the variation is much greater: between 4.1 percent and 25.3 percent. This means that if one species varies from another by 10 percent of cytb, there is a void of 9 percent (10-1/2-1/2). There is no known mechanism that can bridge this void to produce a new species, especially in the short, young earth, timeframe. This is true for all our subjects as shown by the data presented in section 3.0 of this paper. Any variation of bird displaying this genetic void is assumed to be a unique kind and most probably was represented on the Ark.

2.2.4 Deep Sleep History and Hypothesis

Another tool God uses to control His creation is that of "deep sleep." Here are three Biblically documented examples of God using "deep sleep":

- **To make physiological changes** - When God created Eve, he put Adam into a "deep sleep" so Adam would not feel the pain of the surgery in which Adam's rib was removed (Genesis 2:21).
- **To establish a new covenant** - When God established the covenant with Abram (Abraham), he, Abraham, was put into a deep sleep. While Abraham was in this "deep sleep" the Lord dealt with him and prepared Abraham for a new covenant (Genesis 15:12).
- **To separate enemies** - When Saul wanted to kill David and had the opportunity, God put Saul and his entire army of 3000 into a "deep sleep" (1 Samuel 26:2,12) so that David would be spared.

The tool of "deep sleep" may very well have been employed on the Ark providing the perfect solution to all the problems: it would provide the anesthetics for the physiological changes required to reset the DNA; it would give God an opportunity to establish His new covenant with all flesh; it would protect the prey from the predators; and, of course, it would solve all the problems of space, food, waste, and air quality. The design of the Ark is obviously not suited to keep the creatures alive in the full metabolic state, but well suited to the "deep sleep" state.

2.2.5 "Deep Sleep" Mechanisms

The exact mechanism for "deep sleep" is not known, but it is logical to assume that it shares some similarities with the various mechanisms that we observe in nature: hibernation, comas, aestivation, brumation, and dormancy. Each of these mechanisms is different and serves the purpose for which it was designed.

We know that God has masterfully designed the Ark to accommodate the safe and peaceful transportation of the creation from one eco-system to another. He created all things in just six day; this is just one more bit of evidence of His genius.

It is a point of interest that all mammals have the ability to hibernate and that mammalian metabolic rates can be reduced to as little as 1% of normal rates (Carey HV, et. al, 2003).

2.3 Biblical examples of Kinds of Birds

It is not known which birds were on the earth on day 6 of creation, but we do know, generally, which birds are presently on Earth. It is known that a raven and a dove were on the Ark. A bit later, the Bible mentions a turtledove and a young pigeon (Genesis 15:9); this is when God commanded Abraham to make a sacrifice. So, three varieties of dove were mentioned within 378 years of the flood. In Hebrew they were: yônah (dove), tôr tôr (turtle dove), and gôzâl gôzâl (young pigeon). All three dove varieties have different names in ancient Hebrew, implying that they were three different kinds. The English descriptions are a bit misleading in that they imply sub kinds; for example the turtledove being a sub-kind of dove. This is not true for ancient Hebrew, there is the yônah (dove) and the tôr tôr (turtledove) which are distinct names and, therefore, are distinct kinds.

This paper deals with ravens, owls, and doves. The raven and the dove were used in this study since it is documented that some species of raven and some species of dove were on the Ark and the owl was used since the Bible documents five owl species.

2.4 Biblical record of Variations the Kinds of Ravens, Owls, and Doves

The following is a list of some of the Biblical references to our subjects:

Raven

Raven (Hebrew - 'ôrêb 'ôrêb) Deuteronomy 14:14 KJV

Owl

Owl (Hebrew - ya'ănâh) Leviticus 11:18 KJV
 Little Owl (Hebrew - kôs) Leviticus 11:17) KJV
 Great Owl (Hebrew - yanshûph yanshôph) Leviticus 11:17 KJV
 Another Great Owl (Hebrew - qippôz) Isaiah 34:15 KJV
 Screech Owl (Hebrew - lîylîyth) "Isaiah 34:14 KJV

Dove

Dove (Hebrew: yônâh) Genesis 8:8 KJV
 Turtledove (Hebrew: tôr tôr) Genesis 15:9 KJV
 Young Pigeon (Hebrew: gôzâl gôzâl) Genesis 15:9 KJV

Note that, again, the names are different for each kind. In English we say Little Owl, Great Owl, Screech Owl, etc.; all are some type of owls, but in the ancient Hebrew each owl has a different name: kôs, yanshûph yanshôph, lîylîyth, etc.

2.5 Cytochrome b (cytb)

Cytochrome b (cytb) is a gene located in the mitochondria and involved in respiration, electron transport, and generation of ATP. In genetics, cytb has been accepted as a powerful tool in phylogenetic work (e.g. Chen, 2009). This is a very good choice for this creation research in that cytb is of prime importance in the creatures which possess the "breath of life" (Genesis 6:17). Since cytb has been widely accepted in phylogenetic analysis, it is readily available.

2.6 Bird Genotypes and Phenotypes

Birds have what is commonly referred to as instincts. These instincts are poorly understood, but are believed to be hardwired into the DNA. These hardwired qualities include nest building, courtship rituals, sounds, egg incubation, migration, and flight. These characteristics add to the complexity of the DNA and the variation of kinds.

Speech is one of these hardwired, very complex instincts in creatures such as birds. Humans learn language from their parents. A few birds learn their sounds from their parents like humans, but most birds have their sounds hardwired in their DNA. This has been observed by many studies including one (Nottebohm, F., 1970, 1979) where birds were raised in isolation from other birds and were found to sing the same song as their peers raised by their parents. It has also been observed that some birds do have the ability to be taught new songs, but revert back to the hardwired repertoire (Brelands, K., and Brelands, M., 1961) when the learning and/or reinforcement stimulus is removed. In this study, all of our variations of kinds, have a different speech, meaning that this would also be a point of DNA complexity and variance. This complexity would also be difficult to explain through a series of accidents in a very short amount of time.

Bone structure like everything else in life forms is very complex and going into details concerning our subject birds is beyond the scope of this paper. However, it is of interest that the various species of the same genus and family do have different bone configurations. Herons have been classified by secular scientists according to bone structure and a phylogenetic tree is available documenting the results (McCracken, K.G., 1998). The osteological study in the McCracken paper correlates fairly well with the genetic variation. So, variation in bone structure also is responsible for significant DNA changes in the species.

2.7 Mutation rates and Evolutionary Clock

Evolutionary scientist use a wide range of mutation rates to accommodate their interpretation of the fossil record and the genetic record (Nabholz, Benoit, 2009, Spradling, T. , 2001). A study involving cytochrome b was conducted that resulted in a mitochondrial substitution rate for birds which ranged from .003 to .090 substitutions per site per million years (Nabholz, Benoit, 2009). This means that for a cytochrome b sequence 1000 base pairs long, evolutionary thinking would predict between 3 and 90 mutations in one million years. Since we are dealing with mutations in this range, creationists who attribute these mutation to natural causes, are not only accepting evolution, but accepting it at hyper speeds.

3.0 Results

3.1 The Raven

There are approximately 40 species of ravens i.e., members of the *Corvus* genus (crows included). Table 1 presents the variation of cytochrome b for four Common Ravens (*Corvus Corax*) collected in various locations. From the limited data available, it shows that within this one raven species, the cytochrome b nucleotides differ from one another by less than one percent; the maximum nucleotide difference is 8 nucleotides divided by the 1035 possible nucleotides resulting in differences of 0.8 percent. These differences show natural variation in this one species of raven.

Table 1 Cytochrome b Differences Within the Common Raven (*Corvus Corax*) Species

	Common Raven (<i>Corvus Corax</i>) (AY156304) Mongolia	Common Raven (<i>Corvus Corax</i>) (AY156302.1) Alaska	Common Raven (<i>Corvus Corax</i>) (AY156300) Alaska	Common Raven (<i>Corvus Corax</i>) (AY156269) Aleutian Islands
Common Raven (<i>Corvus Corax</i>) (AY156304) Mongolia		8/1035 (.8%)	5/1035 (.5%)	7/1035 (.7%)
Common Raven (<i>Corvus Corax</i>) (AY156302.1) Alaska	8/1035 (.8%)		5/1035 (.5%)	7/1035 (.7%)
Common Raven (<i>Corvus Corax</i>) (AY156300) Alaska	5/1035 (.5%)	5/1035 (.5%)		4/1035 (.4%)
Common Raven (<i>Corvus Corax</i>) (AY156269) Aleutian Islands	7/1035 (.7%)	7/1035 (.7%)	4/1035 (.4%)	

Note: The GenBank (Benson DA, 2007) sequence numbers for each subject is in parenthesis. Alignment and identities were performed by BLAST- Basic Local Alignment Search Tool (Altschul, 1990) and verified using Micro-Soft Excel. When sequences were of different lengths, only the aligned sections were considered. The numbers represent the number of nucleotide differences for one species to another divided by the number of nucleotides of cytochrome b available for the comparison sequence.

Table 2 presents the cytochrome b differences between different species of ravens. The variety of ravens selected was due mainly to availability of DNA sequences. The nucleotide variance between these species of raven varies from 38 nucleotides (4.1%) and 86 nucleotides (8.3 %). This variance is distinctively beyond the one percent of natural variation in the one species. From an evolutionary perspective, the Chihuahuan Raven parted from the Common Raven approximately one million years ago (Marzluff, John M., Angell, Tony. 2007). So, if a creationist assumes that the Chihuahuan Raven parted from the Common Raven in the last 4400 years, the creationist must accept the evolutionary processes at work, and that it progressed 227 (1,000,000/4,400) times faster than what the secular evolutionists predict. All of the ravens in Table 2 are of the genus *Corvus*.

Table 2 Cytochrome b Differences Between Raven Species

	Common Raven	Chihuahuan Raven	White-necked Raven	Australian Raven	Pied Crow
Common Raven (AY156304) (<i>Corvus Corax</i>)		40/925 (4.3%)	38/925 (4.1%)	86/1035 (8.3%)	39/925 (4.2%)
Chihuahuan Raven (AY527264) (<i>Corvus Cryptoleucus</i>)	40/925 (4.3%)		44/925 (4.7%)	71/925 (7.6%)	48/925 (5.2%)
White-necked Raven (AY527263.1) (<i>Corvus Albicollis</i>)	38/925 (4.1%)	44/925 (4.7%)		68/925 (7.4%)	41/925 (4.4%)
Australian Raven (AF197837) (<i>Corvus Coronoides</i>)	86/1035 (8.3%)	71/925 (7.6%)	68/925 (7.4%)		77/925 (8.3%)
Pied Crow (AY527262.1) (<i>Corvus Albus</i>)	39/925 (4.2%)	48/925 (5.2%)	41/925 (4.4%)	77/925 (8.3%)	

Note: The GenBank (Benson DA, 2007) sequence numbers for each subject is in parenthesis. Alignment and identities were performed by BLAST- Basic Local Alignment Search Tool (Altschul, 1990) and verified using Micro-Soft Excel. When sequences were of different lengths, only the aligned sections were considered. The numbers represent the number of nucleotide differences for one species to another divided by the number of nucleotides of cytochrome b available for the comparison sequence.

3.2 The Owl

There are approximately 220 varieties of owls in the world. The Bible refers to five varieties of owls: The Owl - Leviticus 11:18 KJV (Hebrew - ya'ânâh), the Little Owl - Leviticus 11:17 (Hebrew - kôs), one type of Great Owl - Leviticus 11:17 (Hebrew - yanshûph yanshôph), another type of Great Owl - Isaiah 34:15 KJV (Hebrew - qippôz), and the Screech Owl - Isaiah 34:14 KJV (Hebrew - lîylîyth). The first three varieties of owls were mentioned approximately 860 years after the flood, the time of Moses, and the last two were mentioned approximately 1600 years after the flood, during the life of Isaiah.

For this owl analysis, five species of owls were used, three of which are specifically mentioned in the Bible, the others were chosen since DNA sequences were available. The five owls presented show cytochrome b genetic differences within the species and between the species. The following owls were used in this analysis; all are from the Strigiformes order and Strigidae family with the exception of the Barn Owl which is from the Tytonidae Family and Tytoninae sub-family. These are defined in accordance with the secular scientific taxonomy.

<u>Common Name</u>	<u>Subspecies</u>	<u>Species</u>	<u>Genus</u>
Great Horned Owl	<i>Bubo virginianus virginianus</i>	<i>Bubo virginianus</i>	<i>Bubo</i>
Northwestern Great Horned Owl	<i>Bubo virginianus lagophonus</i>	<i>Bubo virginianus</i>	<i>Bubo</i>
Little Owl	-	<i>Athene Noctua</i>	<i>Athene</i>
Barn Owl	-	<i>Tyto alba</i>	<i>Tyto</i>
Eagle Owl	-	<i>Bubo Bubo</i>	<i>Bubo</i>
Spotted Owl	-	<i>Bubo Africanus</i>	<i>Bubo</i>

Table 3 presents the cytochrome b genetic variation within the species of the Great Horned Owl (*Bubo virginianus*). Presented in Table 3 are two subspecies of Great Horned Owl: the Common Great Horned Owl (*Bubo virginianus virginianus*) and the Northwestern Great Horned Owl (*Bubo virginianus lagophonus*). Subspecies are generally considered "races" similar to the human races. This is interesting that the owl races are genetically similar, i.e. overlap, but some phenotypical differences are observable. So, it is probable that only one pair, or two pair depending on the interpretation of Genesis 7:9, of Great Horned Owls was/were aboard the Ark and the other races appeared after disembarkation due to migration and loss of some genetic information, again, similar to humans

Table 3 Differences in cytochrome b Nucleotides for Great Horned Owls

	Great Horned Owl Number 1 (AF168106.1)	Great Horned Owl Number 2 (AJ003974.1)	Northwestern Great Horned Owl Number (AJ003956.1)
Great Horned Owl Number 1 (AF168106.1)		7/968 (.7%)	10/968 (1.0%)
Great Horned Owl Number 2 (AJ003974.1)	7/968 (.7%)		3/968 (.3%)
Northwestern Great Horned Owl Number (AJ003956.1)	10/968 (1.0%)	3/968 (.3%)	

Note: The GenBank (Benson DA, 2007) sequence numbers for each subject is in parenthesis. Alignment and identities were performed by BLAST- Basic Local Alignment Search Tool (Altschul, 1990) and verified using Micro-Soft Excel. When sequences were of different lengths, only the aligned sections were considered. The numbers represent the number of nucleotide differences for one species to another divided by the number of nucleotides of cytochrome b available for the comparison sequence.

Table 4 presents the cytochrome b nucleotide differences of the subject owl species. The Little Owl and the Eagle Owl differ by 197 nucleotides (18.9%), and are categorized as different genera, but the Eagle Owl and the Great Horned Owl, both of genus *Bubo*, differ by 115 nucleotides (11%). These differences are necessary to explain the differences in size, plumage, and other phenotype qualities which include instincts: sounds, mating habits, nest construction, and habitat choice. It is beyond reason to accept that these magnificent owls could be the result of accidental mutations which were selected out in only 870 years for the first three and 1600 years for the last two species of owls. The evolutionary scientists have estimated that the evolutionary processes took nearly 60 million years (Diniz-Filho, J.A.F. and Sant'Ana, C.E.R. 2000) to generate the varieties we have today in just South America. Those who accept owl speciation through natural selection, must realized that it would take full evolution processes racing at the speeds on the order of 60,000 times as fast as the rate of consensus evolutionary thinking.

Table 4 Differences in cytochrome b Nucleotides for Owls

	Great Owl (AF168106.1)	Little Owl (AJ003947)	Barn Owl (FJ588458.1)	Eagle Owl (AJ003956)	Spotted Eagle Owl (AJ003950.1)
Great Owl (AF168106.1)		183/1041 (17.6%)	240/1041 (22.4%)	115/1071 (11.0%)	97/1041 (9.3%)
Little Owl (AJ003947)	183/1041 (17.6%)		247/1041 (23.7%)	197/1041 (18.9%)	194/1041 (18.6%)
Barn Owl (FJ588458.1)	240/1041 (22.4%)	247/1041 (23.7%)		226/1041 (21.7%)	264/1041 (25.3%)
Eagle Owl (AJ003956)	115/1071 (11.0%)	197/1041 (18.9%)	226/1041 (21.7%)		101/1041 (9.7%)
Spotted Eagle Owl (AJ003950.1)	97/1041 (9.3%)	194/1041 (18.6%)	264/1041 (25.3%)	101/1041 (9.7%)	

Note: The GenBank (Benson DA, 2007) sequence numbers for each subject is in parenthesis. Alignment and identities were performed by BLAST- Basic Local Alignment Search Tool (Altschul, 1990) and verified using Micro-Soft Excel. When sequences were of different lengths, only the aligned sections were considered. The numbers represent the number of nucleotide differences for one species to another divided by the number of nucleotides of cytochrome b available for the comparison sequence.

Table 5a presents some comparisons to demonstrate the extent of genetic diversity in owls. Table 5b documents the data used in Table 5a.

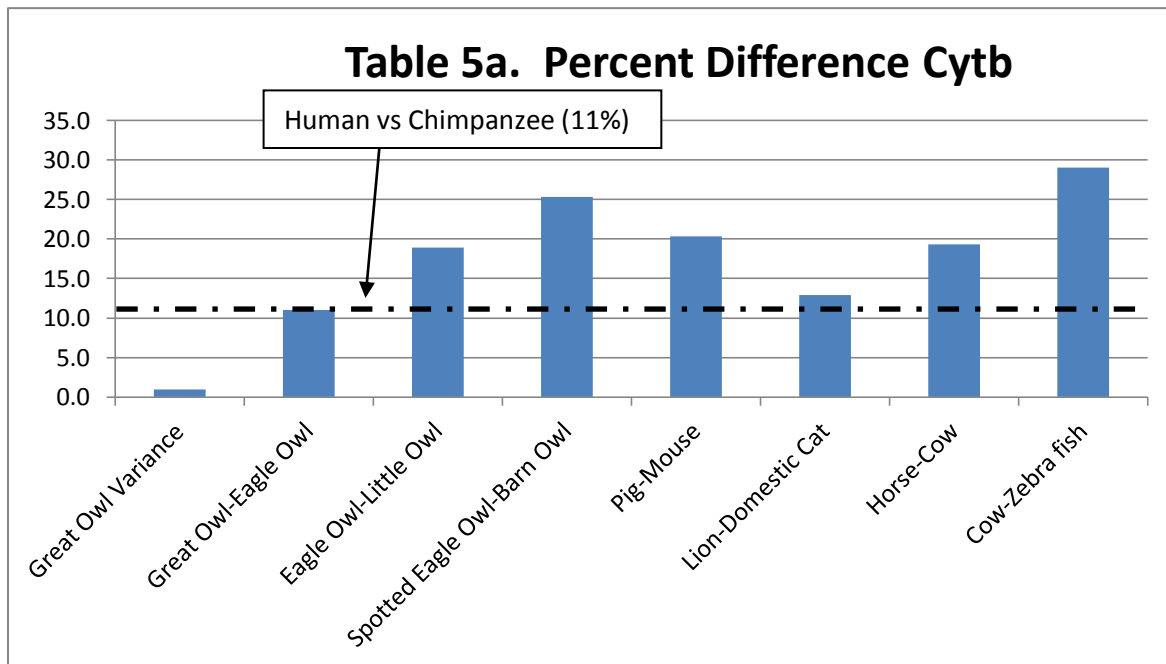


Table 5b. Comparison of Kinds	BLAST Identities
Human(NC_012920.1) to Chimpanzee (NC_001643)	11.0
Great Owl to Great Owl (See Table 4)	1 percent or less
Great Owl (AF168106.1) to Eagle Owl (AJ003956)	11.0
Eagle Owl (AJ003956) to Little Owl (AJ003947)	18.9
Spotted Eagle Owl (FJ003950.1)-Barn Owl (FJ588458.1)	25.3
Pig (GQ338965) to Mouse (JX457724.1)	20.3
African Lion (AF384818) to Domestic Cat (AB194817.1)	12.9
Horse (HQ439448) to Cow (EU807948)	19.3
Cow(NC_013996.1) to Zebra Fish(NC_002333)	29.0

Note: The GenBank (Benson DA, 2007) sequence numbers for each subject is in parenthesis. Alignment and identities were performed by BLAST - Basic Local Alignment Search Tool (Altschul, 1990) and verified using Micro-Soft Excel. When sequences were of different lengths, only the aligned sections were considered. The numbers represent the number of nucleotide differences for one species to another divided by the number of nucleotides of cytochrome b available for the comparison sequence.

Tables 5a. and 5b. show that even owls of the same genus have diversity commensurate with the human compared to chimpanzee variation (11%). So, considering that speciation was involved in generating these owls is tantamount to saying that the ark not need carry a chimpanzee since they could evolve from Noah, or worst yet that Noah was a chimpanzee and evolved to modern humanity. This is a severe logic problem.

It appears from this owl analysis that it is not possible to decide which creatures were on the Ark without having DNA.

3.4 The Dove

There are over 300 species of doves in the world. Table 6 presents the cytochrome b variation of the following five doves:

<u>Common Name</u>	<u>Family</u>	<u>Genus</u>	<u>Species</u>
Turtle Dove	<i>Columbidae</i>	<i>Streptopelia</i>	<i>turtur</i>
Spotted Dove	<i>Columbidae</i>	<i>Streptopelia</i>	<i>chinensis</i>
Speckled Pigeon	<i>Columbidae</i>	<i>Columba</i>	<i>guinea</i>
Slender Billed Cuckoo Dove	<i>Columbidae</i>	<i>Macropygia</i>	<i>amboinensis</i>

Cloven Feathered Dove

*Columbidae**Drepanoptila**holosericea*

Three varieties of doves are mentioned in the Bible and their Hebrew names are : yônah, tôr tôr, and gôzâl gôzâl. It is not known exactly which doves these are compared to our modern classifications, but the tôr tôr is most probably the turtledove; the gôzâl gôzâl is possibly close to the speckled pigeon; and the yônah is some dove, but it is not clear which one. However, it is known that there were at least three varieties of doves approximately 378 years after the flood (Genesis 8:8 and 15:9). Table 5 shows that within the *Streptopelia* genus a variance of at least 107 nucleotides out of 1045 nucleotides (10.2%) exists; and, between the genera, a variance of at least 152 nucleotides (14.5%) exists. This again, if one accepts speciation after the flood, this is core evolution at extreme rates, in this case at least 4,500 times that of evolutionary time frames - see paragraph 2.7

Table 6 Differences in cytochrome b Nucleotides for Dove

	Turtle Dove	Spotted Dove	Speckled Pigeon	Slender Billed Cuckoo Dove	Cloven Feathered Dove
Turtle Dove (<i>Streptopelia turtur</i>) (AF353405)		107/1045 (10.2%)	141/1045 (13.5%)	137/1034 (13.2%)	152/1044 (14.5%)
Spotted Dove (<i>Streptopelia chinensis</i>) (AF483341)	107/1045 (10.2%)		103/1044 (9.9%)	116/1054 (11.0%)	142/1044 (13.6%)
Speckled Pigeon (<i>Columba guinea</i>) (AF279708)	141/1045 (13.5%)	103/1044 (9.9%)		117/1035 (11.3%)	150/1044 (14.4%)
Slender Billed Cuckoo Dove (<i>Macropygia amboinensis</i>) (EF373283)	137/1034 (13.2%)	116/1054 (11.0%)	117/1035 (11.3%)		153/1035 (14.8%)
Cloven Feathered Dove (<i>Drepanoptila holosericea</i>) (AF483345.1)	152/1044 (14.5%)	142/1044 (13.6%)	150/1044 (14.4%)	153/1035 (14.8%)	

Note: The GenBank (Benson DA, 2007) sequence numbers for each subject is in parenthesis. Alignment and identities were performed by BLAST- Basic Local Alignment Search Tool (Altschul, 1990) and verified using Micro-Soft Excel. When sequences were of different lengths, only the aligned sections were

considered. The numbers represent the number of nucleotide differences for one species to another divided by the number of nucleotides of cytochrome b available for the comparison sequence.

The dove cytochrome b differences are approximately the same difference as between human and chimpanzee (11.2 % - GenBank refs. NC_001643 NC_012920.1) .

4.0 Conclusions/Hypothesis

The results of this investigation support the Biblical statement of Genesis 7:14 ". . . and every fowl after his kind, every bird of every sort." All of the birds in this investigation were distinct and differed from one another sufficiently to secure a birth on the Ark. Also, these results support the long held stance of creationists that the species are distinct with no intermediate forms (Morris, 1974).

There is no known mechanism that could explain the genetic diversity of the post-flood birds; even evolution, if it did exist, could not function quickly enough to explain the genetic diversity in the Biblical time frame. Any attempt to explain this genetic diversification by natural processes, such as speciation, is indefensible faced with the DNA evidence.

The following hypotheses are submitted which are in tune with the DNA evidence and the Bible, requiring no reliance on evolutionary principles.

1. The DNA of the original creation was reset to accommodate the new ecosystem.

This is in agreement with the fossil record, the cytochrome b genetics presented in this paper and the Bible. The fossil record is clear, many existing species lived before the flood, but they were somewhat different: usually in size or small differences in bone structure. The genetic reset hypothesis explains this and can be generalized as follows: the genetics of pre-flood creatures are different than the genetics of modern creatures; this was accomplished by God's voice, speaking the required changes into the creation preparing it for the new covenant and the new eco-system. One of the best examples of this is in pre-flood man (Genesis and Genetics, 2011)..

2. The occupants of the Ark were generally in a deep sleep.

The Ark's design is perfectly suited to the deep sleep scenario and in God's own words the goal was to "keep them alive" (Genesis 6:19). There are examples of God using deep sleep in the Bible to make physiological changes, to establish a new covenant, and to protect prey from predator; all of which apply to the state of affairs on the Ark. Contrary to common perception, life on the Ark may have been very peaceful with all of the animals asleep; this presents a comforting picture: all the reset animal DNA necessary to replenish the world with its new eco-system, in one peaceful little Ark.

3. Divine wisdom and creativity

God created all things in six days, it should not be difficult to accept that He had the perfect design for the Ark and made the perfect provisions for those on it; He is not only a divine creator, but He is also full of mercy (Psalm 100:5, et. al.). When God does something it is done right; the Bible implies that not one animal was lost, during the voyage of Noah's Ark (Genesis 8:19). Just

looking at the Ark design should be enough to lead one to believe the animals, and possible Noah, were in a deep, merciful sleep.

4. Defining "Kinds" - Rule of Thumb

From this very limited research, it appears that a kind will vary in cytochrome b from its own kind by generally one percent or less; if the variance is 4 percent or more, the subjects are different "kinds;" and any variance between 1 percent and 4 percent are in a gray area and would need more investigation using additional genes.

4.0 References

Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." *J. Mol. Biol.* 215:403-410.

Benson DA, Karsch-Mizrachi I, Lipman DJ, Ostell J, Wheeler DL. *Nucleic Acids Res.* 2007 Jan; 35(Database issue):D21-5.

Brelands, K., and Brelands, M. (1961). The misbehavior of organisms. *Am. Psychol.* 16, 681-684.

Carey HV, et. al, (2003) Mammalian hibernation: cellular and molecular responses to depressed metabolism and low temperature., *Physiol Rev.* 2003 Oct;83(4):1153-81.

CHEN QL, TANG XS, YAO WJ, LU SQ. Bioinformatics Analysis the Complete Sequences of Cytochrome b of *Takydromus sylvaticus* and Modeling the Tertiary Structure of Encoded Protein. *Int J Biol Sci* 2009; 5(6):596-602. doi:10.7150/ijbs.5.596.

Collins, F.,S., 2006, *The Language of God; A Scientist Presents Evidence for Belief*, Free Press.

Cornell Lab of Ornithology, 2011, http://www.allaboutbirds.org/guide/browse_tax/55/

Deane P. Lewis, 1998, *The Owl Pages* - internet <http://www.owlpages.com/index.php>)

Diniz-Filho, J.A.F. and Sant'Ana, C.E.R. (2000). PHYLOGENETIC CORRELOGRAMS AND THE EVOLUTION OF BODY SIZE IN SOUTH AMERICAN OWLS (STRIGIFORMES), *Genetics and Molecular Biology* vol.23 n.2 .

Feldman, C. R. & Omland, K. E. (2005). Phylogenetics of the common raven complex (*Corvus:Corvidae*) and the utility of ND4, COI and intron 7 of the β -fibrinogen gene in avian molecular systematics. — *Zoologica Scripta*,34, 145–156.

Genesis and Genetics (2011). *Neanderthal and His Biblical Identity*,. Published on www.genesisandgenetics.org.

- Howell, Neil, et. al., (2000). Transmission of the human mitochondrial genome. *Human Reproduction*, vol. 15, (Suppl. 2), pp 235-245.
- Johnson, G. E. Hibernation in mammals. *Quart. Rev. Biol.* 6:439-461, 1931.
- Legros F, Malka F, Frachon P, Lombes A, Rojo M. Organization and dynamics of human mitochondrial DNA. *J Cell Sci* 2004; 117:2653–2662.
- Li, M., et. al. (2010). Detecting heteroplasmy from high-throughput sequencing of complete human mitochondrial DNA genomes. *Am J Hum Genet.* 2010 Aug 13;87(2):237-49.
- Marzluff, John M., Angell, Tony. (2007) *In the Company of Crows and Ravens*, Yale University Press. pp. 86-87.
- McCracken KG, Sheldon FH.(1997). Avian vocalizations and phylogenetic signal. *Proc Natl Acad Sci USA.* 1997;94:3833–3836.
- McCracken, K.G., 1998, *Molecular and Osteological Heron Phylogenies: Sources and Incongruence.*, *The Auk* 115(1):127-141.
- Morris, H. M., 1974, *Scientific Creationism*, Master Books, Green Forest, AR., pp 78-80.
- Nabholz, Benoit, 2009, The erratic mitochondrial clock: variations of mutation rate, not population size, affect mtDNA diversity across birds and mammals, *BMC Evol Biol.* 2009; 9: 54
- Nottebohm, F. (1970). Ontogeny of bird song. *Science* 167, 950-956.
- Nottebohm, F. (1977). Asymmetries in neural control of vocalization in the canary In "Lateralization of the Nervous System" (S. Harnard, ed.). Academic Press, New York and London.
- Nottebohm, F. (1979). Origins and mechanisms in the establishment of cerebral dominance. In "Handbook of Behavioral Neurobiology" (M. Gazzaniza, ed.). Plenum, New York.
- Oard, M. (2007). Where does the Ice Age Fit?, *Answers in Genesis*.
- PAYNE R. B. and RISLEY C. J. (1976). *Systematics and Evolutionary Relationships Among the Herons (Ardeidae)*, MUSEUM OF ZOOLOGY, UNIVERSITY OF MICHIGAN
- Polikanov YS, et. al., (2012) How hibernation factors RMF, HPF, and YfiA turn off protein synthesis. *Science*, 2012 May 18;336(6083):915-8.
- Rivolta MN, Holley CM. Asymmetric segregation of mitochondria and mortalin correlates with the multi-lineage potential of inner ear sensory cell progenitors in vitro. *Brain Res Dev Brain Res* 2002;133:49–56.
- Sibley, Charles G., and Monroe, Burt L., (1991). *Distribution and Taxonomy of Birds of the World*, Yale University Press.
- St. John, Justin C., (2010). Mitochondrial DNA transmission, replication and inheritance: a journey from the gamete through the embryo and into offspring and embryonic stem cells. *Human Reproduction Update*, Vol.16, No.5 pp. 488–509, 2010

Theresa A. Spradling, Mark S. Hafner, and James W. Demastes (2001) DIFFERENCES IN RATE OF CYTOCHROME-*b* EVOLUTION AMONG SPECIES OF RODENTS. *Journal of Mammalogy*: February 2001, Vol. 82, No. 1, pp. 65-80.

Wesley C. Warren, et. al. (2010), The genome of a songbird, *Nature* 464, 757-762

Woodmorappe John, (1996) Noah's Ark: A Feasibility Study, El Cajon: Inst. for Creation Research, 1996.