



# Types of Animal Form

## Evidence from nature accords with the Creation account

### Lindsay Thompson PhD

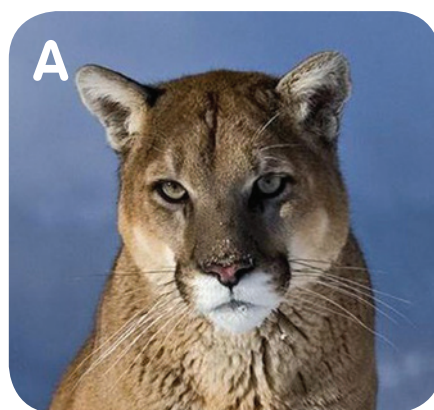
The great diversity of animal forms we see today is often presented as being united together in a “phylogenetic tree” originating from a single, primitive ancestor. This view appears to be at loggerheads with the Creation account in Genesis, in which complex animal forms (such as birds) were present at the beginning. However, the following account indicates that the evidence from nature compellingly supports the Creation narrative.

#### Section 1:

##### The Evidence Base – Hybridization data.

Cross-breeding between species (i.e. inter-specific hybridization) is very common. Abundant data for this exists for birds, mammals, plants and invertebrates such as butterflies. For instance, at least 1 in 10 species of bird hybridize with another species (Grant and Grant 1992). Over 14,000 inter-specific hybrid rhododendrons have been registered with the Royal Horticultural Society. Analysis of such data can indicate which species and genera may be united by hybridization. For hybridization between species to produce live offspring at all, they must share an embryological machinery that is compatible when egg and sperm of the two parent species unite and full development ensues. Thus this method (which employs hybridization data) rests on an empirical basis (i.e. evidence-based), in which the members of a group must share a common developmental plan. Below are a few examples of groups distinguished in this way, which can be

denoted as hybridization groups (HGs). The data is drawn from sources including academic journals, breeders’ records, museum specimens, International Zoo Yearbook records and field reports, cited in the following publications: Mammalian Hybrids (Gray, 1972); Bird Hybrids (Gray, 1958); and Avian Hybrids (McArthur, 2006).



**Fig 1.** Various species within the cat family can cross-breed (hybridize), e.g. A. *Puma concolor* (puma) x B. *Panthera pardus* (leopard). This is also one of many instances of hybridization between species in different genera.

A © Presumed to be in the public domain  
B © Arno Meintjes

**The Cat family (*Felcidae*).** Hybridization unites not only different species, but also links several cat genera together. For instance, two sub-families (Pantherinae and Felinae) are generally recognized within this family (Wilson and Reeder, 2005). However, the above cross links together these sub-families (according to the taxonomy recognized by Zhang and Zhang, 2013), indicating they share a common developmental plan.

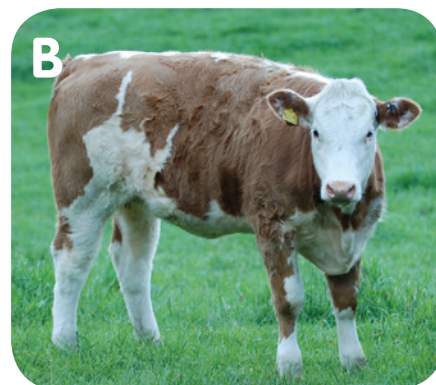
Some of these crosses are fertile, e.g. *Prionailurus bengalensis* (leopard cat) x *Felis catus* (domestic cat). Indeed, this cross was the basis for generating a new pedigree domestic breed, the Bengal cat. When a Ruddy Abyssinian cat was bred with a Seal Point Siamese, then backcrossed to another Siamese in the next generation, the surprising outcome was a spotted cat resembling an extinct Egyptian breed. This is now another accepted new rare breed known as the oicat (Figure 2), because of its resemblance to the ocelot. Neither parent breeds were ever known to express such spots. The oicat spots are an example of an atavism – the reappearance of a character known in distant ancestors and not seen in the parents or recent ancestors (Hall, 2010).

#### Old World Monkeys (*Cercopithecoidea*).

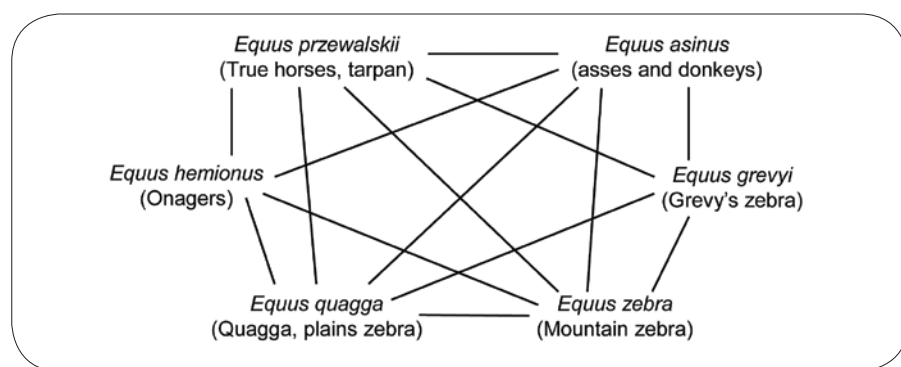
Eight out of 9 genera are connected through hybridization. This links together diverse forms such as the baboons, macaques, mandrills and Barbary apes.



**Fig 2. Ocicat:** Bred from 2 pedigree breeds, neither of which express these spots, indicating that the parents possess a hidden ancestral character known as an atavism. © Helmi Flick



**Fig 4.** Hybridization can occur between different genera within Bovidae, e.g. A. Bison (Genus: *Bison*) x B. Domestic cattle (Genus: *Bos*). A. © US Fish and Wildlife Service B. © Lindsay Thompson



**Fig 3.** Hybridization (indicated by lines) links together all of the species in the horse family (Equidae).

**The Horse family (Equidae).** All of the species in this family are united by hybridization, i.e. horses, donkeys, asses and zebras hybridize together (Figure 3). They do not hybridize with their nearest taxonomic neighbours (the tapirs and rhinoceri). This data, combined with their distinctive horse-like form, such as numerous skull and dental characters (Anderson and Knox Jones, 1984) clearly separates them from these neighbours.

#### **Bovidae.**

Hybridization unites yaks, bison, zebu and cattle (i.e. 2 genera – *Bison* and *Bos*, Figure 4)

#### **Cervidae.**

Deer-like species from 6 different genera can interbreed, linking together the elk, fallow deer, roe deer and chital. This also links 2 of the 3 sub-families together.

#### **Ursidae.**

Hybrids between 6 of the 8 species of

bears can be found. For instance, the polar bear, American black bear, Asiatic black bear, sloth bear and sun bear are known to cross-breed. This also interconnects 4 of the 6 genera recognized by Wilson and Reeder (2005).

#### **Ducks, Geese and Swans (Anatidae).**

In general, the number of species able to hybridize together can be quite large. For instance, 128 species (81 %) of all Anatidae species hybridize. Twenty percent of all these hybrids are fertile, and over 30% of them also connect several tribes (a taxonomic rank between genus and family) (Scherer and Hilsberg, 1982).

#### **Storks (Ciconiidae).**

Seven of the 19 species of storks hybridize, uniting species ranging from those with slender to massive bills. Again, no hybridization between storks and other bird families is evident.

#### **Pelicans (Pelicanidae).**

Six out of 7 of all pelican species can hybridize together, but hybridization between pelican and any other groups is unknown.

#### **Implications.**

These HGs listed above become apparent simply by collating the hybridization data. Appraisal of other hybridization data indicate over 100 further HGs can be obtained, just for birds and mammals alone, with many more likely among plants, and other taxa such as snakes. Some of these are analysed in more detail elsewhere (e.g. Crompton and Winkler, 2006; Hennigan, 2005, 2010). From this data analysis, the following themes emerge:

1. There is a high degree of hybridization within each HG, but none whatsoever outside of it, which suggests a deep natural division between an HG and any proposed neighbours.





- The hybridization data accords with the outward appearance or form shared by members of the HG, for instance, the easily recognized “cat-like” form (Sicuro and Oliveira, 2011) shared by all cats united by hybridization. This is exactly what should be expected if the developmental plan of the hybridizing parents is compatible, which in turn produces the form typical of the group.



**Fig 5.** The stork (A) and pelican (B) “*min*” (kind) found in the Bible may represent a higher taxonomic unit such as the stork and pelican (B) families, rather than just species. “Reproducing after their own kind” can imply maintaining the basic ground-plan of that particular *min* over successive generations, whilst allowing variation within the kind. There is evidence to support this. © Pixabay, © US Fish and Wildlife Service in the public domain

- Although members of the HG have a common essence of form, hybridization often links species with quite variable morphology, suggesting that the developmental plan is sufficiently compatible to generate hybrids between the varying forms throughout the HG.
- The presence of atavisms is suggestive of a hidden ancestral reservoir of genetic potential distributed in the HG, suppressed until both parents possessing the hidden alleles breed together, allowing these alleles to recombine.

According to Hall (1984), atavisms are the visible sign of an enormous hidden potential for morphology change possessed by all organisms, which would explain the capacity for members of the HG to exhibit a range of variations in form. Large subsets of genes, including transcriptional regulators, are known to be reprogrammed during hybridization, which could be driving the generation of new forms occurring during rapid speciation (Tsiantis and Hay, 2003). This could provide the mechanism for expression of this ancestral genetic reservoir.

- The nearest taxonomic equivalent of the above HGs ranges from the genus to the family or super-family level.

## Section 2: The Genesis Kinds.

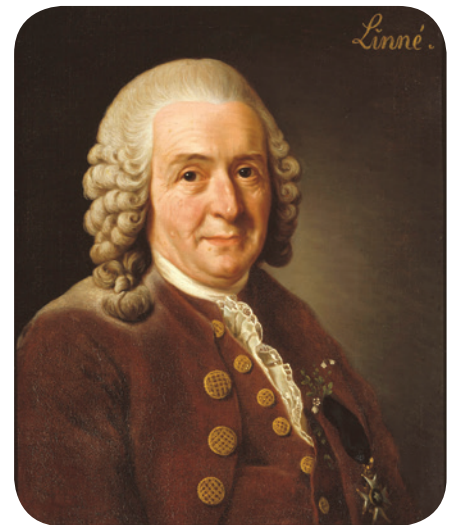
What exactly *were* the Genesis kinds? The original Hebrew word employed in the Bible to describe the animals is *min*. Examples of *min* can be found in Leviticus 11 and Deuteronomy 14:13-18, which list animals using collective words such as the hawk, eagle, owl, heron, stork, seagull and pelican. In these accounts there is a recurrent phrase referring to the particular animal “according to its kind.” Also the Genesis account adds that God created these animals to “*reproduce* after their own kinds”. Moreover, the word *min* always includes the *lamedh* preposition, which indicates reference to a formal standard (Williams, 1967). Together these ideas suggest that the *min* are distinct units of creation (Jones, 1972a).

### Understanding the Biblical text.

Although there are some uncertainties in the correct translation of the animal names

from the original Hebrew, a number of key points emerge:

- There is a real sense conveyed that each word in the list represents a wider group of animals, the members of which reproduce “according to its kind”. Crucially, if this were just a species list, it would surely be much more exhaustive, for there to be no uncertainties as to which were the clean and unclean animals. With the rich species diversity in the Palestinian lands then even more than now, a species list would number in the hundreds.



**Fig 6.** Linnaeus (1707–1778) the founding father of taxonomy, realized that the Bible’s “Kinds” represented higher taxonomic groups than species, and that species could freely hybridize within these kinds. Darwin knew this, but ignored it, imposing his own mistaken view of species fixity on the Bible. His “evidence for variation” thus appeared to demolish the credibility of the Bible. © Painting by Alexander Roslin, National Museum of Sweden

- Most of the Hebrew words cited in those passages provide the identifier for its particular *min*, (although some appear to be terms for several *min*, e.g. ‘*anaphah*’ [long-legged wading birds]). It appears that Moses chiefly has to name each *min*, not all the various members of each *min*, to convey his meaning.
- Some of the *min* listed can be translated with more confidence. Examples include the stork and pelican (Fig. 5). These birds are mentioned elsewhere in the Scriptures, and various authors are in agreement regarding their identity in translation.

From a biological perspective, in section 1 it was demonstrated that inter-specific hybridization within each of the stork and

pelican families provides evidence for uniting them in their respective HGs. This is consistent with the idea that the stork and pelican *min* named in the Scriptures refer to a higher taxonomic unit. It is also consistent with the notion that the members of a *min*, when they breed would reproduce with fidelity the basic ground-plan of that particular *min*.

4. The idea of “fixity of species” is nowhere to be found in Leviticus and Deuteronomy. Indeed the above arguments suggest the opposite – that variation is possible within a *min*. Both “fixity of species” and “species” were alien concepts to the Middle East culture of Moses’ day, as we shall now see.

### Who needs fixity of species? Not the Bible, but Darwin!

Darwin considered that variation provided evidence for evolution. He contrasted this with the concept of fixity of species. Where did this concept arise from?

- i. **Fixity** This sprang from the ancient Greeks, not the Bible, being associated with the Platonic world of perfect and eternal, unchanging or *immutable* ideas.
- ii. **Species** When the Bible was translated into Latin, the Latin word for *min* chosen was “species”. However, this also originates from the Greek word “idea,” associated with fixity and immutability, different to the narrower meaning of the word today.

The great taxonomist, Linnaeus (Fig. 6), came to the conclusion that genera, not his species, were the important units of creation, and that the various species within a genus could freely hybridize to produce new species. In other words, they were mutable, not immutable. Many of the genera first described by Linnaeus have since been elevated to the higher taxonomic level of the family.

When Darwin was informed that Linnaeus had departed from his earlier belief that species are fixed or immutable, he seemed surprised by this. However, Darwin chose to ignore this point when he wrote “On the Origin of species.” In Darwin’s mind, any demonstration of variation refuted the fixity of species, and provided evidence in favour of his theory of evolution. He wrongly assumed that it was the Creation account that demanded species fixity, which he felt was contradicted by his observations of

variation, when he stated “*it is inexplicable on the theory of creation why a part should be liable to variation*” (Darwin, 1872). This did not represent fairly the thoughts of Linnaeus about speciation after God’s original creation by means of hybridization between species (Landgren, 1993). Thus a Greek view of fixity of species was wrongly imposed on the understanding of Genesis. The view that the Bible speaks of fixity is a straw man (Lester and Bohlin, 1986) set up in order to be easily refuted, and is perpetuated to this day.

### Conclusion

Firstly, there is sufficient data to indicate that hybridization unites groupings of animals which, for this to be so, must share the same plan of development, giving rise to a common type of body form between them. The forms do not vary gradually between one HG and its nearest neighbour. Rather, there are distinct gaps, so that the different forms are easy for even the layman to discern. These forms can be identified with the kinds or “*min*” described in various Biblical texts. This is based on examples of *min* which seem to represent a taxonomic unit higher than species, with each *min* denoting a common ground plan of form.

Secondly, the Biblical term “reproducing after their *min*” clearly suggests the ability for the ground plan to be maintained with fidelity, but crucially there is also the opportunity for variation within the *min*. This implies an in-built capacity for variation was created in the beginning, and is consistent with evidence, such as from atavisms, that ancestral reservoirs of genetic variation exist within life’s forms, which recombine to generate new variations in form.

The Genesis account declares that these *min* were created from the beginning. There is evidence to support this also. For instance, the distinctive body forms of the above groupings (e.g. the skin pouch and long beak of the pelicans) are already fundamentally the same as their modern counterparts when they first appear in the fossil record (reviewed by Gish, 1995). The marked absence of proto-forms before these in the fossil record led Gould and Eldridge (1972) to propose that nature’s forms must evolve in jumps, which occurred too fast to leave any fossil remains. But for advanced,

complex vertebrates such as the birds, to arrive without any trace is a very big jump indeed. An alternative is that the sudden appearance of these forms is consistent with the Biblical account, which states that these forms were created in the beginning. Evidence-based reasoning appears to be pointing in this direction. ■

### Dedication.

*This article is dedicated to Annika Landgren*

### References

- Anderson, S. and Knox Jones, J., Jr. (1984). *Orders and families of recent mammals of the World*. N.Y. John Wiley and Sons.
- Crompton, N.E.A. and Winkler, N. (2006). Die Katzenartigen—ein klar abgegrenzter Grundtyp, *Studium Integrale J.* 13, 68–72.
- Darwin, C. (1872). *The Origin of species*. 7th ed. London: John Murray.
- Eldredge, N. and Gould, S.J. (1972). Punctuated equilibria: an alternative to phyletic gradualism. In Schopf, T. J. M., and Thomas, J.M. eds. *Models in Paleobiology*, pp. 82–115. San Francisco: Freeman, Cooper.
- Gish, D. (1995). *Evolution: the fossils still say no*. pp. 142–145. El Cahon, Calif., USA: ICR.
- Grant, P.R. and Grant, B.R. (1992). Hybridization of bird species. *Science* 256, pp 193–197.
- Gray, A. P. (1958). *Bird Hybrids*. England: Commonwealth Agricultural Bureaux.
- Gray, A.P. (1972). *Mammalian Hybrids*. England: Commonwealth Agricultural Bureaux.
- Hall, B.K. (1984). Developmental mechanisms underlying the formation of atavisms. *Biol. Rev. Camb. Philos. Soc.* 59, pp. 89–124.
- Hall, B.K. (2010). Atavisms. *Current Biol*, 20 (20), R871.
- Hennigan, T. (2005). An initial investigation into the baraminology of snakes: Order—Squamata, Suborder Serpentes. *C.R.S.Q.* 42, pp. 153–160.
- Hennigan, T. (2010). The case for holobaraminic status in bears (family Ursidae) and the implications within a creation model of ecology. *C.R.S.Q.* 46, pp. 271–283.
- Jones, A.R. (1972a). A general analysis of the Biblical kind (*min*). *C.R.S.Q.* 9(1), pp. 5357.
- Jones, A.R. (1972b). Boundaries of the *min*: an analysis of the mosaic lists of clean and

## Editorial: Continued.

coding mechanisms are *not* themselves information. Given the paper, the pen, the language, someone still has to write the book! No amount of evolutionary juggling can deal with this logical impasse.

The point of these two illustrations is that evolution is both statistically and logically impossible. By contrast, the evidence of creation and the power of the creator is all around us. The reasons for unbelief are spiritual, not scientific.

Re-reading that first editorial, and the guest editorial from Nigel Cameron, the original editor of *Biblical Creation*, it is extraordinary – and encouraging – to see the same themes persisting. Our original focus and message have not changed, but clearly the numbers of Christians who have regained confidence in the Word of their creator has grown enormously, which gives us cause to rejoice. However as John Peet points out in his last editorial, we need to get the message out to the millions who are totally ignorant of the bible's teaching, for creation is an integral part of the good news: that original sinless relationship with our creator can be restored!

We are now on the verge of a new format again for this publication, for a new age of communication. In *Origins 1* we published an article on computers – now the computer has become the main vehicle of worldwide communication. The truths may be couched in a different medium, but they themselves do not change. They may have assumed a new importance in the eyes of the world (if only as something to be resisted) but their eternal significance has not changed. There may be a wholesale departure in the Western world from belief in the Word of God, but that Word still stands unchangeable, as a witness against our apostasy.

**Mike G Matthews**

unclean animals. *C.R.S.Q.* 9(2), pp. 114-123.

Landgren, P. (1993). On the origin of species: ideological roots of the species concept. In Scherer, S. ed. *Typen des Lebens*, pp. 47-63. Berlin: Pascal Verlag.

Lester, L.P. and Bohlin, R.G. (1986). *The natural limits to biological change.* Zondervan publishing.

McCarthy, E. (2006). *Handbook of avian hybrids of the world.* England: Oxford Univ. Press.

Scherer, S. and Hilsberg, T. (1982). Hybridisation and relationships in the Anatidae – a taxonomic and evolutionary consideration. *Journal für Ornithologie* 123, pp. 357-380.

Sicuro, F. L. and Oliveira, L. F. B. (2011). Skull morphology and functionality of extant Felidae (Mammalia: Carnivora): a phylogenetic and evolutionary perspective. *Zool. J. Linnean Soc.* 161, pp. 414-462.

Tsiantis, M. and Hay, A. (2003). Comparative plant development: the time of the leaf? *Nature Rev. Genet.* 4, pp. 169-180.

Williams, R.J. (1967). *Hebrew syntax: an outline.* Univ. Toronto Press.

Wilson, D.E. and Reeder, D.M.(eds). (2005). *Mammal species of the world. a taxonomic and geographic reference* (3rd ed). Johns Hopkins Univ Press.

Zhang, W.Q. and Zhang, M.H. (2013). Complete mitochondrial genomes reveal phylogeny relationship and evolutionary history of the family Felidae. *Genet. Mol. Res.* 12 (3), pp. 3256-3262.