Doing the Karyotype Shuffle: A Survey of Intrabaraminic Variation in Karyotypes and Chromosome Numbers

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Abstract

Many authors have expressed concern for the inadequacy of the current creation model to explain the rapid diversification of animals post-Flood. This study reviews the latest research on interchromosomal changes within terrestrial mammalian baramins bringing to light one aspect of this diversification, chromosome numbers. It takes a critical look at diploid variations within a baramin and connects the findings to the current creation model of diversification and to baraminology. The results were surprising showing that chromosome number change within this sampling of nine baramins seems to be the rule rather than the exception.

Introduction

Karyotypes and their chromosome numbers have been considered stable. Check any biology text. For example, the diploid number for dogs is 2n =78, cats, 2n = 38, and horses, 2n = 64 (Gregory 2010). However, Lightner (2006) shows that chromosome rearrangements are dynamic by pointing out that members of the same monobaramin can exhibit a range of chromosome numbers. For example, the Indian muntjac (2n=6 in females and 7 in males) and Reeves muntjac (2n=46) have been known to hybridize. Domestic sheep (2n=54) are inferred as having three different translocations derived from an ancestral karyotype preserved in domestic goats (2n=60). Both species are considered to be in the same monobaramin based on hybrid data. Hennigan (2009a) identifies the monobaramin Ursidae as having eight genera: six with diploid number 2n = 74, one with 2n = 52, and one with 2n = 42.

Based on incongruities such as these, many authors expressed concern for the inadequacy of the current creation model of diversification to explain the chromosome number variety and other rapid changes within terrestrial mammalian baramins (Lightner 2006; Wood 2002, 2008a; Hennigan 2009a). The model states that natural selection (microevolution) and Mendelian genetics act on mutations and inherent variability within a kind to produce the diversity of life. Wood (2002) set the stage for a creation model change with a comparison of the three widely used creationist’s speciation explanations: genetic changes through mutations or recombination, hybridization, and the splitting of diverse gene pools. He points out that these mechanisms “are inadequate to explain diversification” (p. 11). He shows through inference that the identified baramin Felidae diversified within a few hundred years after the Flood. Wood (2008a) further argues that family Equidae represents a monobaramin or “created kind” and that rapid post-Flood diversification of the horse kind into the modern horse took place within a period of about 400 years.

The results of studies like these emphasize the need for further research to account for marked and rapid change seen in the past but not, at least on the same scale, in the present. This change includes chromosome numbers as the family Equidae has a range of diploid numbers from 2n=32 to 2n=66 with a total of 10 different karyotypes represented (Bedinger 2010).

The question then presents itself – within the baramins identified thus far in the literature, how many have variations in karyotype and to what extent do these involve changes in diploid number? In keeping with the current line of investigation initiated by Lightner (2006) in karyotype variability within baramins, this study focused on interchromosomal (between chromosomes), particularly fusions and fissions, as opposed to intrachromosomal
Table 1. Chromosome number diversity within baramins. Families whose baraminological status has been studied are listed with the diploid chromosome numbers (both the range and known numbers), number of species with a particular diploid number (in parentheses if greater than one) as reported in the journal articles cited in the text, and the techniques used to analyze the baraminological status. Diploid numbers separated by a slash represent polymorphisms for that species. In order to demonstrate the scope of diploid range, supplemental chromosome numbers marked with an asterisk were obtained from the Animal Genome Size Database (Gregory 2010) and Atlas of Mammalian Chromosomes (O’Brien et al. 2006). Holobaramins are marked with (H) and monobaramins are marked with (M).

<table>
<thead>
<tr>
<th>Baramin</th>
<th>Diploid Range</th>
<th>Diploid Number (2n)</th>
<th>Method of Baramin Determination</th>
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<tr>
<td>Bovini (M)</td>
<td>46-60</td>
<td>46, 48, 50, 52, 58, 60 (5)</td>
<td>Hybridization; inferences based on embryology</td>
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<td>Mormoopidae (H)</td>
<td>38-38</td>
<td>38</td>
<td>BDC analysis***</td>
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<td>Ursidae (H)</td>
<td>42-74</td>
<td>42 (1), 52 (1), 74 (6)</td>
<td>Hybridization; exception: giant panda 2n=42</td>
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<td>Cingulata (H)</td>
<td>38-64</td>
<td>38, 50*, 58*, 60, 62 (2), 64</td>
<td>BDC analysis</td>
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<td>Canidae (M)</td>
<td>34-78</td>
<td>34 + B’s, 36, 38+Bs, 50 (2), 54 + B’s, 64, 66, 72**, 74, 76**, 78 (4)*</td>
<td>Hybridization; exceptions: Canis does not hybridize w/ Vulpes (Gray, 1972)</td>
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<tr>
<td>Camelidae (M)</td>
<td>74-74</td>
<td>74 (6)</td>
<td>Hybridization</td>
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<tr>
<td>Equidae (M)</td>
<td>32-66</td>
<td>32, 44/45, 46, 52/51, 54/55, 56/55, 62/63/64, 62, 64, 66</td>
<td>Hybridization</td>
</tr>
<tr>
<td>Cercopithecinae (M)</td>
<td>42-84</td>
<td>42 (14), 48**, 54 (2), 58*, 60 (7), 66* (2), 70**, 72**, 84*</td>
<td>Basic Type defined from hybridization (Hartwig-Scherer, 1993)</td>
</tr>
</tbody>
</table>

*Supplemental chromosome numbers from Animal Genome Size Database
** Supplemental chromosome numbers from Atlas of Mammalian Chromosomes
***BDC: Baraminic distance correlation

(within chromosomes) rearrangements. To reduce the number of genetic variables only baramins of terrestrial mammals were examined as they represent descent from a single pair of animals disembarking from the Ark (with the exception of clean animals which came on by sevens, Genesis 7:2). Identified baramins were obtained from the latest published list found in Animal and Plant Baramins (Wood 2008b) and confirmed with updated articles whenever possible.

Diploid number is determined from an established karyotype which represents the arrangement of all the chromosomes from a cell on the basis of a universally agreed layout scheme that is specific for each species. Using banding techniques that were developed in the 1970s to improve visibility and thus identification of chromosomes, homologous chromosomes are paired according to the distinctive banding pattern of light and dark band lines and then arranged in descending order according to size. G-banding, a technique still routinely used, stains chromosomes fixed during metaphase with Giemsa. The resulting arrangement becomes standardized when agreed upon worldwide (Chowdhary & Raudsepp 2005). The technique Zoo-FISH “paints” specific DNA probes onto target chromosomes to discern homologies, especially across taxa.

With the assumption of common ancestry, this information is used to construct phylogenies, infer breakpoints for fusions through evolutionary time, estimate the number of rearrangements needed to convert the extant species to the putative ancestor at the time of divergence, and reconstruct an ancestral karyotype (Serov et al. 2005). Chromosomes are classified in several ways: metacentric,
having the centromere near the center; submetacentric, with the centromere obviously off-center; and acrocentric, where the centromere is found near the end of the chromosome (Figure 1).

All genetic information was obtained from literature dated 1983 or later as this represents the timeframe of accelerated growth in technological advances (Table 1).

Results

**Tribe Bovini: monobaramin (Lightner 2008a).** Lightner (2008a) examined intrabaraminic chromosomal morphology variation to assess its diversity and possible origin within the cattle monobaramin. Diploid numbers presented: 2n=60 (Bos taurus, B. indicus, B. banteng, Bison bison, Bison bonasus), 2n= 58 (Bos gaurus), 2n=52 (Syncerus caffer), 2n=50 (Bubalus bubalis), 2n=48 (Bubalus bubalis, Bubalus depressicomis), 2n=46 (Bubalus mindorensis). A Robertsonian translocation (centric fusion), a type of rearrangement commonly found in ruminants, has been identified in a number of domestic cattle breeds. Commonly referred to as “rob (1:29),” it joins the largest acrocentric chromosome, 1, to the smallest acrocentric, 29. Characteristics of this fusion include being monocentric and association with a variable chance of producing unbalanced gametes rendering carriers undesirable for breeding programs.

Though less widespread, numerous other Robertsonian translocations have been identified in domestic cattle such that all 29 autosomal chromosome pairs are documented as being involved in at least one such rearrangement. However, most of these are dicentric and very recent, as indicated by the fact that the majority were only found in one or a few related animals. Often different fusions involving a particular autosome can be found within a genus such as Bubalus. It is believed this would make it impossible for a fertile hybrid to form, if a hybrid could be produced at all. African buffalo (genus Syncerus) morphology is similar to that of other bison (genus Bubalus), however their combination of Robertsonian translocations is expected to result in reproductive barriers.

**Family Mormoopidae: holobaramin; Family Phyllostomidae: monobaramin (Wood 2008b).** Baker and Bickham (1980) extensively studied the families of Mormoopidae, containing the moustache and ghost-faced bats, and Phyllostomidae representing the leaf-nosed bats, to estimate the magnitude of evolutionary chromosomal change and correlate the degree of karyotype change with morphology differences. For family Mormoopidae, all six species evaluated possessed 2n=38. For family Phyllostomidae, the diploid numbers are as follows (parentheses indicate the number of species with the same diploid number): 2n=16 (1), 18 (1), 20 (2), 26 (2), 28 (3), 30 (10), 32 (12), 34 (1), 40 (2), 44 (1), 46 (1). Vampyressa pusilla and Uroderma bilobatum were the most karyotypically divergent phyllostomids. When making comparisons within genera, four species showed totally altered G-banding patterns such that each “karyotype is essentially not relatable to those of its closest relative” (p. 247) and the estimated number of rearrangements between them ranged from 14-20.

**Family Ursidae: monbaramin (Hennigan 2009b).** Nash et al. (1998) compared the ursine bears (black, brown, polar, sun, sloth, and Asiatic black bear), 2n=74 of mostly acrocentric chromosomes, to the spectacled bear, 2n=52 of mostly biarmed chromosomes, to the giant panda, 2n=42 of mostly biarmed chromosomes and finally to a putative ancestral carnivore karyotype, 2n=44. Using G-banding and Zoo-FISH with probes derived from human, cat, brown bear, spectacled bear and giant panda, they reconstructed the now extinct bear ancestor proposed karyotype as 2n=72 and identified the rearrangements that must have occurred up to the present extant bears.

**Suborder Cingulata: holobaramin (Wood 2008b).** G-banding techniques reveal the diverse karyotype of armadillos (Dasypodidae); for example, Chaetophractus villosus – 2n=60, Chaetophractus vellerosus – 2n=62, Dasypus hybridus – 2n=64, Zaedyus pichiy – 2n=62, and Tolypeutes matutus – 2n=38. To better characterize the evolution of armadillos, Lizarralde et al. (2005) analyzed the distribution of a conserved vertebrate telomeric sequence using G- and C-band and FISH on the above mentioned species (minus Tolypeutes matutus). Animals (10) were collected from several locations in Buenos Aires with a minimum of two armadillos representative of each species. The numbers of biarmed (not acrocentric) autosomal chromosome pairs found are as follows: C. villosus, 15; Z. pichiy, 15; C. vellerosus, 14; D. hybridus, 8. Based on G-banding, two chromosomes were conserved in all but D. hybridus and the X chromosome was conserved in all four species. Lizarralde et al. hypothesize that D. hybridus (2n=64 with 8 biarmed chromosomes) represents the armadillo ancestral karyotype. Lizarralde et al. further conclude that evolution of Dasypodidae occurred with a loss of genetic material (shown by G-banding).

**Family Canidae: monobaramin (Wood 2008b).** Graphodatsky et al. (2008) integrated previous canid maps with their current comparative maps of dog, dhole, fennec fox, gray fox, red fox and corsac fox to generate a Canidae phylogeny and reconstruct the likely Canidae ancestral karyotype. G-banding and Zoo-FISH provide most of the data. Diploid numbers were found as follows: dog and dhole, 2n=78; crab-eating fox, 2n=74; gray fox, 2n=66; fennec fox, 2n=64; Chinese raccoon dog, 2n=54 + B’s; arctic fox and kit fox, 2n=50; Japanese raccoon dog, 2n=38 + B’s; corsac fox 2n=36; red fox, 2n=34 + B’s. Only 4.9% of mammals have been described as having B chromosomes, which are composed of heterochromatin and segregate abnormally during meiosis (Pardo-Manuel de Villena 2005). Zoo-FISH chromosome
painting showed dog and dhole have identical karyotypes, one dog probe corresponded to one dhole chromosome. Most dog probes hybridized to fennec fox and gray fox chromosomes in one or two segments. All red fox probes split into segments on different corsac fox chromosomes; not one shared a single entire autosome even though they are from the same genus. One red fox probe lit up telomeric regions of 8 different corsac fox chromosomes (unique to red fox-corsac fox comparisons). Red fox showed one-to-one correspondence to dog chromosome segments. Graphodatsky et al. superimposed their findings onto their latest Canidae phylogeny map making the gray fox lineage the basal group. They concluded the following: position of raccoon dogs and gray fox branches remain uncertain with current morphological, molecular and chromosomal data. The Canidae karyotype shows extensive rearrangement: the Japanese raccoon dog differs by at least 22 fission/fusion rearrangements; the corsac fox by 23 and the red fox by 24 fission/fusion events; and several fusions likely arose independently several times over within Canidae. The similar corsac fox and arctic fox lineages are isolated from the red fox. With their study, Graphodatsky et al. confirmed the highly rearranged karyotypes of the Canidae family and they suggest that more studies will lead to unraveling these unresolved lineages.

**Family Camelidae: monobaramin (Wood 2008b).** Using a total of 12 llamas, guanacos, vicuñas, and alpacas, Bianchi et al. (1985) demonstrated the complete conserved karyotype of the Camelidae. In side by side comparisons, chromosome morphology, diploid number of 2n=74, and G-, C-, and NOR banding patterns, the homology was striking. They integrated the Bactrian camel into this group through previous reports of homology and by inference include the dromedary camel. Bianchi et al. conclude the Camelidae karyotype represents the most extreme case of chromosomal conservation among mammals.

**Family Equidae: monobaramin (Wood 2008b).** Because equid species exhibit different diploid numbers but may have polymorphic chromosome numbers within a normal population, Myka et al. (2003) set out to determine if those polymorphisms involved interspecies homologous chromosomes. Chromosome preparations from eight species of equid representing all groups, two equine BAC probes, and FISH were used in the investigation. The probes mapped to five extant species with metacentric morphology, diploid number of 2n=60, and 2n=56 (2n=55); Transcaspian wild ass, 2n=54 (2n=55); Tibetan wild ass, 2n=52 (2n=51); Grevy’s zebra, 2n=46; Burchell’s zebra, 2n=44 (2n=45); Hartmann’s mountain zebra, 2n=32. Balanced chromosome polymorphisms are rare occurrences though been observed in other species such as domestic cattle with some lowered fertility (Weber et al. as cited by Myka et al. 2003) and domestic sheep (Koop et al. as cited by Myka et al. 2003). The origin of this polymorphism found across five of ten equid species was either one event in the common ancestor or five independent fission events.

**Subfamily Cercopithecinae: monobaramin (Wood 2008b).** A study using G-, Q-, and C-banding compared karyotypes of four genera within family Cercopithecidae (Ponsa et al. 1981). Diploid numbers are as follows: *Erythrocebus patas* and *Miopithecus talapoin*, 2n=54, *Cercopithecus aethiops*, 2n=60, and *Macaca mulatta*, 2n=42. Three *E. patas* females from Spain and the Netherlands were studied. Seven chromosome pairs of the mostly metacentric karyotype were not homologous with *M. talapoin* or *M. mulatta* and five were not found in *C. aethiops* but the remaining pairs had homologs. *E. patas* and *M. talapoin* are closely related phylogenetically and have the same diploid number, yet no equivalent banding pattern could be found for many chromosomes.

**Discussion**

Of the nine baramins surveyed, all contain members with widely diverse diploid numbers except for Camelidae and Mormoopidae, which are conserved (Table 1). The enormous range of chromosome numbers within the sampling of terrestrial mammalian baramins supports the discrepancy between the general sense of stability thought to be within a kind and the actual dynamic rearrangements as brought out by Lightner (2006). From the sample of nine baramins, 78% showed considerable variation in chromosome numbers (a 14-44 point spread) and only 22% exhibited no change. Bovini are considered clean animals and, therefore, more than one pair were taken aboard the ark (Genesis? 7: 2). This would allow for a possibility of diploid number variety at the start. However, removing it from the data set does nothing to improve the statistics. The baramins selected for study represent diverse yet common groups of organisms. Had the sample been made up of unusual mammals that do not fit easily into a category, the data might have been easier to explain as being an exception to the rule. Given the data presented here, it appears diploid number changes are prevalent within a baramin.

This wide diploid number diversity within baramins invokes a multitude of questions. How is it that some families remain stable and others are highly versatile? Based on the survey of species within mammalian families (Wood 2011), separate analyses for mammalian families with numerous species versus those with few would be prudent. Is there any advantage to chromosome number variation? Do the different diploid numbers confer advantage or assist in adaptation in diverse environments? In other words, as Sankoff (2003) asks, is there a functional consequence of chromosomal rearrangements? There has been documentation of recent and rapid chromosomal changes in house mice populations in Madeira (Britton-Davidian et al. 2000). Six different populations exhibited severely reduced diploid numbers from the standard 2n = 40 through Robertsonian translocations (fusions) estimated to have occurred within the last 500 years. In a later study Britton-Davidian et al. (2007) found the correlation between generic and chromosomal distance to be marginally non-significant (Mantel test z=0.75 0.01, P=0.08). “In fact, the most chromosomally divergent races (San and Ade) were not among the most genetically differentiated (P<0.01)” (p. 437). If there is no significant difference, as in the mouse study, and assuming design is involved, why are rearrangements needed or important? Why have rearrangements at all? Is there relevance
between gene function and chromosome location (Serov et al. 2005)? On what scale do chromosome numbers change today? Can karyotype rearrangements be used to help delimit a baramin such as in families with enormous diversity such as Canidae and Phyllostomidae? Future research into each one of these questions will help to refine and clarify the scope and magnitude of actual chromosome diversity within a baramin.

Another question involves patterns. In families where the chromosome numbers proceed by twos (reflecting a fixed rearrangement), such as Phyllostomidae, (2n=16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 44, 46), does the pattern hold true throughout the karyotypes represented within that family? If so, the pattern would predict that intermediate Phyllostomidae species with 2n=42 should exist or is extinct. The same pattern exists for Bovini, 2n=46, 48 and 50 all carry the four same translocations (rob 1:27; 2:23, 8:19, 5:28 plus tandem variations) but there the pattern ends. Robs for Bubalus bubalis, 2n= 48 (river buffalo) and 2n=50 (swamp buffalo) are identical save one tandem fusion, 5:28+7. Bubalus depressicornis, 2n=46, carries two translocations (rob 11:20 and 17:29) not found in any of the other karyotypes. None of the genera follow a clear pattern of step-wise inheritance of translocations to transform one karyotype to the next though 2n=46, 48 and 50 are close. Based at least on this example, it would seem that 2n = 54 or 56 need not be missing. It would be of interest to survey the patterns of Robertsonian translocation inheritance in Phyllostomidae. Of the sampled baramins, two have diploid number changes in increments of two (Bovini and Phyllostomidae) and five do not (Canidae, Cercopithecidae, Cingulata, Equidae and Ursidae). The remaining two were stable (Camelidae and Mormoopidae).

The speciose Phyllostomidae family with ~160 species and 57 genera (Sotero-Caio 2010) has confounded evolutionists with its highly rearranged karyotypes even 20 years after Baker and

Table 2. Rob translocations in Bovini (Lightner, 2008a) relative to 2n=60 Bos taurus (domestic cattle, European descent), Bos indicus (Indian or zebu cattle), Bos banteng (banteng), Bison bison (American bison), and Bison bonasus (European bison or wisent).

<table>
<thead>
<tr>
<th>Rob</th>
<th>2n=58 Bos gaurus (gaur)</th>
<th>2n=52 Syncerus caffer (African buffalo)</th>
<th>2n=50 Bubalus bubalis (water buffalo) swamp</th>
<th>2n=48 Bubalus bubalis (water buffalo) river</th>
<th>2n=46 Bubalus mindorensis (tamaraw)</th>
<th>2n=48 Bubalus depressicornis (lowland anoa)</th>
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identified in Syncerus 2n=52 are unique. Based on their patterns of recombination it is believed Syncerus and Bubalus karyotypes were derived from a common ancestor with a karyotype similar to modern cattle (Lightner, 2008a). Karyotypes 2n=46, 48 and 50 all carry the four same translocations (rob 1:27; 2:23, 8:19, 5:28 plus tandem variations) but there the pattern ends. Robs for Bubalus bubalis, 2n= 48 (river buffalo) and 2n=50 (swamp buffalo) are identical save one tandem fusion, 5:28+7. Bubalus depressicornis, 2n=48, carries two translocations (rob 11:20 and 17:29) not found in any of the other karyotypes. None of the genera follow a clear pattern of step-wise inheritance of translocations to transform one karyotype to the next though 2n=46, 48 and 50 are close. Based at least on this example, it would seem that 2n = 54 or 56 need not be missing. It would be of interest to survey the patterns of Robertsonian translocation inheritance in Phyllostomidae. Of the sampled baramins, two have diploid number changes in increments of two (Bovini and Phyllostomidae) and five do not (Canidae, Cercopithecidae, Cingulata, Equidae and Ursidae). The remaining two were stable (Camelidae and Mormoopidae).
Bickham’s (1980) extensive study was published. In order to accommodate the 36 plus karyotype changes, many known for causing severe meiotic difficulties (such as pericentric inversions), and the four species within a genus that were so radically different from each other that homologous segments were hard to find, they coined the term “megaevolution.” They conclude that “it will be an interesting task determining the factors which result in one species having a totally reorganized genome while a closely related species undergoes no change” (p. 252). From the creationist’s perspective two progenitors of these monobaraminic bats presumably disembarked from the Ark; therefore, either this group includes more than one baramin or a mechanism is indeed needed to explain this vast diversity.

Do chromosome variations play an important part in rapid diversification? This question has been posed by many. For instance, even though they mentioned nothing about the “environments of intense selection” in their study of bears, Nash et al. (1998, p. 192) somehow conclude, “It is as if the genome possesses a built-in capacity to modify chromosome number, such that an increase is triggered by environments characterized by intense selection.” This profound statement can cautiously (as their conclusion was derived from a presupposition of universal common ancestry and only in general supported by their study) be examined in light of a dramatically altered post-Flood world for explaining rapid diversification after a catastrophic global event. Baker and Bickham (1980) concur with Nash et al.’s evaluation by suggesting involvement of genetic and environmental factors though admit to a paradox of rearrangement and fitness issues. Wood (2011) cautioned that rapid diversification in light of speciation is only typical of a small number of terrestrial mammalian families. Within a biblical context “rapid” has been defined as within 400 years of the Flood (Wood 2008a). The multiple fusions and fissions that must be invoked to account for the wide range of interchromosomal changes within baramins, such as in Canidae (26 chromosomal fusion and 4 fission events between the fox, 2n=34 + 0-8 Bs, and dog, 2n=78; Yang et al. 1999), and the magnitude of change that is not seen in the present suggest that diversification, at least at the genetic level, appears accelerated in the past. If this is indeed the case, then it strongly suggests designed features that allow for widespread and potentially devastating changes to take place while preserving the organism. This is supported by Lightner’s conclusion in her study of Bovini that chromosomal rearrangements are the result of designed mechanisms such as those regulating repairs to breaks, silencing a centromere, and adjusting the amount of heterochromatin in order to maintain viability such that organisms adapt and thrive in a fallen world.

Among primates, G-banding of the monobaramin Cercopithecinae shows a surprising lack of equivalent banding patterns between two presumably closely related monkeys that even have the same diploid number, 2n=54, Erythrocebus patas and Miopithecus talapoin. Five or greater chromosome pairs from E. patas were not homologous with M. talapoin, Cercopithecus aethiops or Macaca mulatta. Ponsa et al. (1981) explain these findings by pointing out the difficulty and likelihood of rearrangement misinterpretations and proposes a multistep process for the chromosome diversity. They strongly disagree with Dutrillaux (as cited by Ponsa et al. 1981) who relegates the wide variability to the interesting concept of hybridization without reproductive isolation. The four genera used in the study of Ponsa et al. are included within the monobaramin containing two tribes – “the Cercopithecini and the Papionini - with nine genera (Allenopithecus, Cercopithecus, Erythrocebus, Miopithecus, Cercocetus, Papio, Mandrillus, Theropithecus, Macaca) and 50 to 60 species altogether” (Hartwig-Scherer 1993; Hartwig-Scherer referred to the group as a “basic type”, which is delimited strictly on hybridization and is equivalent to a monobaramin). Compiling a hybridization network (Figure 2) shows that all but three genera within the original monobaramin hybridize with at least one other member (Gray 1972). No record was found for any hybridization of the monobaramin with Subfamily Colobinae. Within the monobaramin no record was found for

Figure 2. Hybridization Network of Monobaramin: Cercopithecini and Papionini (Gray, 1972).
explaining his model of highly regulated number changes within a baramin (Hennigan 2009a, Lightner also does not have the explanatory power to resolve chromosome at present, the basic creation model of natural selection and in part with the unraveling of the canid conundrum. However, deciphering the mystery of karyotype rearrangements might lie on.” This assumes that the baramin boundaries are correct as investigation as there is still “a whole lot of shuffling going 

be taken into account for the derivation of the ancestral Canidae disembarking from the Ark. The underlying assumptions must be taken into account for the derivation of the ancestral Canidae karyotype but even so, the Canidae monobaramin warrants further investigation as there is still “a whole lot of shuffling going on.” This assumes that the baramin boundaries are correct as hybridization data separates Canis from Vulpes (Gray 1972) and zoo-FISH does not resolve the family. That being said, the key to deciphering the mystery of karyotype rearrangements might lie in part with the unraveling of the canid conundrum. However, at present, the basic creation model of natural selection and Mendelian genetics acting on mutations and variation within kind also does not have the explanatory power to resolve chromosome number changes within a baramin (Hennigan 2009a, Lightner 2006, 2008b; Wood 2008a).

Several proposals have been made to expand the current creation model to explain rapid diversification after the Flood and genetic changes. Lammerts (Lammerts and Howe 1974, as cited by Wood 2002) suggested divine intervention was responsible for altering genetics as well as languages during the Babel dispersion. Later, based on recent studies on mobile DNA, Wood (2002) proposed that transposable elements are responsible for bringing about intrabaraminic diversification after the Flood through mediated and coordinated alterations in the genome.

These mobile elements or Altruistic Genetic Elements (AGEs) are inferred to act on the genome by creating new recombination sites and by promoting, enhancing or disrupting gene coding regions through a high specificity for their positional insertion or removal into a region. His model of AGEing was refined and expanded (Wood 2003) to come under the umbrella of a larger concept, that of highly regulated genomic modularity capable of responding to stress. He further incorporated genomic modularity into the bigger picture of an overall biological model, which includes unresolved concepts such as: biological similarity, genomic architecture and complexity, and intrabaraminic genomic plasticity (Wood 2006). Borger (2009) proposes a slight twist on transposable elements calling them VIGEs, short for Variation-Inducing Genetic Elements. He argues that VIGEs play a key role in variation, adaptations, and speciation events with strategic positional gene regulation and by facilitating karyotype rearrangements. His premise is that created kinds have inherently plastic genomes he calls baranomes with the ability to induce variation from within, through VIGEs. Several others have elaborated on various themes of these concepts (Williams 2005; Shan 2009).

The common thread found in these models involves coordinated modularity of the genome be it through a single inspired event or inherent design. Shapiro (2005) has developed a similar model of non-random, coordinated genomic modularity to counter conventional evolutionary theory. Though an evolutionist, he deems Darwinian Theory as inadequate to explain the complexity of the cell. In 2011 he published Evolution, a View from the 21st Century explaining his model of highly regulated machinery within the cell which looks very much like design, and incorporates many of the ideas discussed by Borger and Wood.

Significant karyotype variations within a large percentage of a sampling of nine terrestrial mammalian baramins were found. Given the data presented here, it appears diploid number changes are the rule within a baramin and the exception is stasis, however a larger data set is needed to confirm this generalization. Following Wood’s lead (2011) of approximating terrestrial mammalian baramins to be at the level of the family or subfamily, a study is underway to examine chromosome number variation on a larger scale. For baramins like Camelidae and Marmoopaedidae, their diploid numbers are stable. But for others, such as Canidae, Phyllostomidae, and Cercopithecidae, extreme chromosome rearrangements are so common that even evolutionists concede to having trouble reconciling their phylogenies. These data suggests either that the baramin boundaries may be in need of adjustment or that designed mechanisms that can orchestrate numerous chromosome rearrangements are at work. At present, however, neither the current creation model of diversification nor the evolutionary model can adequately explain the mystery of the karyotype shuffle.
References


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