

Karyotype Variability within the Cattle Monobaramin

Jean K. Lightner, Independent Scholar, Mentor, OH

Abstract

The Genesis account states that God created all living things according to their kinds. Cattle, bison, and buffalo are identified as being derived from a single created kind (i.e., they belong to a monobaramin). Karyotype variability is examined within this monobaramin. I conclude that chromosomal rearrangements, particularly centric fusions, have played an important role in developing the chromosomal patterns that are seen in these animals today. Furthermore, it appears that these rearrangements are dependent on numerous mechanisms (to repair breaks, deactivate a centromere, and restructure heterochromatin) that allow for such changes while maintaining the viability of the animal. Since different fusions have become fixed in different populations, it is proposed that these changes are likely beneficial. The precision necessary to fuse two chromosomes, inactivate one centromere, and adjust the amount of heterochromatin suggests that the chromosomal translocation mechanisms were designed by God to provide for His creatures in this present fallen world.

Keywords; baraminology, cattle, chromosomes, chromosomal rearrangements, cytogenetics, fusion, karyotype, translocation

Introduction

The historical account of origins presented in Genesis details that God created animals “according to their kinds” and with the ability to reproduce and fill the earth (Genesis 1:20–31). The study of created kinds is called baraminology (from Hebrew *bārā’*—create, *mîn*—kind). One method to determine if two species of animals belong to the same baramin is to attempt to form an interspecific hybrid. Interspecific hybrids are relatively common within genera and sometimes occur between genera within families (Gray 1972; Brophy 2006). There are even a few examples, such as in galliform birds, of hybrids between species in different families (McCarthy 2006). However, failure to form a hybrid can result from any number of differences which can arise between parents sharing common ancestry (Moore et al. 1981¹; Dodd 1989; Hemberger et al. 2001). For this reason, lack of hybridization data is inconclusive. Therefore, a number of statistical methods have been developed which use various character traits to assess for continuity (implying subjects may belong to the same baramin) or discontinuity (implying the subjects may be from different baramin). The history, methods, and some of the findings of baraminology are reviewed in greater detail elsewhere (Wood et al. 2003; Wood 2006).

It is recognized that intrabaraminic (within kind) changes have occurred since Creation. Most notably,

degenerative changes have occurred as a result of the Curse (Genesis 3; Romans 8:19–23). Additionally, since it is clear that God intends the earth to be inhabited and He cares for His creation (Genesis 8:17; Isaiah 45:18; Psalm 147:8, 9; Matthew 6:25–34), adaptive changes are consistent with the biblical record as well. Some of these changes have been observed to occur quite rapidly under the right conditions (Arendt and Reznick 2005; Grant and Grant 2006; Herrel et al. 2008). These are in contrast with the “creative” information-gaining mutations from chance events required to support an evolutionary origin.

An evaluation of intrabaraminic variability is crucial to further our understanding of baraminology and the world God created. Some variability was present at creation, yet more variability has arisen from changes which have occurred since creation. How do animals change over time? What are the underlying mechanisms? Are all these changes purely chance, random events, or are some programmed? Do some of these changes have an underlying purpose (i.e., to help animals adapt)? The answer to these questions will help us better appreciate the effects of both the Curse and God’s provision which are simultaneously active in our world today. It may also be valuable in guiding character selection for future baraminological research.

Previous baraminological research has established that species within the genera *Bos* and *Bison* belong

¹ Although Barbary sheep (*Ammotragus lervia*), domestic sheep (*Ovis aries*) and domestic goats (*Capra hircus*) have been identified from hybrid data as belonging to the same baramin (Lightner 2006b) and would be considered to have ancestors that were interfertile, today many crosses do not result in live offspring.

to a monobaramin since live hybrid offspring have resulted from interspecific mating (Lightner 2007a). Although mating has been observed between water buffalo (*Bubalus bubalis*) and the gaur (*Bos gaurus*, previously *Bos frontalis*) and hybrids between these genera have been reported in China, no well documented live hybrid is recorded in the scientific literature (Gray 1972). However, I have argued that species within the genus *Bubalus* should be included within the cattle monobaramin based on a study which yielded hybrid embryos which developed to the advanced blastocyst stage (Kochhar et al. 2002). I suggested that this stage indicates development past the maternal phase and requires the coordinated expression of both maternal and paternal morphogenetic genes (Lightner 2007a).

Chromosome numbers are generally considered to be stable within a species. Yet, this is not always the case (Lightner 2006a). Evolutionary apologists have suggested that molecular evidence of a translocation on human chromosome 2 is powerful evidence that humans descended from apes (Miller 2007). It has been shown that this argument naïvely ignores much current scientific knowledge (Lightner 2007b). Unfortunately, some creationist attempts to highlight differences between humans and chimps have also failed to account for current scientific understanding of translocations and their effect on populations (e.g. Harrub and Thompson 2002). By examining intrabaraminic variation in chromosome morphology, a better understanding of the types of changes that occur and their effect can be acquired. In this way we will have a more robust creationist model and be better prepared to comment intelligently on interbaraminic similarities and differences. Here the karyotypes of members of the cattle monobaramin are examined to assess the diversity that exists today and inferences are made about the origin of this diversity.

Robertsonian Translocations in Domestic Cattle, *Bos taurus*

Domestic cattle of European descent, *Bos taurus*, normally possess 60 chromosomes. These consist of 29 pairs of acrocentric autosomes and two submetacentric sex chromosomes. The autosomes vary in size with 1 designating those of the largest pair and 29 being the smallest. This karyotype is used as a basis of comparison for other bovid karyotypes.

The most common type of chromosomal rearrangement found in ruminants is known as a Robertsonian translocation (ROB) or a centric fusion. In this type of rearrangement two acrocentric chromosomes fuse to form a large metacentric or submetacentric chromosome. The most commonly identified ROB in domestic cattle is a fusion involving chromosomes 1 and 29, rob(1;29). This was first

identified in 1964 in the Swedish Red and White cattle breed (Gustavsson 1979). During the next thirty years several hundred articles appeared describing this ROB in scores of different breeds from all six continents inhabited by cattle. There is considerable variation in the incidence of rob(1;29) between breeds and even within breeds (Popescu and Pech 1991). A few breeds, such as the Barrosã breed of Portugal, have a high incidence resulting in a significant number of homozygous individuals (Rangel-Figueiredo and Iannuzzi 1991).

This translocation has been determined to be monocentric in contrast to the dicentric nature of many other ROBs. While satellite (SAT) I DNA is found in the centromeric region of all cattle acrocentrics (including 1 and 29), it is not found in the submetacentric rob(1;29) or sex (X and Y) chromosomes (Chaves, Heslop-Harrison, and Guedes-Pinto 2000). SAT III (from BTA 1) and SAT IV (from BTA 29) remain largely intact in rob(1;29). While SAT I from chromosome 1 may have been lost during the translocation event (which involves chromosomal breaks and the loss of a small amount of DNA), SAT I from BTA 29 is located behind SAT IV and was presumably lost during a separate and most likely subsequent process (Chaves et al. 2003).

A study using both banding and FISH-mapping techniques revealed that in addition to the translocation and loss of centromeric material, further rearrangement had occurred. Di Meo et al. (2006) suggest a double pericentric inversion or, more likely in their opinion, a chromosomal transposition of a small segment from the proximal p-arm to the proximal q-arm. Additionally, “polymorphisms between different rob(1;29) chromosomes in both centromeric and intercalary regions” have been observed in a homozygous bull (Chaves, Heslop-Harrison, and Guedes-Pinto 2000).

The monocentric nature of the chromosome has been cited as evidence that it has an ancient origin since recent translocations are generally dicentric. Some have argued that a single ancient translocation event can explain the widespread nature of rob(1;29) (Gustavsson 1979). Others have considered recurrent mutation a more likely explanation given that the many breeds in which it appears have presumably undergone genetic bottlenecks that would make the introduction of a preexisting rob(1;29) unlikely (Wilson 1990; Chaves et al. 2003). Chaves et al. (2003) suggested that loss of SAT I from the BTA 29 side is a pre-programmed, controlled event. Studies in humans indicate that more commonly occurring ROBs have common breakpoints suggesting a common mechanism to their formation (Bandyopadhyay et al. 2002). While a *de novo* rob(1;29) has never been confirmed by karyotypic analysis of the parents,

there is some evidence that some may have occurred recently. For example, a British Friesian bull was found to be heterozygous for rob(1;29). Cytogenetic analysis of 23 closely related animals revealed only one carried rob(1;29). Yet 19 of its 35 daughters (54.3%) were found to be carriers (Wilson 1990). Since this ROB is commonly inherited in a Mendelian fashion, with approximately 50% of the offspring carriers (Rybar et al. 2005; McWhir et al. 1987), the low incidence in close relatives suggests a relatively recent origin for the rob(1;29) carried in these British Friesians.

The rob(1;29) can be associated with decreased fertility in heterozygous carriers. This appears to be primarily from early loss of embryos formed by unbalanced gametes (Schmutz et al. 1991; Molteni et al. 2005). The degree of infertility appears to be quite variable. The first study of carrier bulls failed to demonstrate any decrease in fertility, but it was pointed out that these bulls were selected for fertility. Subsequent studies on unselected bulls revealed a 3 to 3.5% decrease in the 28-day non-return rate and a 4.5% decrease in the 56-day non-return rate. Several studies in Brown Swiss cattle failed to show any significant difference in fertility of heterozygous females compared to those of normal karyotype (Blazak and Eldridge 1977; Kneubühler et al. 2003). In contrast, a very large study clearly showed that daughters of five Norwegian Red heterozygous bulls had reduced fertility (Refsdal 1976). Other studies have confirmed this reduced fertility including one study in which 36% of embryos from superovulated carrier cows crossed with normal bulls had unbalanced karyotypes which would result in embryonic death (Schmutz et al. 1991). Since fertility is an important trait in modern livestock production, known carriers of rob(1;29) are now commonly selected against in most breeds.

If demonstrating reduction of fertility can sometimes be difficult, finding evidence of other factors associated with the ROB has proven even more elusive. Several studies have found a significant increase in milk production (Kneubühler et al. 2003) or milk fat in carrier animals. Yet the finding that age at first service is significantly higher in carriers may be a confounding factor (Kovács and Csukly 1980). The ROB appears to be more common in beef cattle than dairy cattle. While it had been suggested the translocation was correlated with increased meat production, it now appears that was coincidental. There is no conclusive evidence that rob(1;29) is consistently associated with any production trait, coloration pattern, or disease condition (Gustavsson 1979). One study found a significant increase in the mean sister chromatid exchange (SCE) values in animals with rob(1;29), but the differences were still

not large (normal: 6.6 ± 3.6 ; heterozygotes: 7.1 ± 3.3 ; homozygotes: 8.1 ± 3.8). The researchers were not certain what to make of this pattern. They did point out that generally increased mean SCE-values indicate potential cell fragility under harsher environments or different dietary conditions. They also mention that SCE values have been reported as being lower in the more selected Friesian breed than in less carefully selected local breeds (Rangel-Figueiredo, DiMeo, and Iannuzzi 1995).

Several dozen other ROB's have been identified in cattle (Table 1). All of the 29 pairs have been involved in at least one ROB described in the literature. Two of these ROB, rob(1;25) and rob(1;27) are believed to be identical to the rob(1;29) (Pearce et al. 1997; Eldridge 1975). The reason for the discrepancy is that chromosomes 25, 27 and 29 are the most difficult chromosomes to distinguish in cattle, particularly with older banding methods. Additionally, inconsistencies existed between the G- and R-banded karyotypes of chromosomes 25 and 29 in the International System for Cytogenetic Nomenclature of Domestic Animals, 1989 (Di Bernardino et al. 2001).

Other ROB's generally contain two blocks of constitutive heterochromatin implying they are dicentric. They tend to be found in isolated animals and their progeny and appear to have occurred de novo or very recently. Many are detected by routine cytogenetic analysis of bulls being considered for use in artificial insemination (AI) programs. Most are from phenotypically normal animals and the few examples of those with abnormalities are likely coincidental (Ellsworth, Paul, and Bunch 1979; Miyake and Kaneda 1987). The dicentric nature of these translocations can make them unstable so they sometimes disappear after several cell divisions (Iannuzzi et al. 1992). This is one possible explanation why they are generally not found in many relatives of carriers (the other being that they are de novo). It is interesting to note that one study examining embryos of a rob(16;20) carrier bull failed to demonstrate any embryos carrying the translocation while approximately 50% of the embryos of a rob(1;29) bull carried the latter ROB (Rybar et al. 2005). However, not all dicentrics are unstable; it appears that one of the centromeres can be inactivated. Some dicentrics are inherited in a Mendelian fashion (e.g., rob(14;20) in Simmental, McWhir et al. 1987). Instability from failure to deactivate one centromere may explain the bull that was mosaic for rob(13;21) (Kovács and Papp 1977). It is possible that the mosaic pattern of the translocation was the result of somatic reversions. It should be noted that sometimes specific, recurrent rearrangements are identified in a few of the cells examined that are the result of the processing procedures and a higher level of such translocations is sometimes found in disease

Table 1. A summary of Robertsonian translocations (ROBs) identified in cattle excluding the common rob(1;29). Characteristics may refer to the translocation or the animal(s) carrying them. (?) some uncertainty exists as to the actual chromosomes involved. Note that all cattle acrocentrics have been identified in at least one ROB.

ROB	Animal(s)	Breed/Country	Characteristics	Reference
1;4	bull	Czechoslovakia	low fertility	Lojda et al. 1976
1;7				cited in Fries and Ruvinsky, eds 1999
1;21	bull and progeny	Holstein-Friesian	apparently de novo: not found in 5 half-sibs	Miyake, Murakami, and Kaneda 1991
	bull	Holstein-Friesian	sperm: 51.8% normal, 47.0 % balanced, 0.6% unbalanced	Tateno et al. 1994
1;22	bull	Czechoslovakia	low fertility	Lojda et al. 1976
1;23	bull	Czechoslovakia	along with 6;28 in sire of calves with hereditary defects	Lojda et al. 1976
1;25		Blonde d'Aquitaine/New Zealand	believed same as 1;29	Pearce et al. 1997
		Piebald/Germany		cited in Fries and Ruvinsky, eds 1999
1;26	bull	Holstein-Friesian/Japan	dicentric, probably de novo	Miyake and Kaneda 1987
1;27		British White	believed same as 1;29	Eldridge 1975
1;28	bull	Czechoslovakia	low fertility	Lojda et al. 1976
2;8		Friesian/England		cited in Fries and Ruvinsky, eds 1999
2;27				cited in Fries and Ruvinsky, eds 1999
2;28		Vietnamese cattle	reduced heterochromatin: possibly monocentric; same as in Gaur	Tanaka et al. 2000a
3;4	cow	Limousine/France	dicentric	Popescu 1977
3;27		Friesian/Romania		cited in Fries and Ruvinsky, eds 1999
4;4		Czechoslovakia		cited in Fries and Ruvinsky, eds 1999
4;10	2 cows	Blonde d'Aquitaine/France	dicentric, cows were paternal half sibs	Bahri-Darwich et al. 1993
5;18	bull	Simmental	dicentric	Papp and Kovacs 1980
5;21		Japanese Black/Japan	dicentric (Slota and Switonski 1992)	cited in Fries and Ruvinsky, eds 1999
5;22	bull	Polish Red and White/Poland	dicentric	Slota and Switonski 1992
5;23		Brune Roumaine/Romania		cited in Fries and Ruvinsky, eds 1999
6;8	bull	Chianina/Italy	dicentric (originally reported as 4;8)	Bouvet et al. 1989; Di Meo et al. 2000
6;16 (?)	cow	Dexter/UK	dicentric; mosaic (8% of cells 60XX)	Eldridge 1974; Slota and Switonski 1992
6;28	bull	Czechoslovakia	along with 1;23 in sire of calves with hereditary defects	Lojda et al. 1976
7;21	bull	Japanese Black Cattle	sperm: 47.3% normal, 50.0% balanced, 2.7% unbalanced	Tateno et al. 1994
	several	Japanese Black Cattle/Japan	reduced fertility from unbalanced embryos in bulls (5.4%) and cows (8.3%)	Hanada, Geshi, and Suzuki 1995
8;9		Brown Swiss/Switzerland		cited in Fries and Ruvinsky, eds 1999
8;23		Ukainian Grey		cited in Fries and Ruvinsky, eds 1999
9;23	bull	Blonde d'Aquitaine	dicentric	Cribiu et al. 1989
11;16	bull	Simmenthal (sic)/Hungary		Kovacs and Papp 1977
11;22		Czechoslovakia		cited in Fries and Ruvinsky, eds 1999
12;12		Simmental/Germany		cited in Fries and Ruvinsky, eds 1999
12;15		Holstein Friesian/Argentina		cited in Fries and Ruvinsky, eds 1999
13;19	bull	Marchigiana/Italy	de novo, dicentric	Molteni et al. 1998
13;21	bull	Holstein-Friesian/Hungary	bull mosaic for the translocation	Kovacs and Papp 1977
13;24	cow		fallout region of a metallurgical plant	Holeckova, Sutiakova, and Pijakova 1995
14;17	bull	Marchigiana/Italy		Molteni et al. 1998
14;19		Braunvieh/Switzerland		cited in Fries and Ruvinsky, eds 1999
14;20	several	Simmental/Switzerland	dicentric, reduced fertility due to unbalanced embryos (22%)	Logue and Harvey 1978; Schmutz et al. 1997
14;21		Simmental/Hungary		cited in Fries and Ruvinsky, eds 1999
14;24	cow	Podolian	dicentric	Di Berardino et al. 1979
14;28	cow	Holstein/USA	dicentric, behavioral/phenotypic anomalies discussed	Ellsworth, Paul, and Bunch 1979
15;25	cow	Barrosã/Portugal	dicentric	Iannuzzi et al. 1992
16;18	bull	Barrosã/Portugal	dicentric	Iannuzzi et al. 1993
16;19		Marchigiana/Italy		cited in Fries and Ruvinsky, eds 1999
16;20	bull	Czech Simmental (sic)	de novo, dicentric, subfertile bull failed to pass this ROB to offspring	Rybar et al. 2005
	bull	German x Czech Red Pied	dicentric, apparently de novo: not found in dam or 26 paternal half sibs	Rubes et al. 1996
16;21		Germ x Czech Red Pied/Czechoslovakia		cited in Fries and Ruvinsky, eds 1999
19;21	cow	Holstein-Friesian	dicentric	Pinton et al. 1997
20;20		Simmental/Germany		cited in Fries and Ruvinsky, eds 1999
21;27	bull and progeny	Blonde d'Aquitaine	dicentric	Berland et al. 1988
24;27		Holstein hybrid/Egypt		cited in Fries and Ruvinsky, eds 1999
26;29	several	Alpine Grey/Italy	dicentric, reduced fertility (originally reported as 25;27)	Di Meo et al. 2000; Molteni et al. 2005
27;29	bull	Guernsey/Canada	non-return rate higher than breed average	Bongso and Basur 1976

conditions, at least in humans (Stern et al. 1989). Considering the fact that the translocation was found during routine cytogenetic examination of bulls at an AI station, somatic reversion seems a more likely explanation than an underlying pathologic condition. In contrast to humans, cytogenetic exams of diseased bovines are not as frequently performed and there is not a significant amount of literature on this. Thus, a discussion of karyotype anomalies appearing in somatic cells in correlation with particular disease conditions is beyond the scope of this paper.

Some of the ROBs listed in Table 1 have also been demonstrated to adversely affect fertility. Again, the degree varies. Unbalanced spermatozoa have been reported at 0.6% and 2.7% for rob(1;21) and rob(7;21) respectively (Tateno et al. 1994). Another study involving rob(7;21) carriers found a higher percentage of unbalanced embryos from bulls (5.4%) and cows (8.3%) (Hanada, Geshi, Suzuki 1995). In contrast, rob(27;29) was found in a Canadian Guernsey bull who had a non-return rate higher than the breed average (Bongso and Basur 1976).

One of the ROBs listed in Table 1 is quite unique, the rob(2;28) identified in Vietnamese Cattle. These cattle are of the Indian or zebu type (*Bos indicus* or *Bos taurus indicus*) which differ from European cattle phenotypically (e.g., pronounced hump over the shoulders and a dewlap) although they have the same normal diploid number ($2n=60$). The rob(2;28) had reduced amounts of SAT I which led the researchers to suggest it might be monocentric and of ancient origin. The same ROB is carried as part of the normal karyotype in the gaur (*Bos gaurus*). Since the gaur can cross with other *Bos* species and produce fertile female offspring, it appears that interspecific mating is a plausible source of the translocation (Tanaka et al. 2000a).

Tandem Fusions in Domestic Cattle

Tandem fusions have rarely been identified in cattle. In this type of fusion, the centromeric end of one chromosome attaches to the telomeric end of another. Rather than creating a metacentric chromosome, this type of fusion forms a longer acrocentric while reducing the chromosome number. Two cases that appear in the literature are from abnormal animals. The first was a 1;16 tandem fusion found in a bull with trisomy, a very unusual condition in cattle (Kovács, Foote, and Lein 1990). The second was found in a freemartin. A freemartin is a female calf that developed *in utero* with a male twin. The embryonic membranes usually communicate and the development of the male's reproductive system adversely affects that of the female, so the freemartin is sterile. This freemartin carried cells from her male twin with a 4;21 tandem fusion. The male twin was never found and may have

died by the time the investigation was carried out (Pinheiro et al. 1995).

Reciprocal Translocations in Domestic Cattle

Reciprocal translocations, while more common than tandem fusions, have not been described as often as ROBs. This may be partly due to the difficulty of identifying them in routine karyotyping procedures since they do not affect chromosome number. Occasionally the resulting chromosomes differ significantly in size, although various techniques in addition to banding methods may be necessary to definitively identify the chromosomes involved (Iannuzzi et al. 2001b; Molteni et al. 2007). The balanced reciprocal translocations that have been described are from otherwise phenotypically normal animals with poor fertility (Mayr et al. 1983; Andersson, Aalto, and Gustavsson 1992; Villagómez et al. 1993; Ducos et al. 2000; Iannuzzi et al. 2001b) or even infertility/azoospermia (De Schepper, Aalbers, and Te Brake 1982; Ansari et al. 1993; Molteni et al. 2007). There has been a case where a reciprocal translocation occurred between an autosome (BTA9) and the Y chromosome resulting in azoospermia (Iannuzzi et al. 2001c).

Inferred Chromosomal Fusions of Autosomes within the Cattle Monobaramin

Many members of the cattle monobaramin have the same normal diploid number, $2n=60$. This includes domestic cattle of European descent (*Bos taurus*), zebu cattle (*Bos indicus*), the yak (*Bos grunniens*), the banteng (*Bos javanicus*), American bison (*Bison bison*), and European bison or wisent (*Bison bonasus*). This is believed to be the ancestral karyotype and differences in chromosome number in other members of the Bovidae family are primarily attributed to ROBs.

As alluded to above, the gaur (*Bos gaurus*) has a normal diploid number of 58, ($2n=58$). It is homozygous for rob(2;28) relative to cattle. There is evidence that there is a decreased heterochromatin block suggesting that it is an older translocation. Interestingly, a rob(1;29) homologue has been identified in a captive gaur. It was determined to be monocentric as evidenced by a single heterochromatic block observed by C-banding. Mastromonaco et al. (2004) give reasons why they believe this was inherited from a gaur ancestor rather than introduced recently from domestic cattle.

As summarized in Table 2, river buffalo (a subspecies of *Bubalus bubalis*, $2n=50$) carry five Robertsonian translocations relative to cattle: 1;27, 2;23, 8;19, 5;28, and 16;29 (Di Berardino et al 2001; Tanaka et al. 1999; the latter ROB is reported as 16;25 in Gallagher et al. 1999). Swamp buffalo (the other subspecies of *Bubalus bubalis*, $2n=48$) have an additional tandem fusion involving BBU4 and

Table 2. Comparison of the normal karyotype of animals in the tribe Bovini (cattle, bison, and buffalo) to the cattle karyotype. NAA= number of autosomal arms; sm= submetacentric; a = acrocentric; ROB= Robertsonian translocation. Adapted from Tanaka et al. 2000b and Gallagher et al. 1999. Chromosomes listed as 25 in Gallagher et al. are listed as 29 here so as to be consistent with other sources; a previous version of the standard karyotype had been inconsistent in the listing of chromosomes 25 and 29 (Di Bernardino et al. 2001).

Species	2n	NAA	X	Y	Translocations of Autosomes	Type of Translocation(s)
<i>Bos taurus</i> (domestic cattle, European descent)	60	58	sm	m	none	
<i>Bos indicus</i> (Indian or zebu cattle)	60	58	sm	a	none	
<i>Bos banteng</i> (banteng)	60	58	sm	m	none	
<i>Bos gaurus</i> (gaur)	58	58	sm	m	2;28	1 ROB
<i>Bison bison</i> (American bison)	60	58	sm	a	none	
<i>Bison bonasus</i> (European bison or wisent)	60	58	sm	a	none	
<i>Bubalus bubalis</i> (water buffalo)						
river buffalo variety	50	58	a	a	1;27 2;23 8;19 5;28 16;29	5 ROBs
swamp buffalo variety	48	56	a	a	1;27 2;23 8;19 5;28+7 16;29	5 ROBs and 1 tandem fusion
<i>Bubalus depressicornis</i> (lowland anoa)	48	58	a	a	1;27 2;23 8;19 5;28 11;20 17;29	6 ROBs
<i>Bubalus mindorensis</i> (tamaraw)	46	56	a	a	1;27 2;23 4;14 8;19 5;28+11 16;29	6 ROBs and 1 tandem fusion
<i>Syncerus caffer</i> (African buffalo)	52	58	a	a	1;13 2;3 5;20 11;29	4 ROBs

BBU9 (BTA5;28 and BTA 7). The decreased fertility of river×swamp buffalo hybrids is believed to be from unusual synaptic behavior of the tandem fusion during meiosis (Świtoński and Stranzinger 1998). The tamaraw (*Bubalus mindorensis*, 2n=46) has a different tandem fusion relative to river buffalo, BBU4 and BBU12 (BTA5;28 and BTA11). Additionally, they carry a rob(4;14) relative to cattle that has been demonstrated to contain larger amounts of satellite I DNA compared to the other banded chromosomes, suggesting it is of more recent origin (Tanaka et al. 1999). Lowland anoa (*Bubalus depressicornis*, 2n=48) share the first four translocations (1;27, 2;23, 8;19, 5;28) and have two unique ROBs (11;20 and 17;29). (The latter is reported as 17;25 in Gallagher et al. 1999. This discrepancy between sources is presumed to be because of the difficulty in distinguishing BTA 25 and BTA 29 and the discrepancy between them in an earlier (1989) published version of the standard karyotype of cattle. See Di Bernardino et al. 2001.)

It should be noted that water buffalo, both the river and swamp varieties, are domestic animals kept in poorer regions of the world. From a veterinary standpoint, they are a type of cattle. They are generally multi-purpose (i.e., dairy, meat, and draft). As such they are not as productive as the specialized beef or dairy cattle with which most westerners are familiar. They are better able to tolerate the harsh conditions and marginal diets in developing countries. While the only solid hybrid data connecting them to cattle (*Bos* species) is the development of hybrid embryos to the advanced blastocyst stage, phenotypically the similarities also strongly support their inclusion in the cattle monobaramin. A comparison of the translocations characteristic of various *Bubalus* species shows that several chromosomes have been involved in different translocations in different species. This would be expected to cause more serious

problems in chromosomal pairing were a hybrid to be attempted than a single translocation (e.g., rob(1;29)) causes. Therefore, it would not be expected that a fertile hybrid (or perhaps even any hybrid) could be produced between the swamp buffalo and the tamaraw because they have a different tandem fusion involving BBU4 (BTA5;28). Ironically, it might be possible for a fertile hybrid to form between the river buffalo (which is classified as the same species as swamp buffalo although they differ in chromosome number) and the tamaraw. Similarly, it would seem improbable that the lowland anoa could form a fertile hybrid with any of the other *Bubalus* species listed.

While the African buffalo (*Syncerus caffer*, 2n=52) has no hybrid data directly linking it to the cattle monobaramin, it is within the tribe Bovini (cattle, bison, and buffalo). While phenotypically it is similar to other buffalo (*Bubalus* spp.) it carries distinct translocations relative to cattle: 1;13, 2;3, 5;20, and 11;29 (Gallagher et al. 1999; again the latter is reported as 11;25, but referred to as 11;29 here to be consistent with the other sources). It seems significant that many of the same chromosomes (i.e., BTA homologues 1, 2, 5, 29) are involved in different ROBs compared to the *Bubalus* species mentioned. Again, despite their phenotypic similarities, the differences in chromosome structure would be expected to create problems should the African buffalo be crossed with any *Bubalus* species. While a single translocation does not automatically lead to speciation, the accumulation of different translocations over time can lead to a real reproductive barrier between populations. Furthermore, the pattern of inferred translocations in these two genera strongly supports the inference that they originated from an ancestor with a karyotype much like that of modern cattle.

Parentetically, it is interesting to note that similar patterns of chromosomal rearrangements were

found within the Tsoan (sheep-goat) monobaramin. In addition to recent translocations identified in domestic sheep and goats today (Lightner 2006a), there has been a history of such rearrangements such that different species within this monobaramin are sometimes characterized by different diploid chromosome numbers. For example the domestic sheep (*Ovis aries*, $2n=54$) karyotype differs from that of the goat (*Capra hircus*, $2n=60$ with banding patterns very similar to cattle) by three ROBs. OAR 1 is equivalent to CHI (and BTA) 1 and 3; OAR 2 corresponds to CHI/BTA 2 and 8; OAR 3 is equivalent to CHI/BTA 5 and 11 (Maddox 2005). Thus homologues to BTA 1, 2, and 5 are involved in the fusions seen in both genera of buffalo (*Syncerus*, *Bubalus*) and in domestic sheep (*Ovis aries*). While much similarity has been identified between cattle (subfamily Bovinae) and the Tsoan (subfamily Caprinae), further investigation needs to be done to determine if the Tsoan monobaramin and the cattle monobaramin are both part of a single holobaramin (Lightner 2006b). Additionally, further investigation is needed to determine if there is truly a significant bias in which acrocentric chromosomes are involved in fusions and what types of physiologic changes might be associated with these fusions.

Variability of the X Chromosome

While members of *Bos* and *Bison* have a submetacentric X chromosome, *Bubalus* and *Syncerus* have an acrocentric X (Table 2). Comparative FISH mapping has revealed that the order of loci is the same on BTA X and BBU X, suggesting a centromere translocation occurred along with a change in amount of constitutive heterochromatin (Iannuzzi et al. 2000). Since the acrocentric BBU X contains greater amount of heterochromatin including some SAT I DNA normally found only on autosomes in other bovids, it has been suggested that this is the ancestral state and the metacentric X is derived (Gallagher et al. 1999).

It should be pointed out that constitutive heterochromatin is not some inert portion of DNA. Different types of genes have been identified in regions labeled as constitutive heterochromatin (Yasuhara and Wakimoto 2006). These areas mediate “various nuclear processes including centromere function, gene silencing and nuclear organization” (Grewal and Rice 2004). Therefore the difference in the amount of heterochromatin evident in the X chromosomes and in the inferred autosomal translocations discussed previously is not likely to be the result of purely chance processes. Instead, it appears that there are mechanisms that alter the amount of heterochromatin in a controlled manner so viability can be maintained. Within this monobaramin the amount of heterochromatin tends to be greater in acrocentrics than in stable metacentrics.

If acrocentrics are indeed ancestral, then it appears that heterochromatin is reduced after translocations to stabilize the derived chromosome. Similarly, it would seem that transposition of a centromere, to be successful and allow for viability, would also need to be a controlled event.

Variability of the Y Chromosome

Three species of *Bos* (*B. taurus*, *B. banteng*, and *B. gaurus*) are identified as having a metacentric Y chromosome (Table 2). *B. indicus* has an acrocentric Y with a small p-arm. BTA-Y and BIN-Y retain the same gene order in their distal chromosome regions despite the difference in centromere placement, suggesting a pericentric inversion or centromere transposition has occurred (Di Meo et al. 2005). A probable pericentric inversion (or possible centromere transposition) was identified BTA-Y in a Podolian sire and 11 male offspring, only one of which had an abnormal phenotype (Iannuzzi et al. 2001a). Additionally, significant variation in the size of BTA-Y has been documented in animals of the same breed (Genero et al. 1998). Differences between breeds have also been identified in both relative length and ratio of the long arm to the total length of BTA-Y (Stranzinger et al. 2007).

Bison, *Bubalus*, and *Syncerus* possess an acrocentric Y. While the Y chromosome of river buffalo is larger than that of *Bos* or *Bison*, the Y chromosome of the African buffalo is smaller. The size differences appear to be largely from variations in the amount of heterochromatin. Both *Bubalus* and *Syncerus* appear to have acquired X-specific repetitive DNA on their Y chromosomes (Gallagher et al. 1999). In addition to variations in the amount of heterochromatin, the gene order differs between BTA-Y and BBU-Y. It appears that these differences could be explained by a pericentric inversion (Di Meo et al. 2005).

It is often difficult to distinguish between a pericentric inversion and centromere transposition unless sufficient loci are identified close to the centromere. Sometimes a pericentric inversion is assumed since it is presumed to be the simpler rearrangement (Iannuzzi et al. 2001a). Yet there has been accumulating evidence that centromere transpositions might not be that rare, again reinforcing the suggestion that there is a mechanism that controls this type of rearrangement (see Ventura et al. 2004²).

Conclusions

Given that in the beginning God commanded the creatures He created reproduce and fill the earth, it would seem that variation that poses a significant barrier to reproduction within a monobaramin has developed subsequent to Creation, and may very likely

be post-Curse. It could be argued that some variation, such as rob(1;29), was actually created because it does not always significantly impair reproduction and perhaps it never would in a perfect pre-Fall world. However, we see *de novo* translocations today. Additionally, many similar inferred translocations discussed would impede reproduction between certain members within a monobaramin. Thus, it seems most likely that all of these presumed translocations discussed are truly translocations that have occurred post-Creation.

Since translocations have been identified in animals of normal phenotype, it is highly doubtful that chromosomal fusions are merely accidental occurrences that can be attributed to purely chance events. In addition to the breaks in the chromosomes (which may be somewhat random), these rearrangements require important mechanisms that repair breaks, silence a centromere, and apparently adjust the amount of constitutive heterochromatin over time in a way that maintains viability. The inference that decreased amounts of satellite DNA implies an older translocation may not have been rigorously tested, but it is consistent with the observed data.

Furthermore, these translocations can become fixed in different populations. This implies that there is some purpose and benefit to them. Although they may come at a cost (usually reduced fertility in heterozygotes), chromosomal translocations may provide a degree of plasticity that is necessary for animals to adapt in a sin-cursed world. Perhaps certain harsh environments or marginal diets trigger chromosomal fragility which may result in translocations. These may allow for certain new gene associations that are beneficial to the animal. Other animals not carrying these traits may not do as well and perhaps choose to move elsewhere. The few animals carrying the rearrangement may be better able to exploit a particular environment. Thus, essentially the founder effect helps the translocation to become established within the population. Therefore, it appears plausible that chromosomal rearrangements are the result of designed mechanisms that provide a source of variability that allows animals to adapt in our fallen world. Further research into the physiologic effects of such rearrangements would be helpful to confirm this conclusion.

Glossary of Terms:

Acrocentric—a chromosome with the centromere very near one end.

Autosome—a chromosome that is not a sex (i.e. X or Y) chromosome.

Baraminological—an adjective derived from the noun baraminology.

Baraminology—the study of created kinds (from Hebrew *bārā'*—create, *min*—kind).

BBU—from *Bubalus bubalis*, designates chromosomes from the river buffalo karyotype.

BIN—from *Bos indicus*, designates chromosomes from the zebu cattle karyotype.

BTA—from *Bos taurus*, designates chromosomes from the cattle karyotype.

CHI—from *Capra hircus*, designates chromosomes from the goat karyotype.

Constitutive heterochromatin—sections of DNA, generally concentrated around the centromeres and telomeres, containing highly repetitive sequences.

Dicentric—a chromosome with two centromeres (blocks of constitutive heterochromatin).

FISH—fluorescent *in-situ* hybridization, a technique useful for gene mapping and identifying chromosomal abnormalities.

Heterozygous—possessing two different forms of a gene or chromosome.

Holobaramin—the entire group of animals belonging to a particular kind.

Interspecific—between different species.

Intrabaraminic—within a baramin (created kind).

Karyotype—the chromosomes possessed by an individual animal.

Metacentric—a chromosome with the centromere very near the middle.

Monobaramin—a group of animals believed to be derived from a single created kind.

Monocentric—a chromosome with a single centromere.

Non-return rate—a measure of fertility; the percentage of females that do not return to heat (and are thus likely pregnant) after being bred.

OAR—from *Ovis aries*, designates chromosomes from the domestic sheep karyotype.

p-arm—the short arm of a (submetacentric or acrocentric) chromosome

q-arm—the long arm of a (submetacentric or

² This paper reviews a number of studies. Some are within what creationists would consider monobaramins, such as in the family Equidae and in the galliform family Phasianidae. Others made comparisons between baramins, such as between humans and primates and between humans and cattle. The studies involving intrabaraminic comparisons reviewed by Venture et al. 2004, by me in this paper, and in Lightner 2006a indicate that translocations have occurred a number of times in different created kinds. The Bible does make it clear that man does not share a common ancestor with other animals, but it does not provide information on the original karyotype in man or created kinds. The possibility exists that all mammals may have been created with essentially identical karyotypes (i.e., the same chromosome number and banding patterns). If so, this has implications for apologetic arguments. Additionally, although evolutionists are incorrect in their assumption of common ancestry, some of their conclusions about rearrangements by comparing different baramins could still have value if karyotypes were in fact very similar at Creation.

acrocentric) chromosome.
 submetacentric—a chromosome with a centromere closer to the middle than the end.

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