

Towards a creationary view of why speciation occurs

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While informed creationists recognize that species are not equivalent to kinds, we don't have an adequate understanding of why different species exist within the various created kinds. Using the biblical history and information from the scientific literature, it appears there is good reason why speciation occurs. Organisms diversify as they reproduce and fill the earth. Maintaining separate diverse populations, which biologists usually classify as different species, provides a reservoir for variability. Through hybridization, this variability can be shared between the populations. There are examples where this has enabled a population to recover from unusually harsh environmental extremes. It has also been proposed that it provides the basis for adaptive radiation, where organisms rapidly diversify and fill a variety of environmental niches. In the end, the process we call speciation appears to be an important means by which God provides for His creatures even in the current fallen world.

The Bible gives us a historical framework for understanding the origin of life and some key events in natural history. We know that God created plant and animal life according to their kinds and blessed them with the ability to reproduce and fill the earth (Genesis 1:11–12; 20–22; 24–25). We are also aware of a severe genetic bottleneck, particularly in unclean flying and terrestrial creatures, at the time of the global Flood (Genesis 6–8). From this historical information and the biological and genetic information we have from observing the world today, it is clear that many animals have diversified and speciated since creation and the Flood.^{1–3}

This brings up several important questions that are crucial to understanding biology. What is the source of this diversity? What processes are involved in diversification and speciation? In a biblical model, why does speciation occur? There is enough information available that we should be able to get some handle on speciation from a biblical worldview.

The origin of diversity

It would seem that some of the diversity seen within kinds was created. At a very minimum, there was a male and female for (dioecious) sexually reproducing kinds. For diploid creatures, it is quite possible that many loci were created heterozygous, containing two distinct alleles, or versions of the gene.

While currently available data does not permit us to make a good estimate of created diversity in most vertebrate kinds, Dr Robert Carter has made a rough estimate of created diversity in humans. Using HapMap data, he proposed that a significant proportion of common single nucleotide polymorphisms (SNPs) found in humans were probably

created alleles. There are about 10 million common variants, and the HapMap data covers a significant sampling of these. He noted that there are two nucleotides at each of these positions that appear to be widely distributed in humans. Widely distributed alleles are generally ancestral and he proposes that 10 million positions or more were likely heterozygous in Adam and Eve.⁴

It is important to recognize that a designed mechanism that can alter the DNA sequence on a chromosome had to be in place to account for the pattern that we see today in created alleles. This designed mechanism is known as homologous recombination. It operates during meiosis, that special series of cell divisions that produces the cells (egg and sperm) necessary for sexual reproduction. Without it, homologous chromosomes do not pair up and then segregate properly. Further, homologous recombination allows for alleles to be shuffled between the corresponding chromosomes, providing for an incredible number of different combinations that underlies much of the diversity we see today.

Yet there is observed diversity that clearly goes beyond what can be accounted for by created alleles and homologous recombination.⁵

In addition to widely distributed alleles, the human population has many more variants that are called private alleles. Given the number of generations since the Flood, human population size, and known mutation rates, it does not appear to be a problem to account for these in a biblical timeframe.⁴ In fact, several studies by evolutionists have concluded that most rare variants in humans have arisen within the last 10,000 years.⁶ In addition to SNPs, structural variants (e.g. indels, inversions, etc.) appear, not only in humans, but in animals and plants as well.

Some instances of diversity may be from something that has been called latent design, also known as mediated design.^{7,8} For example, there are several different pathways plants use for photosynthesis, and the efficiency of the pathway depends on the environment the plant is in.⁹ From an evolutionary perspective it appears that C₄ photosynthesis has arisen multiple times. Even in a creationary model, which generally recognizes plants in the same family as descending from the same kind, it appears this may have happened. Interestingly, genes for the C₄ pathway have been identified in plants using the C₃ but they are not switched on. One possible explanation is that previously existing genes were merely switched on to account for the ‘appearance’ of C₄ photosynthesis in plants.

Epigenetic change is a mechanism that can switch on or off genes, as is transposable element (TE) movement. Epigenetic changes are used regularly throughout the lifetime of an organism to adjust gene transcription to its needs. There have been examples of environmentally induced epigenetic changes that are passed transgenerationally; it appears this may have been one factor involved in adaptation among Darwin’s finches.¹⁰

TEs could be involved with mediated design or other pathways of designed genomic change. A number of articles by creationists have addressed this.^{11–14} TEs were first identified as a source of phenotypic change in maize. It now appears that they can not only provide an alternative promoter, but may also shift the function of genes through alternative splicing and alternative polyadenylation.¹⁵

While some diversity may be derived from switching things on or around, additional diversity comes from knocking things out. Some of the interesting variety seen in coat colour patterns among many different mammals is from ‘breaking’ a protein receptor or causing it to be permanently switched on. Either way, this receptor is no longer responsive to its signalling molecule.¹⁶ At another locus, changes affect the migration of pigment cells (melanocytes) during embryogenesis and white spotting is the result of no melanocytes in that location.¹⁷

There are several examples where gene duplication followed by concerted evolution (i.e. a series of nucleotide changes that are adaptive) appears to have taken place.^{18,19} Despite the terminology, detailed examination indicates the evolutionary model can’t account for this naturalistically (i.e. via random mutation and natural selection). The idea that programming is involved in germline mutations has been ridiculed by evolutionists but it should be no surprise to creationists. There are several DNA editing enzymes that are used in the immune system.^{20,21} There is no reason why these or other DNA editing enzymes may not also play a valuable role in germline editing. It has been noted that meiosis is mutagenic beyond what is attributable to

homologous recombination and it is perfectly reasonable to suspect some of these changes may have purpose.²²

Thus, diversity has multiple sources. Evolutionists like to propose that all changes to DNA are essentially accidents or the result of unrepaired errors. While accidents and errors certainly do occur, it is unlikely that they have played a major role in adaptive genomic changes given the multiple *designed* mechanisms that could plausibly be involved to induce *strategic* DNA changes. It is important to recognize that adaptive changes can result in specialization and thus may be adaptive in a limited number of conditions. Further, in this fallen world, some adaptive genetic changes come at a significant cost (e.g. sickle-cell trait).

The purpose of diversity

The long-term study of Galápagos finches done by Drs Peter and Rosemary Grant provides an understanding of how diversity can benefit a population of organisms.²³ The medium ground finch (*Geospiza fortis*) was chosen for study because of the variability within the population. Birds with smaller beaks ate smaller, softer seeds and the birds with larger beaks ate larger, harder seeds. When a drought hit that eliminated the supply of smaller seeds, the birds with smaller beaks were more profoundly affected by starvation. Yet the population survived. Thus, variability within the population was important to help it withstand harsh environmental conditions that can arise in years with extreme weather conditions. It would have also been useful if there was a gradual shift in food source, but that was not observed.

A hedge against environmental uncertainties, the ability to overcome environmental challenges, and the ability to exploit new environmental niches as creatures fill the earth are very reasonable suggestions as purposes for diversity within a population. Yet from a creationist perspective there is more: it also shows God’s provision as He sustains life (Psalm 147:8,9; Matthew 6:25–34; Colossians 1:17)²⁴ and has been seen as evidence of His overflowing abundance and mercy in this fallen world.²⁵ This should become even more evident as we move on.

The origin of diverse populations / separate species

In the allopatric model of speciation, separate populations form when there is a barrier of some sort that prevents them from interbreeding. This can be a geographic barrier, such as a mountain range, a wide sea, or a great distance between optimal habitats. Over time these populations can diverge enough that biologists consider them separate species. Interestingly, this process is believed to have played an important role in the radiation of finches on the Galápagos Islands. It is thought that if these populations come back into

contact again, they will have diverged enough that they will not normally interbreed.²⁶

The Grants observed examples of closely related species coming in contact with each other on the island of Daphne Major. Some of these species were residents at the time the study began; others migrated in.²⁷ The Grants noted that normally there are behavioural barriers which prevent mating between species.²⁸ Young males normally learn to sing the same song as their fathers, and females tend to mate with birds that are morphologically similar to their fathers and sing the same song. This is usually enough to keep the birds mating within their own species. Occasional breakdowns occur for various reasons. For example, the father may die and the offspring may learn the song of a neighbour that belongs to a different species.

The phenotypic divergence that takes place during speciation may often be from the mechanisms discussed previously under the origin of diversity. Presumably many of the genetic (or epigenetic) changes would be adaptive. It would take volumes to fully explore the origin of diverse populations and mechanisms of diversification between them, and this is beyond the scope of this paper. For now, this provides enough of a basis to begin to explore the purpose of separate species.

The purpose of diverse populations / separate species

Based on field observations, there are several obvious benefits for separate, diverse populations that are classified as separate species based on morphology. In the example with the Galápagos finches, the effects of the periodic droughts (mainly due to the El Niño/La Niña cycle) on the medium ground finch (*G. fortis*; figure 1) varied depending on weather conditions in the previous years. While one drought preferentially eliminated birds with smaller beaks, another drought, which occurred after a series of very wet years, preferentially eliminated birds with larger beaks. This difference was because the seed abundance at the beginning of the drought was different, so a different food source was depleted first. However, the droughts were not the only factor identified as affecting the average beak size of the birds. The medium ground finch hybridized with several

other species that lived on the island (i.e. the cactus finch, *G. scandens*, and the small ground finch, *G. fuliginosa*) and regained some of the lost variability in beak size.

While the number of individuals in the population which hybridize with a second species is generally quite low, hybridization is a widespread phenomenon where closely related species come into contact with each other. It is being increasingly recognized that adaptive alleles can enter a population through these hybridization events. This is termed ‘adaptive introgression’.²⁹

In addition to providing a valuable reservoir of adaptive alleles to recover from harsh environmental extremes (natural selection in action), many are proposing examples where hybridization is involved in speciation.³⁰ In some cases the hybrids go on to form a distinct species.³¹ Beyond this, in certain conditions hybridization appears to provide a basis for adaptive radiation, the rapid diversification of organisms into new forms which can effectively exploit the resources in a variety of niches.^{32–34} In other words, speciation through hybridization appears to be one of the means by which God’s creatures reproduce and fill the earth (Genesis 1:22; 8:17).



Figure 1. The medium ground finch population was affected by a severe drought which changed the average beak size. Some of the lost variability was recovered by hybridizing with closely related species.

Many details as to why this occurs remain to be fully elucidated, though it appears both genetic and epigenetic factors can play a role.³⁵ From what is known already, it should be more likely for adaptive alleles to arise where there are more individuals, and multiple populations/species would provide this. Further, the effect of a mutation is often dependent on the genetic background; it could be that the likelihood that they will appear is influenced by this as well. Finally, hybridization sometimes releases a burst of transposable element activity. This has been recognized in the creation literature.³⁶ Many more examples have appeared in the secular literature since then.³⁷ This may be one source by which diversity is increased so adaptive radiation can occur.

The origin of hybrid sterility/inviability

There are situations where there is little or no discernable difference in the viability or fertility of the hybrids.³⁸ At other times hybridization results in hybrid vigour, a condition where offspring perform better than the parents. This phenomenon is often exploited in domestic species for agricultural purposes. The opposite can occur as well and is known as outbreeding depression.³⁰ From both a biblical and a scientific perspective, perhaps the most challenging aspect of speciation to explain is the origin and purpose of hybrid sterility or inviability.

There are many types of changes that may contribute to sterility or inviability. Pairing during meiosis depends on sequence similarity between homologous chromosomes. Significant differences in sequence can impair pairing, potentially resulting in failure to complete meiosis. Chromosomal rearrangements can contribute to this sequence divergence.³⁹ The effects vary from no perceivable difference, to reduced fertility (when only some cells fail to complete meiosis), to infertility associated with complete meiotic arrest. In addition to affecting fertility, sequence changes, including sizeable inversions, can affect viability.⁴⁰

In crops, male sterility can have several sources. There is cytoplasmic male sterility and germline male sterility. In the former, mutations in mitochondrial genes that affect the regulation of nuclear genes are the basis of the infertility. Several dozen such mutations have been identified in over a dozen different crop species. In the case of the latter, the sequence changes are within nuclear genes that affect the regulation of other nuclear genes affecting reproduction. In some cases of germline male sterility, environmental factors are involved. Epigenetic regulation by non-coding RNAs may allow for restoration of fertility with changes in growing conditions such as temperature or photoperiod.⁴¹

One fairly common pattern associated with speciation in animals is a rapid sequence divergence in male sex-biased

genes (e.g. in *Drosophila*⁴² and mice⁴³). These are often non-synonymous changes which appear to be correlated with abnormal patterns of gene expression in hybrid offspring. A large proportion of these genes are on the X chromosome, which is often referred to as the ‘large X effect’. The genes are normally expressed during spermatogenesis, but are misexpressed in hybrids which are infertile. Both *Drosophila* and mammalian males are heterogametic (XO and XY respectively), and are more likely than female hybrids to be affected by infertility. This phenomenon is described by Haldane’s Rule, which states: “When in the F1 [hybrid] offspring of two different animal races one sex is absent, rare, or sterile, that sex is the heterozygous [heterogametic] sex.”⁴⁴ This rapid divergence in X chromosome sequence of male-biased genes appears to be at least one reason why this pattern of male infertility is observed in these taxa.

The sequence changes are not limited to male-biased genes or the X chromosome. Autosomal loci have been shown to contribute as well. For example, in the house mouse (*Mus musculus*; figure 2) there are several subspecies where crosses can result in infertile males. In crosses between the subspecies *M. musculus musculus* and *M. musculus domesticus*, both a region on the X chromosome and another on chromosome 17 are found to be essential in the complete meiotic arrest associated with hybrid males having *M. musculus musculus* mothers. Despite being essential, incompatibility between alleles at these two loci is not sufficient to cause this phenotype; other loci are involved as well.⁴³

An underlying cause of meiotic breakdown appears to be asynapsis of chromosomes derived from different subspecies (i.e. heterosubspecific chromosomes). This suggests a divergence on the chromosomes themselves influencing the incompatibility. Thus, infertility is a result of a complex interaction between *trans* (loci on another chromosome)



Figure 2. The house mouse is undergoing speciation. Despite the fact that males are infertile in some crosses, there is significant gene flow in hybrid zones in Europe.

and *cis* (loci on the same chromosome) factors. Not only are multiple genetic loci involved, but sterility is associated with large-scale alteration of gene expression that shows a complex pattern of interaction.⁴⁵

While one might be inclined to suggest that incompatibilities arise from purely degenerative genomic changes (i.e. errors), this does not account for the pattern seen. Instead, there appear to be coordinated changes that occur within a species (or subspecies) that maintain fertility and viability.⁴⁶ Appropriate compensatory change is not something that can arise by chance processes. Instead, these changes appear to be possible because developmental systems and gene networks are designed with plasticity that allows for adaptation.⁴⁷

The purpose of post-zygotic reproductive isolation (hybrid infertility)

The effects of hybrid infertility are interesting. The infertility is often partial, affecting only one sex, usually males in mammals and females in birds (females are the heterogametic sex in birds). In some cases it is further limited to crosses in one direction. This is the case in the house mouse example already discussed, as only males with mothers from the *musculus* subspecies are normally affected. The severe sterility phenotype was not generally seen when the hybrids were crossed (F2), though the range of phenotypes suggests additional recessive loci affecting fertility.⁴⁵ All of this allows for considerable gene exchange in hybrid zones, though often the regions of the genome most strongly associated with the infertile phenotype do not cross the boundary well.⁴⁸

It has long been recognized that various regulatory changes can be associated with phenotypic diversity and adaptation.⁴⁹ These types of changes are involved in hybrid infertility as well. Thus, it is possible that hybrid infertility is not purposeful in itself, but is a side effect of effective adaptive changes accumulating separately in different populations. This would seem to make sense, given that the ability to reproduce and fill the earth was a blessing God bestowed on His creatures at Creation (Genesis 1).

However, since the phenomenon of hybrid infertility does alter gene flow between separate populations, it could be argued that it may serve a purpose in limiting the flow of particular genes. Certainly it does limit the gene flow of particular genic regions, but we are a long way from understanding if this is ever a truly beneficial phenomenon.

There is a case where infertility is a beneficial phenomenon; it is related to its appearance in crop species and has significantly benefited agricultural production. In order to harness the advantages of hybrid vigour, inbred lines need to be crossed. The problem is that crops such as corn are

monoecious; both sexes are in the same plant. To produce hybrid seed, the male portion of one of the lines must be inactivated to avoid self-pollination. At one time this was done manually (by cutting off the tassels), mechanically or chemically. This was expensive and had potentially harmful effects on the environment. However, with the appearance of male infertility genes, plants can now be bred so male sterility can be activated when needed and then restored if desired.⁴¹

Conclusions

This brief overview of some of the basic components of speciation shows that this phenomenon fits well within the biblical model. God blessed his creatures to reproduce and fill the earth, and so they have. The underlying mechanisms of diversification show design and forethought. This includes genomic networks that were designed to change adaptively. The origin and maintenance of separate populations allows for further adaptation of each, as well as a source of genetic variety that can be transferred between them as they adapt to the challenges they face in the world today. Thus, God's abundant provision and care for His creatures can be seen in what is currently known about speciation.

References

1. Lightner, J.K., Life: Designed by God to Adapt, *Answers in Depth* 3(1), www.answersingenesis.org/articles/aid/v3/n1/life-designed-to-adapt, 4 June 2008.
2. Lightner, J.K., Identification of species within the sheep-goat kind (Tsoan monobaramin), *J. Creation* 20(3):61–65, 2006; creation.com/images/pdfs/tj/j20_3/j20_3_61-65.pdf.
3. Lightner, J.K., Identification of a large sparrow-finch monobaramin in perching birds (Aves: Passeriformes), *J. Creation* 24(3):117–121; 2010, creation.com/sparrow-finch-baramin.
4. Carter, R.W., The Non-Mythical Adam and Eve! Refuting errors by Francis Collins and Biologos, creation.com/historical-adam-biologos.
5. Lightner, J.K., Karyotypic and allelic diversity within the canid baramin (Canidae), *J. Creation* 23(1):94–98, 2009; creation.com/images/pdfs/tj/j23_1/j23_1_94-98.pdf.
6. Tennesen, J.A., Bigham, A.W. and O'Conner, T.D. *et al.*, Evolution and functional impact of rare coding variation from deep sequencing of human genomes, *Science* 337(6090):64–69, 2012; and Fu, W., O'Conner, T.D. and Jun, G., *et al.*, Analysis of 6,515 exomes reveals recent origin of most human protein-coding variants, *Nature* 493(7431):216–220, 2013.
7. Wood, T.C. and Cavanaugh, D.P., A baraminological analysis of subtribe Flaveriinae (Asteraceae: Helenieae) and the origin of biological complexity, *Origins* 52:7–27, 2001.
8. Wood, T.C., Mediated design, ICR Impact #363, www.icr.org/i/pdf/imp/imp-363.pdf.
9. Gowik, U. and Westhoff, P., The path from C3 to C4 photosynthesis, *Plant Physiology* 155:56–63, 2011.
10. Skinner, M.K., Gurrero-Bosagna, C., Haque, M.M., Nilsson, E.E., Koop, J.A.H., Knutie, S.A. and Clayton, D.H., Epigenetics and the evolution of Darwin's Finches, *Genome Biology and Evolution* 6(8):1972–1989, 2014.
11. Wood, T.C., The AGEing process: Rapid post-Flood intrabaraminic diversification caused by Altruistic Genetic Elements (AGEs), *Origins* 54: 5–34, 2002.
12. Terborg, P., The design of life: part 3—an introduction to variation-inducing genetic elements, *J. Creation* 23(1):99–106, 2009.

13. Terborg, P., The design of life: part 4—variation-inducing genetic elements and their function, *J. Creation* **23**(1):107–114, 2009.
14. Shan, E.L., Transposon amplification in rapid intrabaraminic diversification, *J. Creation* **23**(2):110–117, 2009.
15. Ayarpadikannan, S., Lee, H.E., Han, K. and Kim, H.S., Transposable element-driven transcript diversification and its relevance to genetic disorders, *Gene* **558**(2): 187–194, 2015.
16. Lightner, J.K., Genetics of coat color I: The melanocortin 1 receptor, *Answers Research J.* **1**:109–116, 2008.
17. Lightner, J.K., Post-Flood mutations of the KIT gene and the rise of white colouration patterns, *J. Creation* **24**(3):67–72, 2010.
18. Lightner, J.K., Gene duplications and nonrandom mutations in the family cercopitheciidae: evidence for designed mechanisms driving adaptive genomic mutations, *CRSQ* **46**(1): 1–5, 2009.
19. Lightner, J.K., Gene duplication, protein evolution, and the origin of shrew venom, *J. Creation* **24**(2):3–5, 2010; creation.com/images/pdfs/tj/j24_2/j24_2_3-5.pdf.
20. Chandra, V., Bortnick, A. and Murre, C., AID targeting: old mysteries and new challenges, *Trends in Immunology* **36**(9):527–535, 2015.
21. Harris, R.S. and Dudley, J.P., APOBECs and virus restriction, *Virology* **479–480**: 131–145, 2015.
22. Lightner, J.K., Meiotic recombination—designed for inducing genomic change, *J. Creation* **27**(1):7–10, 2013.
23. Grant, P.R. and Grant, B.R., *40 Years of Evolution: Darwin's Finches on Daphne Major Island*, Princeton University Press, Princeton, NJ, 2014.
24. Lightner, J.K., The effect of mutations down on the farm, *Answers in Depth* 2010, from answersingenesis.org/genetics/mutations/the-effect-of-mutations-down-on-the-farm/ accessed, 4 September 2015.
25. Sanders, R., The best seat in the house, *Answers* **3**(3): 66–68, 2008.
26. Grant and Grant, ref. 23, pp. 4–8.
27. Grant and Grant, ref. 23, pp. 35–39; 103–121; 140.
28. Grant and Grant, ref. 23, pp. 138–165.
29. Hedrick, P.W., Adaptive introgression in animals: examples and comparison to new mutation and standing variation as sources of adaptive variation, *Molecular Ecology* **22**(18):4606–4618, 2013.
30. Abbott, R. *et al.*, Hybridization and speciation, *J. Evolutionary Biology* **26**(2): 229–246, 2013.
31. This appears to have happened on Daphne in the Galápagos Islands. See chapter 13 in Grant and Grant, ref. 23.
32. Palmer, D.H. and Kronforst, M.R., Divergence and gene flow among Darwin's finches: A genome-wide view of adaptive radiation driven by interspecies allele sharing, *Bioessays* **37**(9):968–974, 2015.
33. Litsios, G. and Salamin, N., Hybridisation and diversification in the adaptive radiation of clownfishes, *BMC Evolutionary Biology* **14**:245, 2014.
34. Stankowski, S. and Streisfeld, M.A., Introgressive hybridization facilitates adaptive divergence in a recent radiation of monkeyflowers, *Proceedings of the Royal Society: Biological sciences* **282**(1814), 2015.
35. Greaves, I.K., Gonzalez-Bayon, R., Wang, L., Zhu, A., Liu, P.C., Groszmann, M., Peacock, W.J. and Dennis, E.S., Epigenetic changes in hybrids, *Plant Physiology* **168**(4):1197–1205, 2015.
36. Jerlström, P., Jumping wallaby genes and post-Flood speciation, *J. Creation* **14**(1): 9–10, 2000.
37. Belyayev, A., Bursts of transposable elements as an evolutionary driving force, *J. Evolutionary Biology* **27**(12):2573–2584, 2014.
38. Grant and Grant, ref. 23, pp. 156–157.
39. Lightner, J.K., Karyotype variability within the cattle monobaramin, *Answers Research J.* **1**:77–88, 2008.
40. Sugimoto, M., Developmental genetics of the mouse t-complex, *Genes & Genetic Systems* **89**(3):109–120, 2014.
41. Chen, L. and Liu, Y.G., Male sterility and fertility restoration in crops, *Annual Review of Plant Biology* **65**:579–606, 2014.
42. Ortiz-Barrrientos, D., Counterman, B.A. and Noor, M.A.F., Gene expression divergence and the origin of hybrid dysfunctions, *Genetica* **129**:71–81, 2007.
43. Bhattacharyya, T., Reifova, R., Gregorova, S., Simecek, P., Gergelits, V., Mistrík, M., Martincova, I., Pialek, J. and Forejt, J., X chromosome control of meiotic chromosome synapsis in mouse inter-subspecific hybrids, *PLoS Genetics* **10**(2):e1004088.
44. Haldane, J.B.S., Sex-ratio and unisexual sterility in hybrid animals, *J. Genetics* **12**:101–109, 1922.
45. Turner, L.M., White, M.A., Tautz, D. and Payseur, B.A., Genomic networks of hybrid sterility, *PLoS Genetics* **10**(2):e1004162, 2014.
46. A similar pattern with different specifics is documented in hybrids between *M. musculus* subspecies *domesticus* and *molossinus*. Oka, A., Takada, T., Fujisawa, H. and Shiroishi, T., Evolutionarily diverged regulation of X-chromosomal genes as a primal event in mouse reproductive isolation, *PLoS Genetics* **10**(4):e1004301, 2014.
47. Lightner, J.K., Developmental system plasticity—a brief initial assessment of extent, design, and purpose within the creation model, *J. Creation* **28**(3):67–72, 2014.
48. Macholán, M., Baird, S.J.E., Dufková, P., Munclinger, P., Bimová, B.V. and Piálek, J., Assessing multilocus introgression patterns: a case study on the mouse X chromosome in central Europe, *Evolution* **65**(5):1428–1446, 2011.
49. Wray, G.A., The evolutionary significance of cis-regulatory mutations, *Nature Reviews Genetics* **8**(3):206–216, 2007.

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