



## THE CRS eKINDS RESEARCH INITIATIVE: WHERE WE HAVE BEEN AND WHERE WE ARE HEADED FROM HERE

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### ABSTRACT

The eKINDS research initiative began in 2016 in an effort to accelerate research on numerous outstanding questions related the diversification and speciation of plants and animals. The research encompasses three broad topics: a) identification of created kinds, b) identification of mechanisms that drive diversification and speciation within created kinds, and c) detailed analysis of individual created kinds in an attempt to propose a robust natural history that delineates key events as organisms reproduced and filled the earth following the time of the Flood.

As part of the eKINDS project, a new statistical tool is being developed to take advantage of the steadily increasing pools of molecular data. It compares expressed proteins, which typically cluster organisms into discreet groups, suggesting that members of a group may belong to a single kind. This method has been applied to insects and fungi. Additionally, analysis has begun on primates and other vertebrates. There are plans to use it on more taxa as proteomic data accumulates.

The eKINDS project is also investigating the possibility that designed mechanisms exist for the generation of adaptive alleles. Some work has been done to explore the significance of founding events in post-Flood diversification and speciation. Other mechanisms are slated to be explored as well. Several avian kinds are being investigated in an attempt to piece together key aspects of their natural history. Our hope is that, by God's grace, more researchers will be mobilized to address these critical questions so we, as believers, can make substantial contributions to science and demonstrate the robustness of the biblical creation model.

### KEY WORDS

Speciation, diversification, adaptation, evolution, post-Flood, baraminology, mutation, eKINDS

### INTRODUCTION

The acronym eKINDS stands for *examination of kinds in natural diversification and speciation*. This Creation Research Society (CRS) research initiative was developed to help resolve numerous outstanding questions surrounding the post-Flood repopulation of the earth by plants and animals. These questions can be broadly grouped as follows: 1) Which organisms today are descended from the same created kind?, 2) What mechanisms are involved in creating the diversity that we see within created kinds?, and 3) Can we trace the natural history of various animal kinds as they moved from the Ark and repopulated the earth?

While considerable work has been done in the last decade to estimate the kinds of animals that were present on the Ark, it has highlighted the reality that there is still considerably more work yet to do (Wood 2008; Lightner 2012; Lightner 2013; Hennigan 2013a, b; Hennigan 2014 a, b; Ross 2014; Hennigan 2015). Hybridization between two species is generally considered to be the most reliable way to determine that both descended from the same kind. This is because reproduction is an enormously complex process that requires compatibility on multiple levels, suggesting that reproduction could not occur between two organisms unless they were specifically designed for this possibility. Thus, hybridization indicates holistic similarity (continuity) suggesting both species belong to the same kind (Wood et al. 2003; Lightner et al. 2011). Hybrid data has shown continuity between different genera in a family, and in some cases between multiple families to the point of showing continuity in an entire order (Lightner 2012; Lightner

2013).

For a variety of reasons, hybrid data may be unavailable for specific organisms. The absence of hybrid data, itself, does nothing to indicate if a species belongs to a particular kind. Sometimes there is a lack of mating opportunity, or hybridization may occur but we have not observed it. However, it is also recognized that the ability to hybridize can be lost over time. This can be due to regulatory shifts, as seen in the house mouse (Larson et al. 2016), and may affect life history traits including food preferences, as seen in mosquitoes (Byrne and Nichols 1999). To help ascertain the baramin status of species when hybridization data is not available, statistical tests, i.e., Baraminic Distance Correlation (BDC) and Multidimensional Scaling (MDS), have been developed. There is clearly value to these tests. However, as with any statistical method, they have their limitations (Lightner et al. 2011). Most notably, they rely on the availability of suitable datasets for analysis.

Many of the recent works attempting to estimate the number of kinds in various vertebrate taxa have defaulted to the level of the family simply because insufficient data was available to make a case for the kind to fall elsewhere along current taxonomic boundaries (Lightner 2012; Lightner 2013; Hennigan 2013a, b; Hennigan 2014 a, b; Ross 2014; Hennigan 2015). Since molecular data is rapidly accumulating for many species, the eKINDS project is sponsoring research to develop a statistical tool that can use this data to make initial estimates of created kinds. This approach

involves comparing all cataloged proteins expressed in different species to known orthology groups, and grouping organisms based on similar orthology content (O’Micks 2017).

For those groups where sizable monobaramins have been identified based on hybrid data, it is clear that considerable diversity exists. At the lay level, creationists have often attributed this to recombination of created alleles, mutation (which is often attributed to random error), and natural selection. Certainly these mechanisms were in operation, but numerous lines of evidence suggest these are insufficient to solely account for many of the patterns we observe today (Rupe and Sanford 2013; Lightner 2015; Anderson 2016). For example, many adaptive alleles are rare and only advantageous in specific environments. This suggests they are not created alleles, but arose rapidly when a particular trait was needed by the organism. Neo-Darwinian mechanisms (random mutation and natural selection) are not genetically adequate for explaining this pattern (Lightner 2014; Lightner 2015).

The eKINDS project is investigating alternative mechanisms for the production of new, potentially adaptive alleles in vertebrates, such as mechanisms of directed mutation. It is well known that DNA editing occurs during meiosis in a process known as homologous recombination, which encompasses both crossing over and gene conversion. DNA editing is also involved in antibody formation as part of the immune system; this includes somatic hypermutation and class switch recombination. These processes are essential for life. It has been noted that one of the enzymes used in antibody formation, activation-induced cytidine deaminase (AID), has also been found in the germline (e.g., see discussion in Lightner 2016). As part of the eKINDS project, we intend to look for evidence that this enzyme may have been active in making heritable genetic changes.

The generation of new alleles is only one factor involved in diversification and speciation. There also are mechanisms that can increase or decrease the prevalence of alleles in a population. Natural selection has been reviewed in detail elsewhere (Lightner 2015). Genetic drift is considered to be important in small or declining populations. Other factors, some of which we have begun to explore in more detail as part of the eKINDS project, are founder events, hybridization, and non-Mendelian inheritance. Non-Mendelian inheritance, often termed “meiotic drive,” was first recognized over sixty ago. It involves the preferential transmission of one allele over the other in a heterozygous genotype. Probably the best known example is biased gene conversion (Lightner 2015).

Based on their world-view, evolutionists have assumed that meiotic drive is always random with respect to fitness, which appears to be a convenient excuse to ignore its effects. However, the reality that complex designed mechanisms underlie gene conversion suggests that various forms of meiotic drive may actually be designed to facilitate the spread of potentially adaptive alleles. Thus, meiotic drive is important to examine in more detail.

Finally, evolutionists have often taken biologic and fossil data and attempted to infer the natural history of organisms as they have transformed through time. The problem with their explanations is that they assume universal common ancestry and do not account

for the global Flood of Noah’s time. Creationists are in a position to propose a more robust natural history of life, based upon both biblical history and physical evidence from creation. As we attempt to do this, we should continue to uncover evidence that substantiates (or possibly modifies) our current understanding of kinds, and how God designed them to reproduce and fill the earth.

### IDENTIFYING KINDS

The molecular based baraminology method the eKINDS project has been developing measures the similarity in expressed orthologous protein content (using the Jaccard Coefficient Value, or JCV) between species and assigns them to individual baramins. It is based on the assumption that different created kinds were likely endowed with a different array of protein coding genes, which have remained largely conserved throughout history. It assumes similarity in phenotype has been retained within baramins, and an analogous set of core proteins underlies this similarity. The method has been applied to various prokaryotic groups, and clustering based on orthologous proteins was found. It should be noted that the term “orthologous” is used for simplicity, but the evolutionary interpretation that similar protein coding genes have all arisen from common ancestry is rejected (O’Micks 2017). In a creation paradigm, similar proteins may have been provided for separate kinds when there was a biologically sound reason for doing so (just as reuse of design elements is common in human engineering).

Within the eKINDS project, this method was first applied to 104 insect species from four orders (Diptera, Hemiptera, Hymenoptera, and Lepidoptera) (O’Micks and Lightner, unpublished data). Diptera forms two clear clusters. The first cluster was comprised of the species in the suborder Nematocera, which included five species of mosquitos (family Culicidae). The second dipteran cluster included members from four of the numerous families in the suborder Brachycera. These four families are in different superfamilies, and represent a sizable portion of this suborder. Hemiptera split into two clusters, only one of which was statistically significant. The pattern was unpredicted based on current taxonomic status, and many members of the cluster that lack statistical significance had far fewer orthologs than the others (<7500).

All 43 species of Hymenoptera that were included in this study fell into one cluster. They represented 14 different families across the three major groupings in the order: Aculeata (ants, bees and stinging wasps), “Symphyta” (sawflies, horntails and wood wasps), and “Parasitica” (parasitic Apocrita) (BugGuide.net). The ten species of Lepidoptera, which represented six different superfamilies, clustered together, though two of them with fewer orthologs (<6000) did not group as strongly as the others.

Comparisons have also been run between humans and other primates. In this case humans (*Homo sapiens*, Denisovans and Neanderthals) formed a clear cluster, and great apes clustered with the Old World and New World monkeys. When a larger group that included other mammals and birds was analyzed, differences between humans and other primates were comparable to the differences between humans and some of the cats (Fig. 1).

There are several conclusions we can draw from these comparisons. First, there is clear discontinuity within the class Insecta, and sometimes it is below the level of the order (e.g., Diptera). There

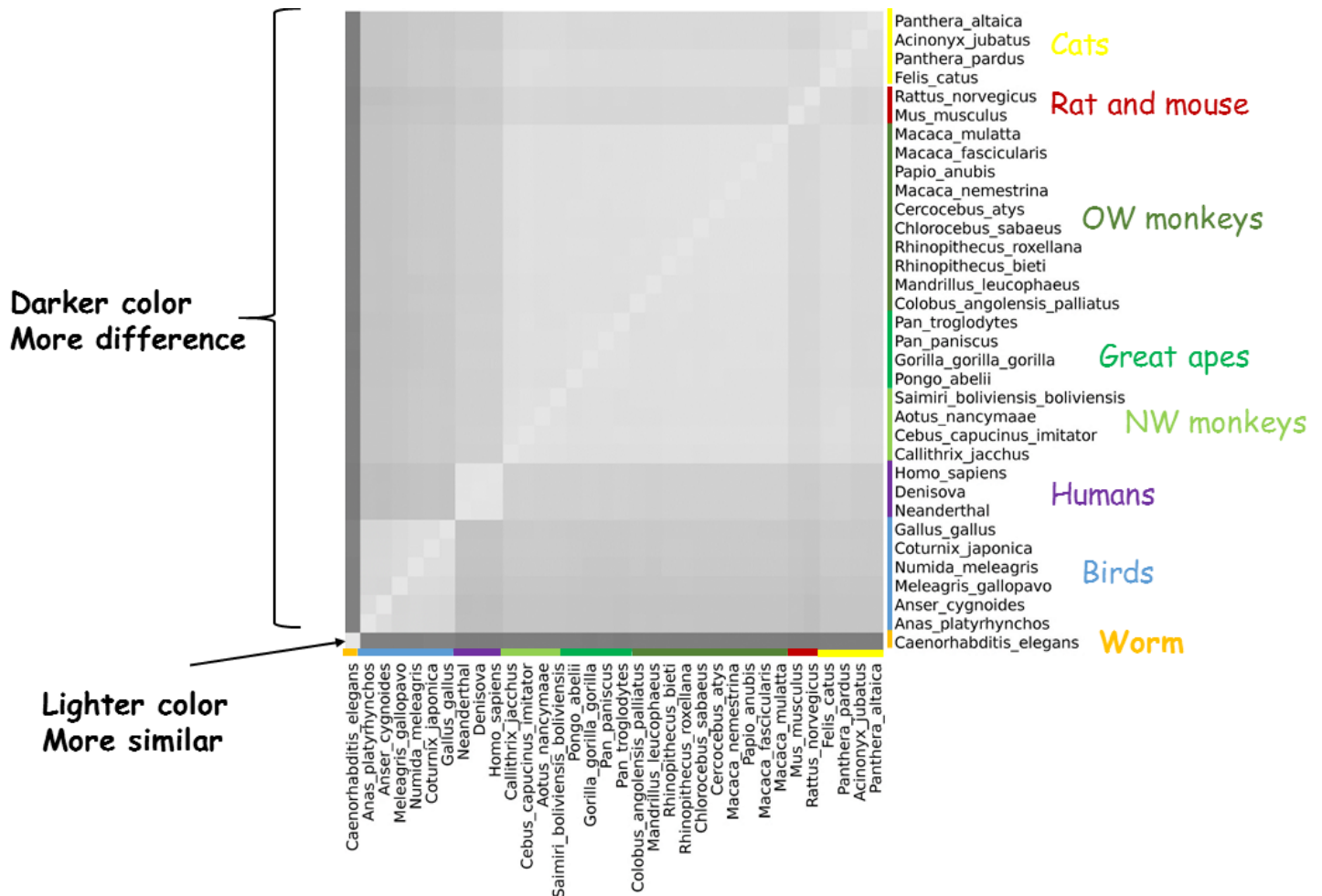
is also clear discontinuity between humans and all other mammals, including primates (Fig.1). These types of gaps are not predicted if all life shares common ancestry. It is consistent with the view held by many creationists that discontinuity should be evident, especially between separately created kinds. It is fully consistent with the belief that humans were separately created in the image of God, and should not be too surprising given that a significant number of genes are either unique to humans or distinct in humans (Genesis 1:26-28; 2:7; Stahl and Wainszelbaum 2009; Tomkins 2016).

It is worth noting that the eminent entomologist Erich Wasmann (1859-1931), who rejected universal common ancestry, used detailed morphological comparisons to conclude that Termitoxeniidae (now placed in Phoridae), Muscidae and Phoridae are from the same “branch of Diptera stock.” (Wasmann 1910, p. 383). This is consistent with the Brachyceran cluster found in our

study that includes species from Muscidae and Phoridae, families that are currently placed in two different sections in Brachycera: “Aschiza” and Schizophora (though sources vary since insect taxonomy is in flux).

Superficially, large baramins encompassing suborders or even orders of insects may seem in conflict with accumulating data on taxonomically restricted genes, or orphan genes, which creationists have suggested may help delineate created kinds (Tomkins 2013). This is especially relevant given that many taxonomically restricted genes were found in ants, members of the insect order Hymenoptera (Simola et al. 2013). All hymenopteran species included in our study, which included ants, bees, and wasps, grouped in a single cluster.

As it turns out, one needs to use taxonomically restricted *essential* genes to determine if two species can be part of the same family tree (Tan 2015). This works well when the assumption is that the



**Figure 1.** A heat map, or diagram indicating similarity of expressed “orthologous” proteins in various vertebrates, with an invertebrate nematode (worm) as an outgroup. The term orthologous is used for convenience to indicate proteins of similar sequence; the assumption they are derived from a common ancestor is not retained in interpreting the results. Each species listed on the right is also listed at the bottom. The nearly white individual boxes running on a diagonal from the lower left to upper right are where each species is compared to itself. They are very light colored because they share all their “orthologous” proteins with themselves. When comparing any individuals, the lighter the color, the greater the similarity; the darker the color, the greater the dissimilarity. Note that the birds in this study form a cluster (with a possible subtle division within them). Humans strongly cluster together. The great apes, which evolutionists claim are our closest ancestors, do not cluster with human, but instead are found in a large cluster between Old World and New World monkeys. In the row containing the three humans (*Homo sapiens*, Denisova, and Neanderthal), the dark regions indicate we are most dissimilar to invertebrates, as compared to birds. The data indicates that we share a fair amount of similarity to other mammals, but clearly are distinct from them.



(hypothetical) common ancestor was less genetically complex. However, it is not as straightforward if the common ancestor was more complex, with significant genetic redundancy. While the evolutionary paradigm sees organisms as progressing from simple to complex, the creationary view is different. Creationists have pointed out that significant redundancy is part of the design of organisms (Terborg 2008). This is believed to provide a basis for organisms to adapt via genomic editing as they have reproduced and filled the earth (Terborg 2009). This implies that as redundancy is lost through genetic adaptation to diverse environments, different genes may become essential in different lineages. This would be a consequence of significant changes in genes that could previously take over for another function if the primary gene is inactivated.

It is also noteworthy that molecular data from insects has prompted evolutionists to postulate massive gene gains to account for various insect orders from a common ancestor. This is because there are thousands of genes unique to these insect orders. In contrast, at lower taxonomic levels, there is primarily a pattern of gene loss that can account for the origin of the numerous extant species from a common ancestor (Rosenfeld et al. 2016). Thus, insect baramins encompassing an order, or a similar high taxonomic level, seem to be consistent with several lines of evidence.

#### MECHANISMS OF DIVERSIFICATION AND SPECIATION

The amount of diversity observed within species of domestic animals and cultivated plants can be significant, sometimes with hundreds or even thousands of breeds or cultivars being recognized (FAO 2015; Janick and Moore 1996). In some monobaramins that were identified based upon hybrid data, diversity can be surprisingly large as well (Lightner 2010). The eKINDS project includes research on the origin of diversity, and the partitioning out of diversity to produce the wide variety of species we have today.

Activation-induced cytidine deaminase (AID) is an enzyme active during antibody formation. It targets a specific motif of DNA (WRC; W = A or T, R = A or G) to induce mutations necessary for forming antibodies (e.g., see Lightner 2016). A program was written to identify regions of the human genome where the WRC motif occurs at high frequency. We hope to analyze the data to see if these regions correspond to highly polymorphic regions in the human genome, which might suggest AID has been active in this region.

Scientists recognize the environmentally based sorting of ancestral alleles as a key factor in diversification and speciation. While the “culling” effect of natural selection is one means by which this may occur, the eKINDS project examined another mechanism: founder events. The history of the development of ideas on the founder effect was reviewed, including observational and theoretical work (Lightner and Ahlquist 2017). While evolutionists generally assume the founder effect is a form of genetic drift (i.e., the alleles involved are random with respect to fitness), observational data suggests many animals choose the environments to which they are best suited. The post-Flood spread of animals, as they invaded newly forming habitats, would have led to an unprecedented number of founding events. Theoretical work on this subject suggests this would have set the stage for rapid diversification and speciation.

#### NATURAL HISTORY OF SPECIFIC KINDS

Observations of patterns within paradise kingfishers formed part of the basis for Ernst Mayr’s proposal of the founder effect (Mayr 1954). Thus, in conjunction with our recent paper on founder events (Lightner and Ahlquist 2017), we are examining kingfishers in general and paradise kingfishers in particular. Morphological traits, geographical distribution, and habits are being investigated to propose a biblically based natural history for this taxonomic group. The landfowl (Galliformes) are similarly being investigated. Ideally, we would like to use our newly developed statistical test on these taxa, but the necessary data for adequate testing to be performed is currently unavailable.

#### CONCLUSIONS

The eKINDS project has begun to explore new datasets and synthesize relevant scientific literature as it investigates created kinds, including the means by which they have diversified and filled the earth. Our newly developed statistical tool has used proteomic data, and initial results suggest that the level of the kind may be fairly high among insects (suborder to order), which is similar to what was found in some avian taxa based on known hybridization. Further work is needed to see what factors (e.g., number of taxa, taxonomic level(s) included, etc.) may influence our results, and if clusters can sometimes be above or below the level of the kind. The results need to be validated, and baramins should be considered tentative until confirmed by other lines of evidence that point to the same conclusion. As with other statistical tests, our method is limited by available data. Ideally, we would have the means to sequence and submit proteomic data from species of our choice. Perhaps God will open that door in the future. In the meantime, we are constrained to wait until sufficient data becomes available to investigate a specific taxon. Nevertheless, this tool appears to hold considerable promise for future creation research.

Mechanisms by which organisms have diversified and filled the earth have begun to be studied in more detail. Investigations have begun on an enzyme known to be active in immune system DNA editing (AID). This enzyme is known to be expressed in the germline, but so far it has not been demonstrated to play a role in generating potentially adaptive mutations that can be passed on to the next generation. The founder effect has also been studied in detail, including both theoretical and observational based evidence on how it can play a role in diversification and speciation. Based on the biblical history of post-Flood migration to repopulate the earth, it is clear that founder events must have played a significant role in the sorting of ancestral alleles in many animal kinds. This would have set the stage for further mechanisms to increase the divergence between populations, eventually leading “in some cases” to speciation. Other mechanisms, including non-Mendelian inheritance (meiotic drive), need to be investigated in more detail.

Finally, in depth study of various created kinds has begun with two avian taxa: kingfishers (Alcedinidae) and landfowl (Galliformes). By examining morphological, geographical, and life history data, we should be able to accomplish several things. First, it provides other lines of evidence to corroborate (or contradict) the boundaries of the created kind proposed by other methods. Second, it may provide a glimpse at what type of mechanisms are operating in particular circumstances as organisms diversify and speciate.

In concert with this, it should allow us to discern what types of traits tend to be variable, and which traits are more fixed. Finally, multiple lines of evidence can be synthesized to propose a robust natural history within various kinds of animals as they left the Ark and filled the earth.

The eKINDS project has already helped to expand the creation model regarding diversification and adaptation of the original kinds. It is our hope that, by the grace of God, the project will gain momentum and more researchers will contribute. This would enable us, as believers, to significantly advance the creation model as we come to more fully understand the world God created.

#### ACKNOWLEDGEMENTS

We wish to express our thanks to Matthew Cserhati for providing the heat map and reviewing a draft of this paper. We also wish to thank the donors of the eKINDS project, which makes this work possible.

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### THE AUTHORS

Dr. Lightner has participated in creation research, especially as it relates to vertebrates, for well over a decade. She has published in numerous creation publications, both at the technical and lay-level. In 2009 she joined the Board of Directors of Creation Research Society (CRS). In 2016 she helped launch the CRS eKINDS (examination of Kinds In Natural Diversification and Speciation) project to help bring together researchers to address many of the outstanding questions about diversification and speciation in the post-Flood world.

Dr. Anderson holds a Ph.D. in microbiology and was an N.I.H. post-doctoral fellow. He has held university professorships as well

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### NOMENCLATURE

**Apobaramin** – a group of known organisms that are discontinuous with all other known organisms, and may be divided internal by discontinuity.

**Archaeobaramin** – the originally created ancestors in a created kind

**Holobaramin** – the group of all known organisms that show continuity within, but are discontinuous with any other group. In theory this means all known members from a single created kind.

**Monobaramin** – a group of known organisms that shares continuity, and may or may not be separated from other known organisms by discontinuity.