Mendelian speciation: part 4—adaptive radiations and *cis*-evolution

Nigel E.A. Crompton, Thomas Sprague, Royal Truman, and Reinhard Junker

When an abundance of new species arises in a restricted geographical location, a logical consequence of Mendelian speciation, the process is referred to as an 'adaptive radiation'. A number of well-researched examples confirms that adaptive radiations occur far more quickly than can be explained by random mutations. All the various species that arise over time and in various geographic locations via Mendelian speciation, including any and all adaptive radiations, give rise to a single genetic family. The range of variation possible, from all potential combinations of pre-existing genetic information, defines phenotypic limits to such genetic families. Biodiversity observed within these genetically constrained, yet modifiable, limits is called, here, '*cis*-evolution'. These genetic families are considered equivalent to Genesis kinds or baramins. Mendelian speciation is consistent with straightforward reading of Genesis. It provides an eminently reasonable and entirely satisfactory solution to rapid speciation as required by a young-earth understanding of origins.

This fourth paper looks at the consequence of Mendelian speciation over a series of generations. It describes adaptive radiations observed in nature and how these result from poly-heterozygous ancestors. They are a natural consequence of Mendelian speciation. The paper also clarifies the difference between *cis*-evolution, speciation radiations observed to occur within genetic families (baramin) based on pre-existing genetic programs, and *trans*-evolution, speciation radiations claimed to occur between genetic families (baramin) but for which no realistic genetic mechanisms are currently known.

Adaptive radiations rely on pre-existing genetic programs

Why is loss of heterogeneity so important for speciation? If only complete heterogeneity were present, only the pan-dominant phenotype would be seen, as discussed in part 2 of this series.[1] All those potential phenotypes, resulting from combinations of recessive and hypostatic trait expression, would be invisible. Loss of heterozygosity must occur so that the enormous wealth of phenotypic potential that otherwise lies latent in a genome can be revealed.

Mendelian speciation gives rise to many new phenotypes (potential species). As few as 10 two-trait characters allow for the emergence of a thousand ($2^{10} = 1{,}024$) distinct phenotypes. Very few vertebrate families show so much variation (or species). Most mammalian families have fewer than 100 distinct species. Furthermore, Mendelian speciation can give rise to all these new species within relatively few generations. If these are maintained in populations, separated by reproductive isolation, the result is a sudden burst of species referred to as an 'adaptive radiation'.

Would all the possible variations ever be observed in nature? That is very unlikely. Nevertheless, dramatic examples of extensive variability and speciation are seen in adaptive radiations. In molecular sequencing studies, these have been confirmed to arise from existing genetic information, as will be described below. Remarkable examples include:

- the picture-wing Drosophilas (sometimes called the birds of paradise of the insect world) on Hawaii
- the silversword plant group also on Hawaii
- the cichlids in the Great East African Lakes, and
- the finches on the Galápagos islands, and also on Hawaii.

A question that immediately comes to mind when studying adaptive radiations is, why do some plants and animals display prominent adaptive radiations, whereas others, in similar situations, display little or no speciation? In Hawaii the finches (honeycreepers) underwent a significant diversification, producing 20 genera and 51 species, but the thrushes and owls produced very few; four species and one subspecies, respectively. Adaptive radiations result from Mendelian speciation; therefore, an immediate answer is found in the degree of heterozygosity carried by any founder species. Those species with significant numbers of heterozygous genes can give rise to many new species, but those with few heterozygous genes can only give rise to a few.

Radiation of *Drosophila*

The nearly 1,000 *Drosophila* species native to Hawaii are believed to have arisen from a single ancestral species. Carson analyzed all the chromosome structures (karyotypes)

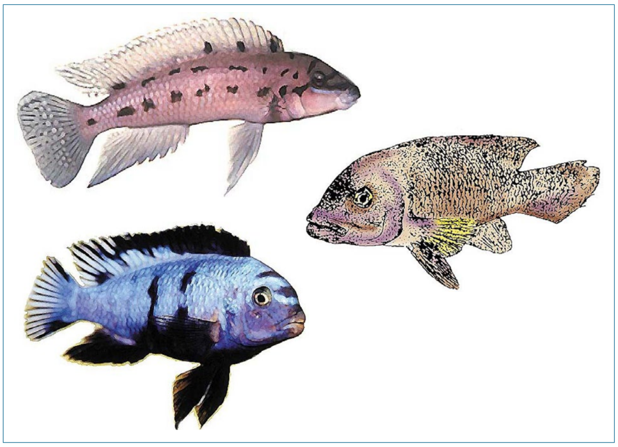

Figure 1. Examples of the diversity of cichlids in East African lakes. From above: *Pseudotropheus saulosi, Lamprologus* spec. and *Chalinochromus ndobhoi*.

of the existing species in the picture-winged Drosophila group.[2] Recognizing that chromosome inversions had occurred allowed him to trace the speciation events back to the original founder karyotype—possibly from South America.

The inversions *per se* do not explain how the phenotypic changes came about.[3] It is known that the radiation of the ~112 species in the picture-winged group proceeded with relatively few changes in DNA sequence.[4] If this radiation resulted from the loss of heterozygosity, as we propose, then few DNA sequence changes would have been required, merely recombination and homozygosity in new combinations of already existing alleles.

Radiation of silverswords

The silversword plants of Hawaii include trees, shrubs, subshrubs, semi-woody rosette plants, carpet plants, cushion plants, and lianas. This group includes three genera: *Argyroxiphium*, *Dubautia* and *Wilkesia*, and 33 species. Despite the great variety of forms, most can be interbred, and molecular phylogenetic analysis indicates it is a monophyletic species group that arose from a single founder event.

The plants are allopolyploid (their usual chromosome number n = 14) and are believed to have arisen from a cross between *Anisocarpus scabridus* (n = 7) and *Carlquistia muirii* (n = 8), two species of California tarweeds, followed by chromosome number reduction to n = 14. Studies of their homeotic flower genes, *ASAP1* and *ASAP 3*, provide strong experimental confirmation for the hybrid origin of these plants.[5]

Detecting translocation events in the different genera allowed researchers to trace back lineages, similar to *Drosophila*.[6] However, these translocation events were not the mechanism responsible for the different morphological forms but only important markers of the divergences that took place.

It is loss of heterozygosity that offers an explanation for the extensive phenotypic diversity observed in this group of plants and for their potential to adapt so extensively and to segregate into a large number of forms. The tetraploid state of the original tarweed cross might have unmasked various genes in the resultant silversword genome, potentially altering the dosage of regulatory proteins, which could have led to the rich phenotypic diversity. Because silverswords derive from tarweeds, they are only a part of a larger family. Their radiation has given rise to a whole taxonomic clade, with either tribe or subfamily status.[7,8]

Radiation of cichlids

Cichlids found in the large East African lakes display significant morphological differences, as illustrated in figure 1. Species vary in length from a few centimetres to about 30 centimetres.

There are many trait reiterations between species in the cichlid radiations in these three lakes, which are understood to arise from pre-existing genetic programs and common ancestry. There is a consensus that dramatically rapid adaptive radiations occurred in these cichlids, serving as examples of sympatric speciation.[9]

The cichlids display a wide variety of specialized anatomical features related to feeding. The range of alternatives includes: feeding on other fish or on their eggs and larvae, chewing off fins, scraping algae, tearing off scales, or crushing molluscs. A multitude of other anatomical features are also observed in these fish in the three lakes: Tanganyika, Victoria, and Malawi.[10]

In Lake Victoria there are >500 cichlid species based on only two lineages.[11] However, in spite of these enormous phenotypic differences, DNA analysis has revealed that the large majority of cichlids in Lake Victoria are descended almost entirely from a single lineage of mouth brooders. Since all the different phenotypes are found in multiple lakes, the obvious explanation is that almost identical species evolved many times independently.[10]

Detailed analysis has led to the conclusion that algae scrapers in Lake Victoria and Lake Malawi diverged independently from an ancestor from Lake Tanganyika, which had more generalized feeding capabilities. The >500 species of cichlids in Lake Malawi were shown to be descended from only a single ancestor.[12]

Significantly, it was shown that the huge variety of cichlids in Lake Victoria must have developed extremely rapidly from a conventional evolutionary point of view. The >500 species contained less genetic variation than the single species *Homo sapiens*. Since palaeoclimatological data is believed to show that Lake Victoria dried out almost completely less than 14,000 radiometric years ago, killing all or virtually all, the fish living there, the huge morphological variety must have arisen since then from a small founder or surviving population.

A similar explosive radiation of cichlids, occurring during a short window of ecological opportunity, appears to have occurred in the dried-up prehistoric Makgadikgadi Paleo Lake and appears to have seeded various river systems in southern Africa.[13]

Recombination and loss of heterozygosity

Given the time constraints, the cause for these very different genotypes could not have been multiple beneficial mutations. But recombining large numbers of alleles (traits) through meiosis provides a very reasonable solution, especially if the alleles had been designed to compatibly work together to generate new biologically relevant features.

Stiassny and Meyer claimed that "The genetic studies thus show that evolution repeatedly discovers the same solutions to the same ecological challenges."[10] However, they found significant divergence in genotypes *within* species but *conservation* of genotypes when comparing more distantly related species. This demonstrated that DNA differences *per se* are not a sufficient explanation for speciation.

Of course, the best way to quickly generate a functional biological response to an environmental challenge is to already have genetic programs available, latent in the genome. This would also provide an elegant explanation for the evolutionary observation of 'convergent evolution' at, and below, the family taxonomic level.

Loss of heterozygosity offers a reasonable explanation for the enormous diversity observed. Sequencing studies were performed on five cichlid fish by Brawand *et al.*, one from each of the larger cichlid lineages, to investigate the origin of diversity.[14] The 75 authors of this paper came to the collective conclusion that pre-existing variation (i.e., pre-existing genetic programs) was important for evolutionary diversification. Commenting on the decisive study, Jiggins confirmed that the data on cichlids complemented work "ranging from sticklebacks to butterflies", demonstrating that adaptive radiations arise "from ancient common variations".

This prediction by Jiggins, based on numerous field studies of species emergence in adaptive radiations, was critically reviewed by Berner and Salzburger. They concluded that

> "… the genomes of these species contain adaptive allelic variants that originated long before the actual species or populations have [sic] formed."[15]

This corresponds exactly to what Mendelian speciation predicts concerning pre-existing genetic programs.

Stiassny and Meyer and others have suggested a very reasonable mechanism for the speciation of cichlids, once variants have arisen. That is, repeated isolation during which new species could form, exquisitely adapted to their local feeding requirements; followed by subsequent contact with other species with which they now could no longer interbreed.[10,16]

Seehausen and his colleagues sequenced 450 whole cichlid genomes, representing 150 species from African lakes.[17] They conclude that the fish in the various major lakes had experienced reproductive isolation and, on rare occasions, were reunited with their ancestral cousins and then separated again, a process they called 'fission-fusion-fission', and a mechanism of hybridization they referred to as "the most powerful engine for the formation of new species and new adaptations".

Their results were presented at an Origins of Adaptive Radiation conference in Honolulu, Hawaii.[18] Pennisi summarized what all the genetic data had revealed:

> "Genomic studies have shown they arose from a few ancestral species in just 15,000 years, a pace that has left researchers baffled about how so much genetic variation could have evolved so quickly. Now, extensive sequencing of cichlids from around Lake Victoria suggests much of it was there at the start, in the cichlids' ancestors."[18]

Evolutionary biologist Dolph Schluter also commented on the results: "It's mind-blowing. All the variation required for speciation is already there in the hybrids."[18]

These researchers clearly acknowledge the existence of pre-existing genetic programs. Latent phenotypic information, expressed through cycles of hybridization and through loss of heterozygosity, explains the origin of the species observed in these adaptive radiations; and clearly confirms the importance of Mendelian speciation.

Past adaptive radiations and family limits to speciation

Darwin's finches (tanager species), the Hawaiian honeycreepers (finch species), and other organisms, e.g., Caribbean Dewlap lizards, have all undergone adaptive radiation. Similar adaptive radiations are observed in the fossil record. These, too, can be readily understood to represent different combinations of constant dominant and recessive homozygous traits and to have arisen by Mendelian speciation within a genetic family. The sauropods are an excellent example (see figure 2).

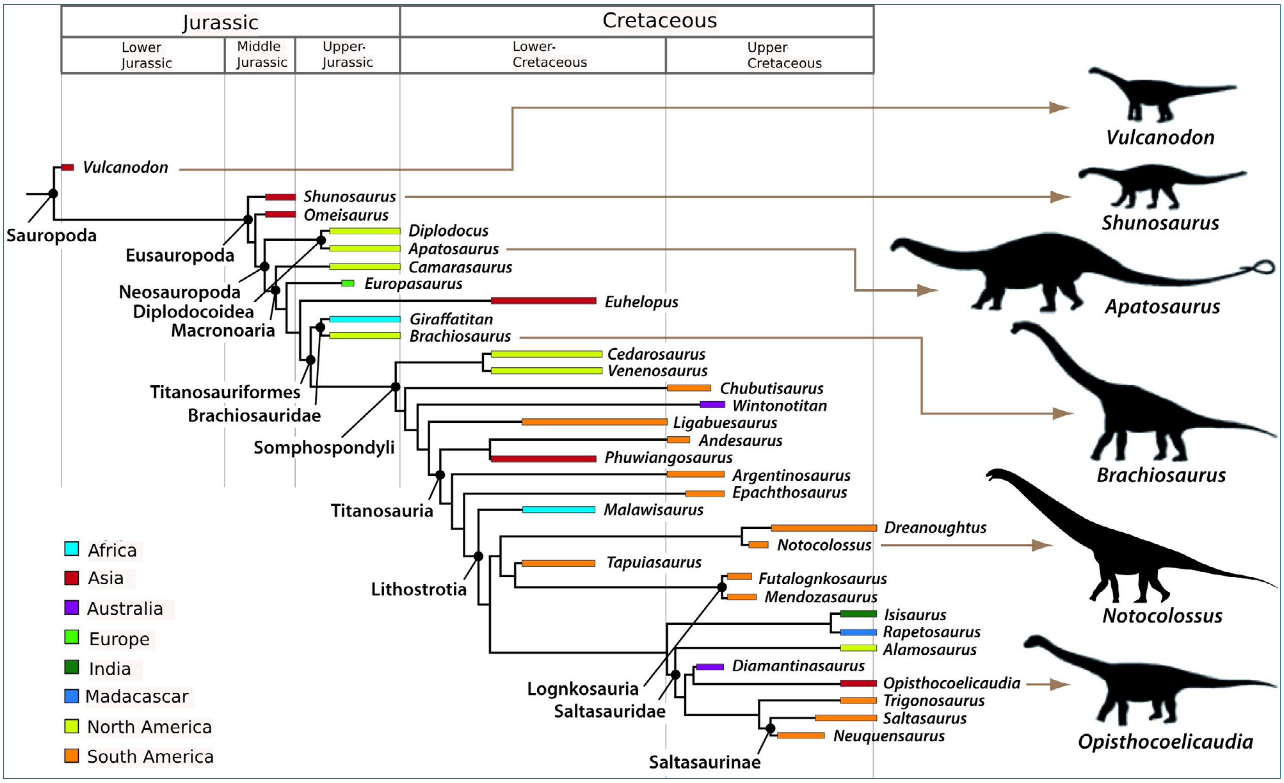

Figure 2. Dendrogram of the Sauropoda. The endpoints correspond to genera. The colours identify the continent(s) where the fossils were discovered. The stratigraphic stages in which the respective groups were found are also shown.

The Sauropoda appear to form a morphogenetic unified family. They certainly appear to have arisen as an adaptive radiation. Their latent pre-existing genetic programs would have segregated according to Mendelian rules, producing this limited but diverse family. Fossils often lack important features necessary for accurate taxonomic classification, and it is possible that the Sauropoda constitute more than one genetic family. However, they certainly appear to reflect a single radiation. Such adaptive radiations can occur quickly, within relatively few generations. There is no genetic reason why vast numbers of generations over tens of millions of years would have been necessary for dinosaur radiations.

Because Mendelian speciation gives rise to significant numbers of species, but fewer with each successive generation, adaptive radiations were originally frequent and extensive, as described in part three of this series.[19] Even in the recent past, however, spectacular adaptive radiations have effortlessly spawned hundreds of new species within plant and animal families based on the expression of genetic information already present in their DNA.

Phenotypic variation and sub-threshold speciation

Towards the end of his scientific treatise,[4] Mendel reflected on how far speciation could vary. If speciation has no boundaries, life could theoretically have originated from a single cell. If speciation has limits, however, not one, but many independent genetic families would exist, and life on Earth can be compared not to one tree, but a forest of many trees. This would be elegant confirmation of what Scripture says about plants and animals being created after their kinds.

Mendel's findings led him to believe there were limits to phenotypic change. He drew attention to experiments by Professor Gärtner, who argued that one species could transform into another, but that there were fixed limits beyond which no further change was possible.[20,21] Mendel was cautious, referring to Gärtner's experiments as confirmation of limited change. However, at the end of his paper, Mendel listed the various species studied by Gärtner, all of which supported this interpretation, and which demonstrated that such an understanding extended well beyond Mendel's own experiments with peas and beans.

Gärtner's argument was correct. Speciation can be shown to result largely from Mendel's Law of Exponential Trait Combinations, and, as this is the case, genetic families have intrinsic phenotypic limits defined by the modifiable potential of their phenotype-defining traits (or pre-existing genetic programs). There are limits to phenotypic change. This all strongly supports a classification of organisms based on a large forest of many separate trees of life, a sylvan taxonomy, with organisms created after their kind.

Because epigenetics and genetic variation is enjoying a prominent position in contemporary genetics, a question often asked is, how does this relate to Mendelian speciation? Epigenetics including structural variants, DNA methylation, and transposable elements, are all important factors in Mendelian speciation. These issues were addressed at a more general level in the second part of this series under the section Transposons and Mendelian speciation.[22]

More than 165 years ago, the importance of genetic variation was emphasized by Darwin in the first chapter, "Variation under domestication", of his famous book.[28] He was familiar with many breeds of pigeon (rock dove), some of them displaying prominent phenotypic differences. Nevertheless, the breeds were, and are, all classified as the same species, *Columba livia*. Similarly, there are many breeds of dog, many of them displaying prominent phenotypic differences, but they are all classified as the same species, *Canis familiaris*. What is observed here is significant genetic variation, but no new species.

A similar observation is made, based on genetic change in humans, which, though extensive, have resulted in no accompanying speciation. Yet another familiar example is seen in the peppered moth, *Biston betularia*, with its light (typica) and dark (carbonaria) forms. In this case, the genetic change is known to be caused by a retrotransposon,[23] and once again there is no accompanying speciation.

Of very great interest in this respect are the *Brassica oleracea* vegetable crops; such as cauliflower, broccoli, cabbage, kale, Brussels sprouts, kohlrabi, *etc*. Very significant phenotypic differences in these common crop varieties, referred to as 'morphotypes', are immediately apparent. A recent paper[24] examining the genetic basis for these phenotypic differences in more than 18 different crop varieties revealed they result from mostly genomic structural variation, predominantly transposition events. However, when the authors referred to the phenotypic morphological changes, they described them as "the role of intra-specific variation … associated with variation in important traits". They, too, acknowledge that these morphotypes are not separate species. It strongly confirms the general principle: there can be significant phenotypic change resulting from significant genetic variation, yet no accompanying speciation.

Without a doubt, epigenetics, DNA methylation, structural variations, and transposable elements are all important agents of genetic change that give rise to significant phenotypic variation. However, the reason the different dog breeds and the different *Brassica* vegetables are not classified as separate species is that they are caused by a limited number of trait or gene differences. Species, however, differ across the whole genome, and such global genomic change requires mechanisms involving very many genes, not just one or a few.

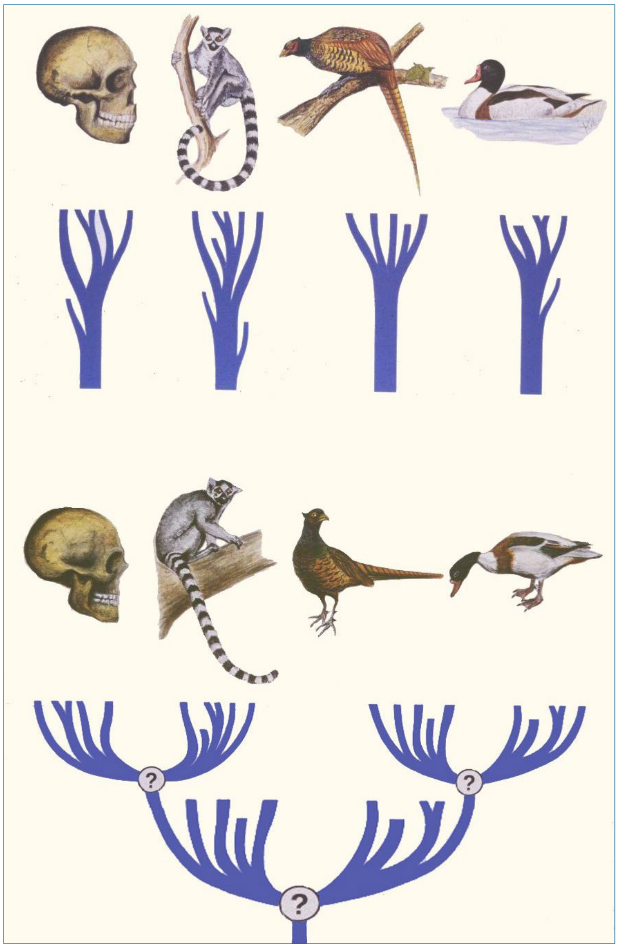

Figure 3. *Cis*-evolution vs *trans*-evolution. In *cis*-evolution (top half) speciation in each genetic family is shown as a separate tree, with the branches being formed by reproductive isolation (though they may sometimes be reunited through hybridization). In *trans*-evolution (bottom half), all genetic families are assumed to have been derived from a common ancestor through random mutations and selection. (From Junker and Scherer, with permission.[25])

Mendelian speciation gives rise to adaptive radiations by employing meiosis and recombination that simultaneously impact the whole genome and not just one or a few select sites. Mutations, transposition, and epigenetics all play a role in Mendelian speciation. On their own, however, they do not give rise to the kind of global phenotypic change needed to warrant classification of organisms as new species. With respect to speciation, they are sub-threshold. The phenotypic changes achieved are insufficient to produce new species. They are also insufficient to produce new characters, which would involve far too many proteins and protein interactions. They are sufficient to produce new traits, and new phenotypic change, and they do this by modifying pre-existing genetic programs.[23] Mendelian speciation is polygenic and is able to account for the characteristically distinctive species observed within genetic families.

Cis-evolution and *trans*-evolution

Worldviews concerning origins collide here. To understand why, one must recognize the difference between evolution *within* genetic families (*cis*-evolution) and evolution *across* genetic families (*trans*-evolution). Only *cis*-evolution is observed in practice, both in the field and in laboratory studies. The difference between *cis*-evolution and *trans*-evolution was discussed in part 2 of this series[1] and is illustrated in figure 3.

Cis-evolution includes examples such as:

- the changes in the light and dark morphs of the peppered moth
- the changes described in Darwin's finches (e.g., in the shape of the beak, body size, or plumage colouration), and
- the diversity observed in the various adaptive radiations listed in the text above.

Cis-evolution occurs because the information required for these changes is already latent in the genome in the form of pre-existing genetic programs. Normally, this information is expressed when meiotic recombination causes loss of heterozygosity. Dominance, epistasis, and also mechanisms associated with transposon activity play a role here.

Pre-existing genetic programs are referred to as 'standing variation' by Brawand *et al*., and as 'ancient genetic variants' by Jiggins[14,26] All three terms express the idea that information for variation that drives adaptive radiations is already present in the genome. The full set of allele pairs of a diploid organism could potentially give rise to an enormous range of phenotypes, one which defines a modifiable but phenotypic limit for a family. The required number of pre-existing genetic programs can be modest. Just 20 biologically important characters, each having two traits (i.e., 40 programs), can generate around 1,000,000 species. If species were defined, on average, by only 10 distinctive trait-pairs (i.e., just 20 programs), families of 1,000 species could theoretically still be produced.

The counterpart to *cis*-evolution, *trans*-evolution, represents unknown, speculative mechanisms that would allow families to transform beyond their phenotypic limits, into other families. Evolutionists believe this type of evolution gave rise to all the separate genetic families, starting from a single common ancestor. A primordial carnivore produced both cats and dogs; and a primordial perissodactyl produced horses, rhinos, and tapirs.

Limits of the genetic family

What kind of mechanism could account for *trans*-evolution? Mendel did not believe that such a mechanism existed. Describing the adaptation of plants to new environments, he wrote:

> "... nothing warrants us to suppose that the tendency to produce varieties is so greatly increased that the species soon lose all independence, and their descendants in an endless series of highly variable forms diverge [our translation.]."[27]

Wallace[28] and Darwin[29] thought otherwise, although neither could provide a feasible mechanism for *trans*-evolution.

Mendelian speciation explains *cis*-evolution but not *trans*-evolution. The only speculated mechanism of *trans*-evolution, mutation/selection, can lead to some *cis*-evolutionary variation, which principally results in loss or impairment or dysregulation of biological function. However, mutations do not explain speciation events, for which extensive phenotypic change is validly necessary. Instead, countless experiments with mutagens confirm the predictably deleterious changes caused by mutations.

Wallace and Darwin recognized that species could give rise to varieties, which, in turn, could give rise to new species. However, they erred in over-extending these findings and assuming that biological change has no limits, which would be a necessary condition if *trans*-evolution is to account for all of life arising from a single tree.

Mendel showed that new biodiversity emerges from latent trait information based on a repertoire of pre-existing traits, and that evolutionary change is essentially confined to this. By all accounts, life is a forest of many trees. This explains why textbooks on evolution give many good examples of *cis*-evolution, but only mere speculation about mechanisms of *trans*-evolution.

Since *cis*-evolution is based on the recombination of alternative traits (pre-existing genetic programs), the logical expectation is that numerous fully functional alternative species will eventually emerge. The same cannot be said for *trans*-evolution as it is based on multiple mutational events that are not designed to produce useful novelty. The logical outcome of multiple mutation events would be a general background of dysfunctional phenotypes.

In contrast, pre-existing genetic programs provide a logical basis for creating the rich diversity of life we see today. Pre-existing genetic programs that give rise to a plethora of healthy and vigorous species is strong evidence that they arose in the mind of an omniscient creator.

Many good examples of *cis*-evolution are known, but only speculation about mechanisms of *trans*-evolution

Mendel's findings open a door onto the enormous phenotypic potential of organisms. This potential is hinted at by several examples:

- In the past, humans tamed the grey wolf, *Canis lupus*, and selected them to produce hundreds of dog breeds with their vast spectrum of phenotypes.

Figure 4. A number of often bizarre forms have been bred from the rock pigeon (far left). (From Junker & Scherer, ref. 25, with permission).

- Man took the common field mustard, *Brassica oleracea*, and, by artificial selection, produced cauliflower, cabbage, broccoli, kale, Brussels sprouts, collards, and kohlrabi.
- Darwin bred the rock pigeon, *Columbia livia*, to produce a number of new breeds, as shown in figure 4. But he clearly over-reached his conclusion after writing: "Under domestication, it may be truly said that the whole organisation becomes in some degree plastic."[30]
- Rose finches appeared in Hawaii and gave birth to the extraordinarily diverse honeycreeper radiation.
- Two precursors (small herbaceous daisy family members, so-called 'tarweeds') of the Hawaiian silversword alliance came from California to the Hawaiian Islands and produced many extremely diverse forms.
- Cichlids entered the great lakes of Africa, and hundreds of new fish species emerged.
- Marine sticklebacks adapted quickly to living in freshwater thanks to a crucial gene variant already present in low percentages in the fishes' marine ancestors.[18]
- Standing variation enabled long-winged beetles to evolve into short-winged ones on the Galápagos Islands.[18]

Mendel's findings provide us with a much better understanding of what species and genetic families are, and also why defining species always proves extraordinarily difficult. Species in a family share a common genetic basis but possess different combinations of dominant and recessive alleles. It sanctions hybridization between different species within families—despite the many mechanisms in place that promote reproductive isolation—and makes defining species somewhat arbitrary.

Reproductive isolation is critical because it allows fixation of recessive or hypostatic allele combinations. This maintains phenotypic diversity that would otherwise be lost through hybridization and subsequent restoration of heterogeneity. The alternate alleles of shared genes offer great potential for phenotypic diversity. They allow a genetic family to evolve into a superabundance of healthy, vibrant species through adaptive radiation.

This non-mutational form of speciation is Mendel's legacy, the fruit of his Law of Exponential Trait Combinations. His experiments on plant hybrids led to extensive and significant ground-breaking insights into genetics and, in particular, into 'the origin of species'.

Conclusions

Mendelian speciation is based on his Law of Exponential Trait Combinations. It provides a powerful explanation for the emergence of biological diversity. It readily explains the most spectacular examples of adaptive radiations within families. Mendelian speciation occurs because the information required for speciation and variability is already present in the genome of organisms, held in a latent state. Mendelian speciation gives rise to extensive, wholesome evolution within a family; *cis*-evolution. It can occur within relatively few generations and provides eminently reasonable and entirely satisfactory solutions to many of the questions that arise when attempting to bring the extensive biodiversity observed in nature and a scriptural understanding of origins into meaningful alignment.

Appendix 1—*cis*-evolution and microevolution

In debates about evolution, the terms 'microevolution' and 'macroevolution' are often used. These two terms are defined differently, and often vaguely, by different groups. Some say macroevolution is evolution within a species; others, within a family. For yet others, both terms only differ quantitatively (i.e., very little or much evolution).

For this reason, the terms '*cis*-evolution' and '*trans*-evolution' are introduced here. It was to express a qualitative and essential difference between these two types of change (cf. figure 3). One can define 'microevolution' and 'macroevolution' as done in Junker and Scherer,[25] which are essentially identical to '*cis*-evolution' and '*trans*-evolution', respectively.[31] According to these two authors, microevolution deals with the question of how existing (latent) information is expressed, whereas macroevolution is about where pre-existing genetic programs and new characters come from.

A glossary of terms is to be found in the accompanying third paper of this series.[19]

References

1. Crompton, N.E.A., Sprague, T., Truman, R., and Junker, R., Mendelian speciation: part 2— latent genetic information, *J. Creation* **38**(1):77–86, 2024.
2. Carson, H.L., Chromosomal sequences and inter-island colonizations in Hawaiian Drosophila, *Genetics* **103**:465–482, 1983.
3. Noor, M.A.F., Grams, K.L., Bertucci, L.A., and Reiland, J., Chromosomal inversions and the reproductive isolation of species, PNAS **98**:12084–12088, 2001.
4. Edwards, K.A., Doescher, L.T., Kaneshiro, K.Y., and Yamamotol, D., A database of wing diversity in the Hawaiian Drosophila, *PloS ONE* **2**:e487, 2007.
5. Barrier, M., Baldwin, B.G., Robichaux, R.H., and Purugganan, M.D., Interspecific hybrid ancestry of a plant adaptive radiation: allopolyploidy of the Hawaiian silversword alliance (Asteraceae) inferred from floral homeotic gene duplication, *Mol. Biol. Evol.* **16**:1105–1113, 1999.
6. Carlquist, S., Baldwin, B.G., and Carr, G.D., *Tarweeds and Silverswords*, Missouri Botanical Garden Press, St. Louis, 2003.
7. Crompton, N.E.A., Die Radiation der Silberschwert Gruppe 1. Indizien für präexistente genetische Programme, *Studium Integrale J.* **29**:80–89, 2022.
8. Crompton, N.E.A., Die Radiation der Silberschwert Gruppe 2. Hybriden und die Geschichte der Silberschwerter, *Studium Integrale J.* **30**:13–21, 2023.
9. Seehausen, O. and van Alphen, J.J.M., The effect of male coloration on female mate choice in closely related Lake Victoria cichlids (*Haplochromis nyererei* complex), *Behavioral Ecology and Sociobiology* **42**:1–8, 1998.
10. Stiassny, M.L.J. and Meyer, A., Cichlids of the Rift Lakes, *Scientific American* **280**:64–69, 1999.
11. Verheyen, E., Salzburger, W., Snoeks, J., and Meyer, A., Origin of the Superflock of cichlid fishes from Lake Victoria, East Africa, *Science* **300**:325–329, 2003.
12. Albertson, R.C., Markert, J.A., Danley, P.D., and Kocher, T.D., Phylogeny of a rapidly evolving clade: the cichlid fishes of Lake Malawi, East Africa, PNAS **96**:5107–5110, 1999.
13. Joyce, D.A., Lunt, D.H., Bills, R., Turner, G.F., Katongo, C., Duftner, N., Sturmbauer, C., and Seehausen, O., An extant cichlid fish radiation emerged in an extinct Pleistocene lake, *Nature* **435**:90–94, 2005.
14. Brawand, D., Wagner, C.E., *et al.*, The genomic substrate for adaptive radiation in African cichlid fish, *Nature* **513**:375–381, 2014.
15. Berner, D., and Salzburger, W., The genomics of organismal diversification illuminated by adaptive radiations, *Trends in Genetics* **31**:491–499, 2015.
16. Salzburger, W. and Meyer, A., The species flocks of East African cichlid fishes: recent advances in molecular phylogenetics and population genetics, *Naturwissenschaften* **91**:277–290, 2004.
17. Meier, J.I., Marques. D.A., Mwaiko, S., Wagner, C.E., Excoffier, L., and Seehausen, O., Ancient hybridization fuels rapid cichlid fish adaptive radiations, *Nature Communicatuons* **8**:14363, 2017.
18. Pennisi, E., Hybrids spawned Lake Victoria's rich fish diversity, *Science* **361**:539, 2018.
19. Crompton, N.E.A., Sprague, T., Truman, R., and Junker, R., Mendelian speciation: part 3—fixation and reproductive isolation, *J. Creation* **38**(2):96–103, 2024.
20. Mendel, G., Versuche über Pflanzenhybriden, *Verh. Naturforschung Vereins Brünn* **4**:3–47, 1866. Republished by Vieweg+Teubner (now Springer Vieweg Verlag) Publishers, Wiesbaden, 1970.
21. Mendel, ref. 20, p. 46.
22. Crompton, N.E.A., Sprague, T., Truman, R., and Junker, R., Mendelian speciation part 2—latent genetic information, *J. Creation* **38**(1):77–86, 2024.
23. Van't Hof, A.E., Campagne, P. *et al.*, The industrial melanism mutation in British peppered moths is a transposable element, *Nature* **534**:102–105, 2016.
24. Li, X., Wang, Y., Cai, C., Ji, J., Han, F., Zhang, L., Chen, S., Zhang, L., Yang, Y., Tang, Q., Bucher, J., Wang, X., Yng, L., Zhuang, M., Zhang, K., Lv, H., Bonnema, G., Zhang, Y., and Chang, F., Large-scale gene expression alterations introduced by structural variation drive morphotype diversification in *Brassica oleracea*, *Nature Genetics* **56**:517–529, 2024.
25. Junker, R. and Scherer, S., *Evolution—ein kritisches Lehrbuch*, Wevel Biologie, Gießen, 7th edn, 2013.
26. Jiggins, C.G., Radiating genomes, *Nature* **513**:318–319, 2014.
27. Mendel, ref. 20, p. 36.
28. Wallace, A.R., On the tendency of varieties to depart indefinitely from the original type, The Ternate Essay, *J. Proceedings of the Linnean Society* **3**:53–62, 1858.
29. Darwin, C., *On the Origin of Species by Means of Natural Selection, or the Preservation of Favoured Races in the Struggle for Life*, John Murray, London, 1859.
30. Darwin, ref. 29, p. 80.
31. Junker and Scherer, ref. 25, pp. 44 and 48.

Nigel E.A. Crompton *has a Ph.D. in biology from the University of Giessen, Germany, and a D.Sc. from the University of Zurich, Switzerland. He worked in mutation and cancer research for twenty years in Germany, the United States, and Switzerland. He was called to teach at Cornerstone University in Grand Rapids, Michigan, where he lectures in biology, genetics, molecular cell biology, and neuroscience.*

Thomas Sprague *has a Ph.D. in mathematics and computer science from Western Michigan University and a masters degree in biblical studies from Dallas Theological Seminary. Prior to retirement, he was a data analyst for a regional affiliate of Feeding America after a thirty-year academic career, most recently as Professor of Mathematics at Cornerstone University in Grand Rapids, Michigan.*

Royal Truman *has bachelor's degrees in chemistry and in computer science from State University of New York; an M.B.A. from the University of Michigan (Ann Arbor); a Ph.D. in organic chemistry from Michigan State University; and a two-year post-graduate 'Fortbildung' in bioinformatics from the Universities of Mannheim and Heidelberg. He works in Germany for a European-based multinational.*

Reinhard Junker *studied biology, mathematics, and theology and gained a Ph.D. in interdisciplinary theology. He has worked as a research assistant at Studiengemeinschaft Wort und Wissen e. V. in Baiersbronn (Black Forest/Germany) for almost 40 years, mainly in the areas of design theory, comparative biology, and palaeontology. He is co-author of* Evolution—a critical textbook *and author of numerous specialist publications and popular books on biological and theological topics.*