

for similar situations. But why, they argue, should a Creator put the same useless pseudo-genes in the same two creatures?

However, it should first be noted that there is no consistent pattern of pseudo-genes in humans, chimps and gorillas from which it could be argued that humans are closer to chimps than they are to gorillas. Some pseudo-genes are shared by humans and chimps, not by gorillas, while others are shared by humans and gorillas, but not chimps.

Thus there is no logical evolutionary picture here — if it is accepted that the human-chimp sharing is due to common ancestry, then the human-gorilla-but-not-chimp sharing has to be explained away as coincidental, or the other way around.

So if these pseudo-genes do not represent common ancestry, how might they have arisen? There have been all sorts of deleterious changes since the Fall. Of interest is the fact that retrovirus infection has been recently observed, in embryonic mouse cells, to turn an ordinary gene into a pseudo-gene.² (The most famous member of the retrovirus family is HIV — human immunodeficiency virus.)

So let us look at three arbitrary (normal, functioning) individually created genes shared by humans,

gorillas and chimps of which there are known pseudo-genes — call the genes A, B and C.

Call A' the pseudo-gene derived from A, and so on. A population which descended from an individual with a retrovirus-caused pseudo-gene, but still with an active version of the normal gene, would then be represented as having A in addition to A'.

Assume retrovirus activity was common in the early years after the Flood in particular, affecting the early ancestral lines of many types of creatures alive today

It is not difficult to envisage a more or less random situation in which the results shown in Figure 1 eventuate.

Looking at the pseudo-gene B', an evolutionist would conclude that humans were closer to chimps than gorillas. The opposite would be the case for C. A' would be argued as showing that the pseudo-gene arose in a common ancestor to all three. Whereas in reality it was just a random pattern of retrovirus infection.

It is as yet unknown whether, and if so why, some genes are more susceptible to becoming pseudo-genes

by such a process than others. The same gene might be vulnerable to pseudo-gene formation many times in the one population. Furthermore, just because retroviral involvement has been observed does not mean it is the only possible mechanism of pseudo-gene formation. Mutational error is always a factor in a fallen world.

In addition, at least some of the 'pseudo-genes' may not properly be such at all, and may turn out to have a function like so many of their 'junkyard' cousins have. Their function may require them to be very similar to 'normal' genes.

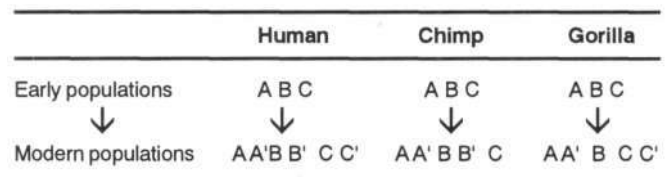


Figure 1. Random generation of pseudo-genes by retrovirus activity.

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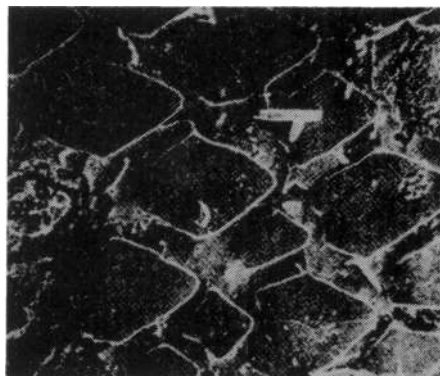
Fish Scales in the Cambrian

Virtually all of the major divisions of life (the phyla) are found in the Cambrian, the rock system which evolutionists maintain is more than 500 million years old. Until recently, it was thought that no vertebrates were found in the Cambrian.

However, last year the enigmatic tooth-like objects known as conodonts, common in upper Cambrian rocks, were shown to be from eel-like creatures. These were identified as true vertebrates on the basis of distinctive eye muscles not found in invertebrates.

Now small fossils found in 1976

appear to be adding more weight to the idea that the Cambrian is not, as



Fish-like scales from Anatolepis.

once thought, free of vertebrates (these were believed not to have evolved yet). They are fish-like scales known as *Anatolepis*.¹ Some have argued that the scales could belong to the arthropod phylum, which includes insects and crustaceans.

However, microscopic studies reveal that the scales contain dentine, which is only known in vertebrates. The researchers feel this is conclusive evidence that these are fish scales.

REFERENCE

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