

# Jumping wallaby genes and post-Flood speciation

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Jumping genes or transposable elements (TEs) are present in virtually all life forms, from bacteria to humans. They are short DNA sequences that can move from site to site in the chromosomes of their hosts. They have been divided into two groups, DNA transposons and retroelements.<sup>1</sup>

DNA transposons can move by a cut-and-paste mechanism or by making copies of themselves. Retroelement jumping involves copying its RNA transcript back into DNA (see figure) using the enzyme reverse transcriptase. In contrast to transposons, however, most retroelements ‘jump’ only occasionally, and there are many which appear to have lost this ability.<sup>1</sup> One exception is an active fruit fly retroelement.<sup>2</sup>

Retroelements have been found in the chromosomes of eukaryotes (which unlike bacteria, have cells with a defined nucleus) such as yeast (the simplest eukaryote), fruit flies, and in vertebrates such as mice and man. The DNA sequence elucidated from the human genome project shows that 35–40% of human DNA is made up of retroelements.<sup>3</sup>

Based on evolutionary presupposition, jumping genes were initially believed to be simply ‘selfish’ DNA with the sole function of self-perpetuation, and with no apparent use to the host (junk!).<sup>4,5</sup> But lately, molecular biologists have been unveiling crucial functions for these elements. For example, retroelements have been found to play an important role in regulating gene expression (switching genes on and off) and in the repair of chromosomes.<sup>1</sup>

## Research on wallabies

In addition, an Australian research group has now proposed that retroelements are involved in mammalian

speciation.<sup>6</sup> The researchers were studying an infertile hybrid wallaby they had found in a wildlife park — a result of crossing two different species: the swamp wallaby and the tammar wallaby. They looked at the genome of this unusual hybrid marsupial, because:

- (a) there are genetic models that predict that rearrangements in the genomes of hybrids can aid reproductive isolation, by preventing hybrid and parent species crossing, leading to the formation of new species,<sup>7</sup> and
- (b) TEs can cause DNA rearrangements in hybrid fruit flies.<sup>2</sup>

They found that a retroelement had jumped profusely in the genome of the hybrid wallaby, and had intergrated around the chromosome centromeres — the region on the chromosome to which the spindle fibres attach during cell division. One of the researchers commented:

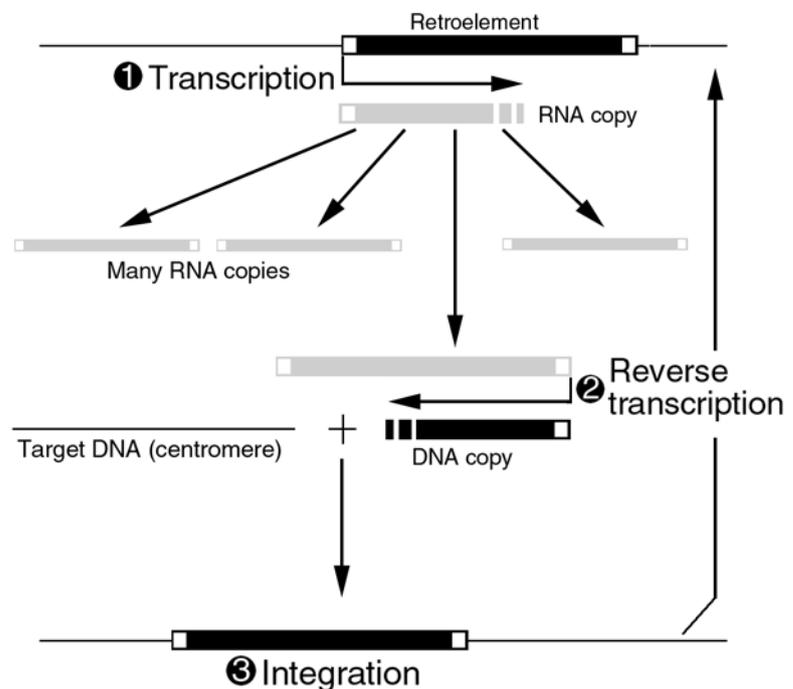
*‘We thought it took millions of years of long-term selection for a jumping gene to be activated.’*

*‘We’ve now shown that it can happen maybe in five minutes after fertilisation.’<sup>8</sup>*

The finding indicated also that the jumping gene in the hybrid had probably been reconstructed (and reactivated) by the genetic combination of two incomplete, inactive segments of a retroelement present in one or both of the parents. This has previously been reported in mice.<sup>9</sup>

Since DNA methylation (the linking of a methyl group to the nucleotide bases adenine or cytosine)<sup>10</sup> is important for switching off genes, it is believed that this process is also used by host cells to stop the movement of TEs.<sup>11</sup> Deficient methylation would then enable jumping. The researchers found that the retroelements in the DNA of the hybrid were indeed unmethylated. This was also the case in two additional hybrids, each from an independent mating between two different wallaby species.

The researchers suggested that the ability of retroelements to produce genomic rearrangements in hybrid



*Retroelement replication cycle. Many RNA copies are transcribed from the integrated retroelement. Some are reverse transcribed into DNA copies, which are reintegrated into the host chromosome. The cycle can then repeat. Boxed regions are retroelements or RNA copies (after Kidwell and Lisch).<sup>13</sup>*

wallabies, due to deficient methylation (eventually resulting in the formation of new species) may be a widespread phenomenon in hybrid mammals. However, this idea has now been challenged by another research group, who did not find any methylation changes in the genomes of a number of mammalian hybrids they studied.<sup>12</sup>

### Evidence supports biblical model

The very rapid genetic changes caused by TEs could help explain the formation of the variants from the original kinds on Noah's Ark in the relatively short biblical time frame.<sup>1</sup> Rapid speciation apparently occurred, since early historical records already show a large variety of types similar to those present today. The various species representing the variants in e.g. the kangaroo/wallaby created kind, would all then stem from the original parent kind present on the ark.

Based on the rapid jumping of retroelements in hybrid wallabies<sup>6</sup> and fruit flies,<sup>2</sup> on their ability to cause DNA rearrangements, and on their role in gene regulation,<sup>1</sup> it is plausible that these TEs were active in the past, and were an original mechanism for expressing God's programmed variation within kinds. Today, the presence of incomplete, inactive segments of retroelements in wallaby chromosomes, which probably recombined in the hybrid to form active elements, as in the case of hybrid mice,<sup>9</sup> may be vestiges from this past mechanism.

Are retroelements involved in wallaby speciation today? The wallaby crosses described here only produce sterile males, a result which is common in interspecific hybridization in mammals.<sup>12</sup> Therefore, most male hybrids cannot produce offspring with female hybrids from a compatible crossing. In the unlikely event of a fertile male successfully mating, there is also no certainty that this will produce viable offspring. These obvious problems, and the fact that TEs are mostly inactive today and are only 'jump started'

by the unlikely events of crossing between species, indicates that the role of retroelements in speciation has been either greatly reduced or has stopped altogether.

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## How different is the cranial-vault thickness of *Homo erectus* from modern man?

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### Introduction

Are the human 'species' that preceded us real taxa, and are they evidences for evolution? A growing body of evidences suggests that they are neither.<sup>1,2</sup> Moreover, the physical features which distinguish 'primitive' from modern man can be accounted for by non-evolutionary explanations.<sup>3,4</sup> These include genetic drift in the small post-Babel populations, adaptations to diet and/or climate, changes in the rate of skeletal maturation, and other consequences of living conditions in the immediate post-Flood period which differed greatly from those enjoyed by subsequent members of the human race.

Everyone with even a remote familiarity with paleoanthropology is aware of the fact that many of the evidences in this field are subjective, and subject to a multiplicity of interpretations. But no one can doubt that *Homo erectus* had a much thicker cranial vault than do modern humans. Or can they? Surely the distinctive cranial features of *Homo erectus* have been arrived at as a result of rigorous scientific investigation? Well, not exactly, as it turns out. Consider the following sobering statements made by Peter Brown,<sup>5</sup> an Australian evolutionary paleoanthropologist:

*'Nearly every introductory and advanced text written on human evolution in the last four decades lists thickened cranial vault bone as one of the features distinguishing Homo erectus from H. sapiens and other hominids. However, data has rarely been presented in support of this statement and it remains unclear whether the distinction that is being drawn is relative,*