



Introns; Darwin's Worst Nightmare?

Introns, those pieces of DNA which interrupt protein coding genes are a curious phenomenon. Why would you want to make life difficult for yourself by adding the need for RNA splicing to the already complex process of gene transcription and translation? One is inevitably drawn to the conclusion that they must have some kind of function, though it isn't clear what that is.

Ideas for the functions of introns vary enormously. At one end of the spectrum they are postulated to have no function. At the other end, some introns are thought to encode proteins themselves, and through the process of alternative splicing it is possible to generate more than one protein from a single gene. It would still seem less of an evolutionary burden to have distinct coding sequences.

It is possible that through chromosomal crossing over it may be a method of generating diversity and thus giving rise to new proteins. What I would like to suggest, however, is that the purpose of introns is exactly the opposite. They are there to stall the evolutionary process as crossing over is more likely to give rise to non viable genetics – functional proteins become non functional by the inclusion of intron DNA without the necessary splicing signals.

Is there any evidence for this? Probably not, but over the years, two observations have stuck in my mind. The first is that introns are principally a eukaryotic phenomenon. Introns are known within the genes of bacteria and archaeobacteria but they occur much more rarely compared to higher organisms. Only 8% of human genes are thought to be intron free.

The second observation is the genetic variability of bacteria. In higher organisms, it has been possible to construct phylogenetic relationships by comparing protein sequences, primarily those of the c type cytochromes. In bacteria this is not possible. In a classic paper in the journal *Nature* (*Nature* **278**, 659 - 660 (12 April 1979; doi:10.1038/278659a0), Ambler and his co-workers determined the amino acid sequences of the principle soluble cytochrome c of representatives of each recognised species of the Rhodospirillaceae, the non-sulphur purple photosynthetic bacteria. This paper probably holds the record for the highest number of new protein sequences published in a single paper. What it shows is that not only is there no correlation between protein sequence and accepted phylogenetic relationship, but there is more variability within this family of Proteobacteria than there is in the entire (known) eukaryotic cytochrome c sequences. For those not familiar with taxonomy, the Kingdom bacteria is hierarchically subdivided into phylum, class, then order before getting to the level of family.

From these two observations, one can formulate the hypothesis that there is greater genetic variability when the incidence of introns within genes is low. Is that generally true? I don't know and would invite readers to submit their own thoughts and observations on the subject. If, through random mutations you have gained an evolutionary advantage, then that advantage is at risk from genetic drift. A mechanism which "stabilised" evolutionary change should lead to periods of stability followed by rapid change when the environmental pressure changed, in other words punctuated evolution. Perhaps that is a third observation in support of the hypothesis that introns function to limit evolutionary change and are Darwin's worst nightmare!

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