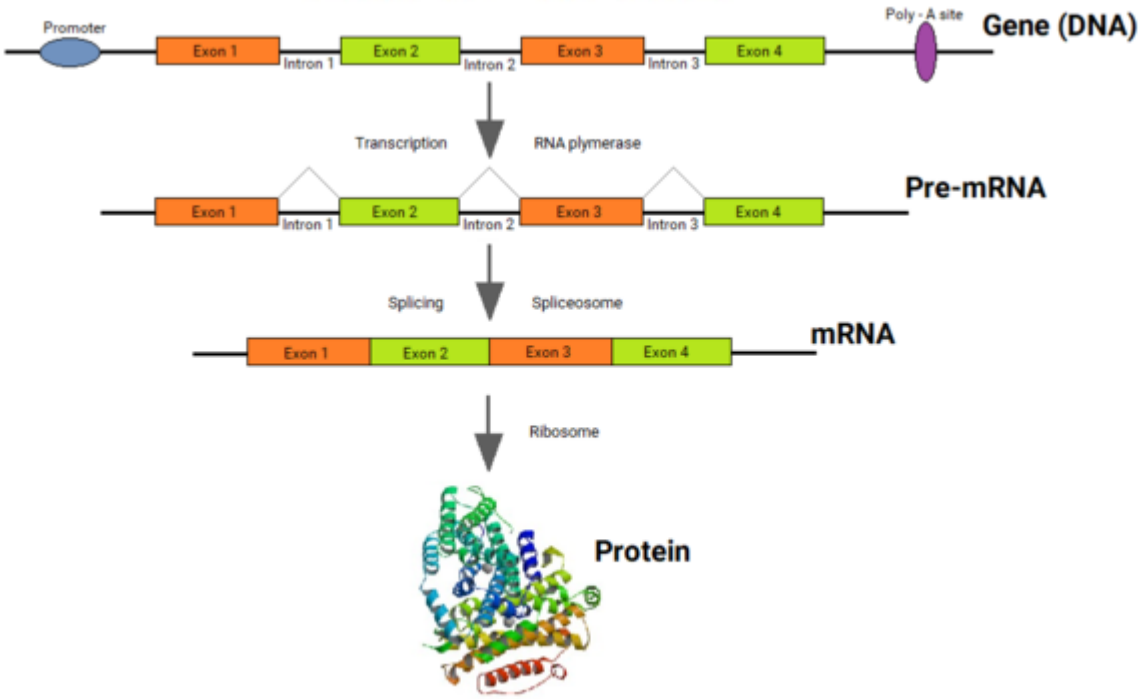
Split Genes

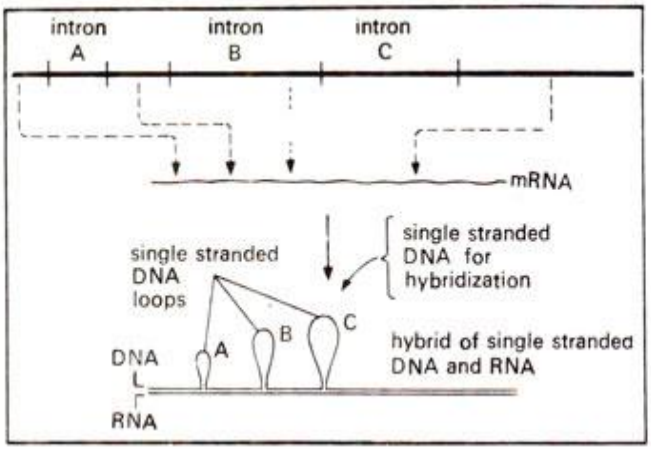
Studies based on Mendel's law considered genes to be a point on the chromosome. Later it was found to be a continuous segment of DNA. Further, colinearity between sequences of nucleotides on DNA and sequence of amino acids in proteins was also proved not only in prokaryotes but also in eukaryotes. But, in 1977, it was found in some mammals, birds an amphibians that genes were not represented by a simple continuous sequence of nucleotides, but was interrupted by some intervening sequences which were not represented in mRNA and not utilised for synthesis of proteins. In other words, it can be noted that eukaryotic genes are composed of few essential sequences-**the exons**, and intervening non-essential or nonsense sequences –**the introns**. Therefore, a single gene responsible for development of a polypeptide is made up of several exons interrupted by introns. **Such genes containing informative exon sequences and non-informative intron sequences lying adjacent to each other are termed as split genes**

From the above discussion it is evident that at the time of enzyme or protein synthesis by the genes, the RNA polymerase would first make a primary transcript of the total gene, including introns and exons. Later this transcript would be processed to remove the introns and re-join the exons with the help of restriction enzymes and ligases respectively. This mechanism of scissoring and joining is otherwise known as **splicing**, which is a characteristic of eukaryotic system and occurs during messenger RNA processing.

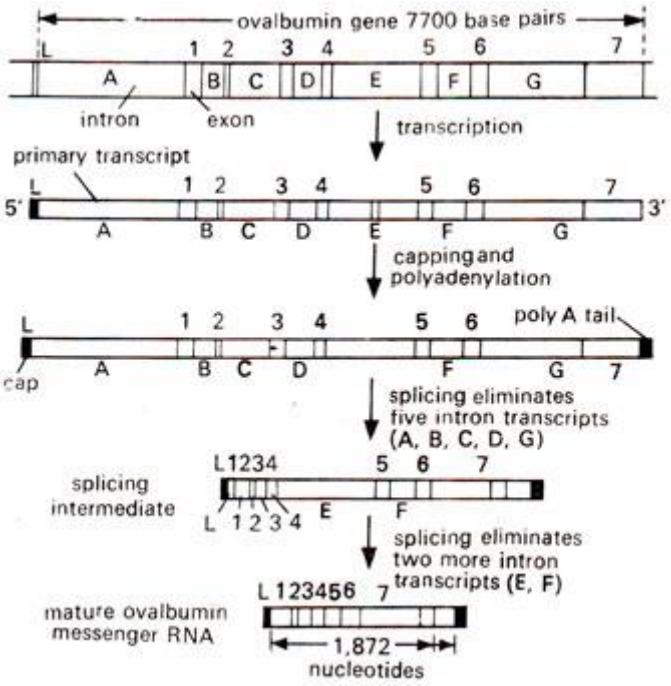


Reports of split genes have been obtained from ovalbumin genes of chicken and β-globin genes of mice (Chambon *et al*), ribosomal genes of *Drossophila* (Hogness *et al*), in hexon genes of adenovirus (Phillip *et al*), tRNA genes of yeast and from many other sources.

The mRNA precursor of globin gene sequence sediments at 15S, while the final globin mRNA has a sedimentation co-efficient of 10S. Tilghman, Leder and others employed the RNA loop formation technology to explain the above relationship. The single stranded complementary DNA strand are capable of binding together. Similarly, single stranded DNA and RNA molecules can also hybridise as long as they have complementary sequences. Tilghman and co-workers found that the globin gene DNA and 15S RNA hybridised to form a continuous double stranded DNA-RNA hybrid. But when the same globin gene DNA was hybridised with the 10S globin mRNA, a large loop was formed by the DNA segment at the centre. The loop resulted from a large intervening sequence in the DNA that was non-complimentary to any part of the globin mRNA.



Similarly, Chambon and his co-workers isolated and hybridised the ovalbumin DNA and mRNA of chickens. The hybrid thus formed contained seven distinct loops corresponding to seven intervening sequences. Subsequent studies have revealed that the introns of a gene are on an average 4-10 times the length of the exons.



Splicing is also found to occur in some tRNA and rRNA molecules of Yeast. In *Neurospora* and Yeast highly repeated sequences are found in introns. Recombinations mostly occur at intron sites leading to exon reshuffling. Intra-exon recombination is rather difficult. It has already been shown in animals that recombination within introns help in the rearrangement of exon as in lysozyme of chicken.