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EDITORIAL

Chromosomes—to date

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Chromosome, the bearer of the basic material of heredity—genes, has come a long way since its discovery. In the evolution of its understanding, starting from Baranetsky, Flemming and others who provided a glimpse of its structure under the microscope, the discovery of Feulgen reaction and absorption at specific wavelength (265 nm) of ultraviolet in later years paved the way for basics of chromosome identification. The revelation of double helical nature of the chemical substance and the alphabets involved along with semi-conservative replication by Watson and Crick were revelations clarifying the structure of the gene. These were all epochal events. A few years later in the post Watson-Crick era, the discovery of repeat sequences of DNA should be considered as the landmark event. Such sequences often occupy a very high percentage of DNA and can reach even 80–90 % as in wheat and rye. In the plant system, such repeats are responsible for large scale C-value paradox providing an explanation of why lilies may have high amount of DNA as compared to man. Moreover, AT/GC Ratio in chromosomes of plants show comparative homogeneity as compared to heterogeneity in animals.

Another startling discovery involved the mobility of large number of repeats. The property of mobility and dispersion are remarkable features of such repeats. The importance of mobile sequences/transposons was clearly demonstrated by AC/DS factor in maize controlling breaks, identified by Barbara McClintock. It gave a new dimension to chromosome structure. The amplification of bases has been recorded even upto 1–4 billion in maize genes. It is often claimed that almost 50 % of the primate genome consists of mobile elements capable of jumping around the genome [1]. These sequences often show diversity, exert pleiotropic effect on surrounding gene, can cause transformation in other genes and can even act as hot spot of integration justifying their tremendous role in evolution. Because of the huge copy number, their role, on evolution of genome, regulation, transcription and species diversification, can be understood. A very interesting case was recorded in melon where transition of male to female has been facilitated by transposon insertion leading to methylation of promoter at transcription factor [3].

The epochal developments also involved RNA molecules, the RNA world and the two essential RNAs—micro RNA and short interfering RNA setting aside other RNAs as well. Their role in different aspects of chromosome metabolism including transposon silencing, function of defence system and differentiation have also been brought out [7]. However, along with the RNA world, the split nature of the genes including exons and introns, though revolutionary developments, have not been kept within the scope of this discussion for the present.

Understanding of the functional segments of chromosomes along with their origin, has been facilitated by technological developments. The use of molecular hybridization on the one hand, and preparation of multiple probes of different origin and colour have made the identification of chromosome sequences of different genotypes and their function, a convenient task, the basic technique being in situ hybridization with fluorescence labeled probe (FISH). Gradually with advancements in technology such probes involved desired sequences or entire genome and so following hybridization (GISH), the genome origin could be determined with absolute accuracy [6]. The chromosome painting therefore, in principle, involves use of multiple probes in in situ hybridization. It can lead to understanding of the genomes participating in evolution and their specific chromosome complements. In the chromosome study, it has become an effective tool on the analysis of evolution.

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Undoubtedly, there have been further developments utilizing various probes of different sizes and origin coupled with amplification.

The study of chromosome structure has gradually been shifted to chemical and histochemical analyses and finally to molecular level giving an understanding of the sequence and functional complexity of minute segments of chromosomes. Along with FISH and GISH, the in situ *hybridization* as mentioned above has also been associated with amplification—through polymerase chain reaction at the chromosome level. This approach often makes possible the identification and localization of even single copy genes in the chromosome complement. The other innovative strategy has been the use and detection of tandem repeated sequence through oligonucleotide primed in situ synthesis (PRINS) [2]. The in situ technique as such is in a position to localize distribution of tandem repeats, dispersed repeats and even single copy sequences. Tracing the complete genes and even genes of different origin have made gene mapping possible under the microscope at the chromosome level.

Finally, the signal development is the discovery of syntenic sequences in chromosomes indicating blocks of primordial genes and colinearity of gene order. The significance of syntenic sequences is immense [4].

The present knowledge of chromosomes owe to a great extent to the rapid advances in technology, unravelling the intricacies of the chromosome structure, the highest complex organic molecule, that one can conceive of. The refinements have made the study a novel combination of microscopic and finer molecular techniques. Coupled with these technological developments, mention must be made of in vitro method which has brought the analysis within the reach of the investigator.

However, another development worth recording is modification of gene expression through epigenetic technology, as mentioned in an earlier editorial [5] providing with a cover on the gene surface by methylation, acetylation, histone positioning etc. which affect significantly the gene expression at the chromosomal level. The technical advancements have undoubtedly unravelled the intricate details of chromosomes on the one hand and their role in evolution on the other, some of which could not be visualized earlier. Not only the knowledge of these sequences, but even their specific manipulation is becoming a routine procedure.

The discovery of the syntenic sequences has further implied that all our progenitors were derived from a few building blocks of gene segments. In grass family, only nineteen such blocks have been visualized, possibly located in one chromosome. The observations as well as the conjecture certainly have tremendous value though specific evidences of modality are yet to be obtained.

With all these discoveries, two more problems have come up as challenges for evolution. Technological advances may ultimately lead to an understanding of the basic sequences of our ancient progenitors. But the mechanisms through which the reshuffling or recombinations and newer and newer arrangements have been affected in an orchestrated manner are yet to be proved. It is true that all chromosomal rearrangements have played crucial roles in the evolution of chromosome structure. But in all probability, their complex functioning leading to the entire biota at present, must have been subjected to some overall control mechanism, responsible for their origin within a period of 4 billion years at the most. The syntenic sequences of chromosomes have utilized, no doubt, transcription factors and regulators, along with all other chromosomal rearrangements. But the control mechanism even for the regulators, to deal with thousands of genes of different groups with absolute accuracy in a predetermined fashion, awaits unravelling.

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