Review Article
Volume 5:10, 2021

Journal of Genetics and Genomes

ISSN: 2165-7920 Open Access

The Principle of modern Genomic Mapping

Yubao Wei*

Department of Medical Genetics, University of Zhengzhou, Shanghai, China

Editorial

Mapping of gene is done as to identify and record the exact loci of the gene; it also helps us to understand the distance present between the genes. Thus, gene mapping is considered to be the backbone for the establishment of the Human Genome Project. It provides a helping hand to the scientists in locating their path around the genetic material. Landmarks on a genome map can include short DNA sequence, control sites genetically modified shutdown and shutdown or the gene itself. The two major types of methods used for the genomic mapping is the genetic mapping and the physical mapping, both these types helps in the location of the gene present on the chromosomes. Genomic mapping plays the major role in identifying the genetic information of the genes which share among themselves in the meiosis process (cell division). The landmarks of these genes are also decided by the crossing over. However, physical mapping observes the distance between the bases in units in a physical manner of the known DNA sequence. Alfred Sturtevant was the first scientist who designed the genetic map of the chromosome of the Drosophila melanogaster (also known as Fruit Fly) in the year of 1913. He also observed that all the genes were arranged in the straight line and every gene were placed at particular places. His theory suggested that the frequency at which the crossing over takes place between the two genes helps in determining their location on the chromosomes.

He also postulated that the genes that are located far apart are said to be inherited separately as the larger space can be observed between the adjacent genes which indicates that recombination have occurred. In the similar fashion, the genes which are separated by less distance are said to be inherited together. Considering the different characteristics inherited together, it can be concluded the units of distance present between the adjacent genes. Thus, a map can be designed which will depict the relationship shared by the genes of that particular chromosomes, which is called as “Linkage Map” Thus, this Linkage map shows the exact loci of the desired gene on the chromosomes. It can be said that the genes which are close to each other and have less linkage distance among themselves are said to be inherited together and the genes which are separated with the large linkage distance are said to be inherited separately, via the crossing over process. If a gene is close to the DNA mark on the chromosome, there is a good chance that the gene and the marker will stay together during the reunification process so there is a good chance they will be passed on to the family line (inherited) together. In the same way, if the DNA marker and the gene are often separated by a regeneration process it suggests that they are too far apart from the chromosome and less likely to inherit together. The more DNA markers on a genetic map, the more likely it is that one of them will be found next to the disease or the genetic mutation that accompanies it.

How to cite this article: Wei Yubao. "The Principle of modern Genomic Mapping ." *J Genet Genom* 6(2022) : 119.

***Address to correspondence:** Yubao Wei, Department of Medical Genetics, University of Zhengzhou, Shanghai, China; E-mail: baowny@gmail.com*

Received: 02 December, 2021; **Accepted:** 10 December, 2021; **Published:** 22 December, 2021