Biospectra : ISSN: 0973-7057, Vol. 17(1), March, 2022, pp. 163-166
An International Biannual Refereed Journal of Life Sciences

34(RA).
Review Article

ISSN : 0973-7057

Int. Database Index: 616 www.mjl.clarivate.com

Parental Mark - Genome Imprinting

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Received : 18th February, 2022 ; Revised : 18th March, 2022

Abstract- Genome imprinting is a vital genetic mechanism in mammals and is thought to influence the transfer of nutrients to the foetus and the newborn from the mother versus father. Imprinting defects can involve multilocus or isolated epigametic changes that may have no evident genetic cause or imprinting disruption can be traced back to alteration of cis-acting elements or transacting factors that control the establishment maintenance and erasure of germiline epigametic imprints. The study at transgene methylation has shown that methylation pattern can be in parent origin in specific manner 3'- 7' suggesting that DNA Methylation may play role in genomic imprinting.

Key words: Heredity, Mendel, Genome Imprinting

INTRODUCTION

Heredity is one of the fundamental characteristics of all life on earth. Naturally, it has been a subject of intense investigation and keen observation since early days. Mendel in the late 19th century unveiled the basic principles guiding the hereditary traits. This virtually became an axiom for the geneticists. But later investigators found some genes showing non-Mendelian behaviours. Genome imprinting is one of such exceptions. It contradicts Mendelian principle of equivalence of traits in reciprocal crosses and shows that the sex of the parents contributing the gene does matter in its expression in the offspring. It is a recent finding. It became known in 1960's after Helen Crouse's experiments on insects. But the interest in the phenomenon really took off in mid 1980s. By now it is well known in Humans triggering several genetic diseases. A large number of investigators are actively engaged in understanding its mechanism and working.

Genome imprinting is the process which imprints or marks the genes passed by males and females in a way that some genes function properly when they are donated by mother while others do this only when they come from father. The phenomenon, thereby, includes all cases where genes have differential expressions depending upon the sex of the parents who inherit it.

The imprints are actually a special kind of modification in gene structure. These arise from varied activity of genes that operate differently in males and females. The imprints are specific to the sex of the individual. Consequently, the behaviour of the alleles varies in effect in succeeding generation. The offspring's

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that receive the gene from mother behave differently from those that receive it from father. Even when parents contribute identical genes, the genes have different effects. However, the imprints are not a permanent modification in gene or chromosome. These do not persist in the next generation. They are, rather, temporary and erasable. Old imprints are erased in each generation and new ones specific to sex of the individual are made during gamete formation.

The sperm and egg cells have chromosomes with new imprints, which are then passed on to the offspring. Thereby both sexes inherit some genes with paternal imprints and some with maternal imprints. The imprints result in differential expressions of alleles during development and in adult.

The mechanism of genome imprinting is not very much clear. Several molecular geneticists consider it as a consequence of vastly different physiology and biochemistry of the gametes. The data, so far available, indicate that the imprints lie within the gene structure itself and are a product of differential Methylation.[1] Methylation occurs after the base has been incorporated into DNA during replication. It is accomplished by ubiquitous nuclear enzyme Methylases. Different genes are methylated differently. Experiments on state of Methylation clearly showed that it is directly associated with the expression of genes. It is critical at specific site or in a restricted region. Many genes are not methylated at 5' end when they are expressed, although they are Methylated at 3' end.

However, the pattern of Methylation is variable in two sexes and hence allelic expressions differ. A gene is more methylated in females than the Males. The more highly methylated a gene the less likely it is to be expressed. The pattern changes as the gene traverses through alternating sexes. The highly Methylated genes become demethylated in Mother's son, Who then makes a new mark, and pass on to its offspring. In other words, female imprints are erased in son and a now one reflecting the male pattern is put on to it. Thereby, genes are methylated differently because of their maternal and paternal origin.

The pattern is believed to be guided by alterations in the chromatin surrounding the gene(s). This implies that the genes lying in tightly wound chromatin regions or in its vicinity are more likely to be imprinted upon. Based on the observations that winding protein may alter gene expression Sapienza *et al.* (1989)[2] suggested that such proteins dictate the process of genome imprinting.

Functions of genome imprinting are also not very clearly understood. There are contrasting views. Some people believe it to be a special case of "Dominance Modification". Many traits respond to the activity of other genes that modify their expressions. The modifier gene is postulated to control imprinting act differently in males and females.

While a widely held view is that imprinted genes regulate growth during development. The opinion is based on the nuclear experiments in Mouse embryo by McGrath and Solter (1984)[3]. It was observed that imprinting process selectively turned off some genes that would act otherwise during development. It was also seen that paternal over expression increased growth and maternal over expression reduced it. It is, thereby, obvious that the differential modification depended upon whether it was maternally or paternally inherited. This view is also substantiated with the evolution of genome imprinting in Mammals alone among vertebrates. Mammalian embryo is nourished directly from maternal tissues. The genes that are expressed in embryos can influence the quantity of resources that the offsprings receive from their mother. But significant effects are not expected in oviparous taxa where the amount of yolk is predetermined.

There are other suggestions also. Moore and Haige (1991)[4] suggested that imprinting in Mammals has evolved to prevent parthenogenesis. Parthenogenetic reproduction is often presumed to have short-term benefit for females but long term disadvantage for the species.

A few are of the opinion that genome imprinting allows flexible gene expressions and sophisticated control.

The problems of genome imprinting remain open for research. For example, it has not been conclusively proved that Methylation is the primary cause for genome imprinting or it merely reflects some hidden and more fundamental biochemical event. Besides, there are also difficulties in assuming that the state of Methylation provides general means for controlling gene expression. In Drosophila melanogaster and other Dipterans there is no methylation of DNA. The other differences between active and inactive, chromatin is the same as in other species that display Methylation, Furthermore, suggestions so far made, do not satisfactorily explain why

among vertebrates mammals alone should require such mechanisms. Future investigations will answer these. The prominent workers engaged in such investigations are Rotondo *et al.* (2013)[1], Sapienza *et al.* (1989)[2], McGrath and Solter (1984)[3], Moore and Haig (1991)[4], Reik and Walter (2001)[5], Barton *et al.* (1984)[6], Herrick and Seger (1999)[7], Ferguson (2011)[8].

CONCLUSION

Sex of the parents does matter in the expression of genes in offsprings. Each parent imprints its genome in a way that some genes function properly when they are donated by mother while others do so only when they come from father. The Imprints are modification in gene structure. Their pattern is specific to sex of the individual. This results in differential expression of alleles during development and growth.

REFERENCES

1. **Rotondo J.C., Selvatici R., Di Domenico M., Marci R., Vesce F., Tognon M. and Martini F. 2013.** Methylation loss at H19 imprinted gene correlates with methylenetetrahydrofolate reductase gene promoter hypermethylation in semen samples from infertile males. *Epigenetics*. **8(9):** 990-997.
2. **Sapienza, C., Paquette, J.E.A.N., Tran, T.H. and Peterson, A.L.A.N., 1989.** Epigenetic and genetic factors affect transgene methylation imprinting. Development, 107(1), pp.165-168.
3. **McGrath J. and Solter D. 1984.** Completion of mouse embryogenesis requires both the maternal and paternal genomes. *Cell*. **37(1):** 179-183.
4. **Moore, T. and Haig, D., 1991.** Genomic imprinting in mammalian development: a parental tug-of-war. *Trends in genetics,* **7(2):** 45-49.
5. **Reik W. and Walter J. 2001.** Genomic imprinting: parental influence on the genome. *Nature Reviews Genetics*. **2(1):** 21-32.
6. **Barton S. C., Surani M. A. H. and Norris M. L., 1984.** Role of paternal and maternal genomes in mouse development. *Nature*. **311(5984):** 374-376.
7. **Herrick G. and Seger J. 1999.** Imprinting and paternal genome elimination in insects. *Genomic Imprinting,* pp.41-71.
8. **Ferguson-Smith A.C. 2011.** Genomic imprinting: the emergence of an epigenetic paradigm. *Nature Reviews Genetics*. **12(8):** 565-575.