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DNA methylation: Atherosclerosis leading to congenital heart diseases

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Madam, Congenital heart diseases (CHD) are the problems that cover the most common type of deformity during birth. The problems could possibly be the accumulation of plaque in the arteries of heart that minimize the supply of oxygen rich blood to the heart muscles thus preventing it from normal workout. Common defects are found inside the walls and valves of heart or the enlarged blood vessels that carry blood towards and from the heart. The CHD can range from simple to much complex and disparaging conditions. CHD takes place in the foetus due to the changes in DNA mutations in particular genes that are inherited. The molecular mechanisms resulting in CHD are multiplex. Several factors can play a part in the development of CHD such as genetic susceptibility, epigenetic mechanism and environmental effects.[1] Among these factors DNA methylation is much known to be associated with CHD, that take place during pregnancy.

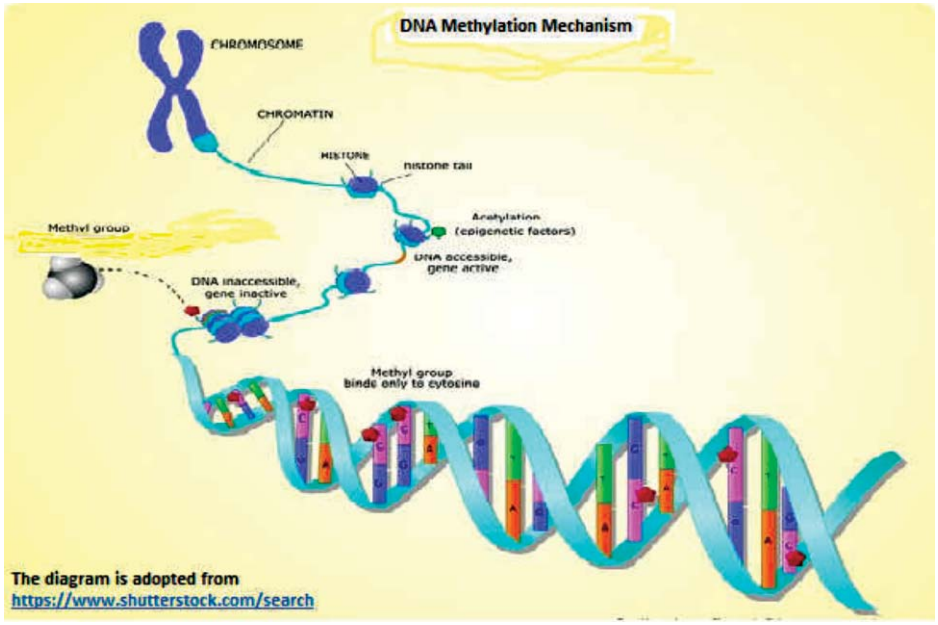

Figure: DNA methylatoin mechanism.

Epigenetic modifications in the genome such as DNA methylation have been suggested to play a role in the processes involved in cardiovascular diseases. DNA methylation is one of the forms of epigenetic gene regulation.[2] This process involves the incorporation of methyl group at the C5 position of cytosine altering the pattern of DNA producing possible changes in the gene expression.[3] DNA methylation is an epigenetic gadget that determines whether or not a gene is expressed, guides stem cells as they get a shape of specialized cells from blank slates.

The association between CHD and DNA methylation is not understood clearly, however many studies have shown substantial findings regarding association between them. Several DNA methylation approaches have been used which differ from one another illustrating the mechanism which include global DNA methylation, candidate gene and epigenome-wide association studies. CHD has been reportedly linked with Antisense non-coding RNA in the INK4 locus (ANRIL) premotor DNA methylation.[4] The differences in DNA methylation in vascular tissues with coronary artery disease may provide insight into the mechanisms underlying the development of atherosclerosis.

Since the studies are ongoing on association between DNA methylation and their consequences in the presentation of CHD, it is expected that the newly developed tools like next generation sequences techniques and further workout on demethylation phenomenon may help us to explore new ways in sorting out the exact epigenetics mechanism of CHD thus helping us in the treatment of complicated heart diseases. DNA methylation abnormalities involved in CHD once explored may help in prediction of

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atherosclerosis leading to CHD.

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