Holger heyn et al. distinct dna methylomes of newborns and centenarians pnas 2012...

Science, Biology

College DNA Methylation and Human Aging Human aging as a topic was the main factor that led to the purpose of this study which was to establish if the DNA methylomes in newborns are different in older people those aged and in between old age and newborns. The main finding of the study was in terms of the number of methylated CpG dinucleotide in newborn, old aged and intermediate sample. The CpG were many in the newborn sample followed by the intermediate and the least were in the old aged sample. Meaning, DNA of the old age has the least of methylated material.

2. The CpG regions acted as target points in the experiment not only because they contain methyl groups but also the researchers wanted to strengthen the study through CpG results, because they make the DNA strands which happen to play a crucial role in human aging. In relation to methylation, CpG regions tend to have a high content of methylomes hence were the most suitable for the study.

3. 12- 16 Whole Genome bisulphite sequencing of all the samples: newborn, centenarian and intermediate, was done to identify the methylation status. Also, a microarray of 450000 CpG methylation samples were included in the experiment. WGBS was hence performed for all the samples. For the newborn, fresh cord blood with permit from the parents was acquired for the experiment while for the old age his CD4 positive T cells were used. The intermediate sample was from a twenty six year old. All the three samples were from Caucasian males.

4. The methylation status in the three samples was different but formed a final curve in the results. The centenarian DNA had low methylomes

compared to those in a newborns DNA. Moreover, there is very low correlation in methylation of the CpG positions that are near the DNA. The intermediate sample was between the two, meaning is was second in the level of methylation. The CpG that were densely methylated in centenarian sample were located in specific genomic regions such as the promoters and more were on Island promoters than the poor promoters.

5. Alternative methods used apart from WGBS included the determination of the DMRS which are the differentiated methylated regions in the DNA of the two main samples. This method involved checking the total length of identical CpGs in the two samples by counting those that have a continuous consistent flow of methylation status. Moreover, an identified map of CpG that showcases a microarray of the 450000 samples use. The results from the map were then compared to those from WGBS.

6. The six genes from WGBS that were identified as differentiated were suspected earlier on following the use of the Epigraph software that helps in detecting and calculating the number of methylated and un-methylated CpGs in their most popular regions such as island promoters in the centenarian sample. The epigraph software tends to bring to surface the probabilities of methylation status of samples.

7. In relation to the CpG promoters, the poor promoters have more un-methylated CpG sites and less in the island promoters in the centenarian sample than in the newborn sample. Ae two main from the methylated CpGs, they were more in island promoters in the centenarian than the newborn sample. The intermediate sample had both methylated and un-methlyated

CpGs in a middle ground compared to two main samples.

Work Cited

http://www. pnas. org/content/109/26/10522. full