Breakthrough in breast cancer research reveals epigenetic link

Decoding the letters of the human genome revolutionised scientists' understanding of the role of genetic mutations in many diseases, including about one in every five cancers.

Now a team of Australian scientists have gone a step further, inventing a way to decipher another layer of information that garnishes genes, called methyl groups, which may explain the cause of many more cancers.

Methyl groups hang off sections of DNA like Christmas lights and act like a switch, affecting how genes are expressed in different cell types. Collectively called the methylome, they can also switch off tumour suppressor genes and switch on cancer promoting genes.

Susan Clark from the Garvan Institute of Medical Research and her team have for first the first time translated the methylome of breast cancer, finding distinct patterns associated with different types of breast cancer.

They have also found a way to classify women with the worst type of breast cancer, triple-negative, into two groups; those with a highly aggressive form and those with a lower-risk variety with a longer survival time. At present there is no reliable way to divide triple-negative cancers, which do not respond to targeted treatment, into these sub-groups.

With further testing, methylation signatures may be used as predictive biomarkers that doctors use to prescribe more appropriate treatments for women diagnosed with breast cancer in the future.

Professor Clark's team are the first in the world to sequence large chunks of the methylome from samples of cancer tissue that had been archived for up to two decades.

Read full, original article: Forget the genome, Australian scientists crack the 'methylome' for an aggressive type of breast cancer