# DNA Methylation

Non-small Cell Lung Cancer

Most frequent aberrant methylation genes in human NSCLC

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Epigenetic and sRNA differences between and within species are relatively poorly described compared with genetic and transcriptome variation.

In agreement, transposable elements (TEs) can be activated in interspecific hybrids, accompanied by changes in DNA methylation (Michalak, 2009)

DNA methylation pattern and gene expression pattern

The functional profile of DNA methylation in the promoter region promoter to skelton the stable relationship between DNA methylation and gene expression.

transgressive segregation

methylation status would transferred with the movement of transposable elements and therefore, lead to gene silence or suppress and then bring some aberrant phenotype.

Methylation status transitivity (MST)

Vary Substantially between difference strains or species, intraspecies

Understanding non-additive interactions between genomes is of both fundamental interest and very practical utility.

Methylome-wide Association Studies (MWAS)

Epigenome-wide association studies (EWASs)

The presence of genetic variation (SNPs) can affect the regulation of methylation and the consequent expression of a phenotype therefore it needs to be addressed when drawing conclusions on methylation-phenotype correlation.

Question. The degree of the SNPs’s effect to modify the relationship between DNA methylation and gene expression?