DNA are compacted as chromatin fibres, more compacted chromatin are less accessible.

Experiment: DNA in undifferentiated leukemia cells and mature erythrocytes treated with DNase, electrophoresis

- DNA in mature cells actively transcribed, less compact, digested by DNase, degraded, no band on autoradiograph. Undigested compact DNA in undifferentiated cells shown as a dark band.

Chromatin Remodelling complexes conduct chromatin remodelling to expose/hide BRE/TATA

- Histone modification: chromatin accessibility determinant:
  - Acetylation: acetyl group transferred from Acetyl-CoA onto lysine residue
    - Enzyme: Histone Acetyltransferase (HAT), Histone deacetylase (HDAC)
    - Neutralise the positive charge of lysine residue, less interaction between +ve tail and -ve DNA
    - Promote expression
    - Acetylated lysine bind with bromodomain of regulatory protein
  - Methylation: Promote/repress
    - Enzyme: Histone methyltransferase (HMT), Histone lysine methyltransferase (HKMT), catalyse in SET domain. Removed by Lysine demethylase (KDM)
    - Add 1/2/3 methyl groups to lysine or arginine on H3 and H4 N-tails
    - Methylated amino acid recognised by chromodomains of effector proteins, recruit other proteins for histone remodelling.
  - Unbiquitination (H2A and H2B C-tails only)
  - Phosphorylation
    - Serine, threonine can be phosphorylated
- H2A H2B expose both C and N tail, H1 H3 H4 expose N tail, most modification is on the N tail.

Histone modification interaction:

- Regulate DNA-histone interaction
- Regulate histone-histone interaction
- Recruit effector proteins
- Influence effect of other histone modifications
- Influence effect of effector

Histone modification transmission:

Parent histones are distributed onto daughter strands, enzymes recognise specific sequences from parental histones and apply the same modifications.

Examples

Experiment on chromatin accessibility

Histone structure

Possible modifications:what, where, who, effect, effectors

General effects 5

Modification transmission