





Double-Strand Breaks causate da radiazioni stress ossidativo farmaci

DSB e CROMATINA

- Higher-order chromatin packaging is a barrier to the detection and repair of DNA damage
- DSBs induce a local decrease in the density of the chromatin fibre, in addition to altering the position of nucleosomes
- DSBs also elicit post-translational modifications on the protruding histone tails

Chromating remodelling and DSBs





complex RSC (remodels the structure of chromatin) ATP-dependent chromatin-remodelling RSC can mediate nucleosome sliding, alter histoneDNA contacts and remove histones from DNA.

The chromatin-remodelling activity of RSC is important for transcriptional regulation of genes that are involved in stress responses and cell-cycle progression

Transcription of Site-specific RNA to be matured by DICER and DROSHA???

POSIZIONAMENTO NUCLEOSOMA Rimodellamento Cromatina





Chromating remodelling and DSBs



MODIFICAZIONE ISTONI

- Eukaryotes have several histone variants, which, as a result of their altered amino-acid composition, can affect both the structure of individual nucleosomes and the ability of nucleosomes to form higher order chromatin structure
- The earliest and most robust modification induced by DSB is phosphorylation of the histone H2A variant H2AX on its extended C-terminal tail.
- Within seconds, phosphorylated H2AX (known as γ-H2AX) spreads over a region spanning thousands to millions of bases surrounding a DSB

PIKKs = phosphatidylinositol-3OH-kinase -like kinases

DNA-damage sensor proteins Ku70–Ku80, MRN, RPA TOPBP1



METODI



METODI



DDR signal spreading



DDR proteins initially accumulate at DSB sites and then spread at distance via a positive feedback loop involving MDC1, which binds gH2AX, the MRN complex, and ATM kinase, which phosphorylates additional H2AX molecules further away from the break site.



Temporal regulation of DDR protein accumulation at DNA breaks







The MDC1 TQXF motifs are ATM targets required for 53BP1 IRIF. (A) Domain architecture of MDC1, with ATM consensus sites (dots).

Specialized binding modules for recognition of post-translational

modifications (PTMs) at DNA breaks.



Specialized binding modules for recognition of post-translational

modifications (PTMs) at DNA breaks.





complex RSC (remodels the structure of chromatin) ATP-dependent chromatin-remodelling RSC can mediate nucleosome sliding, alter histoneDNA contacts and remove histones from DNA.

The chromatin-remodelling activity of RSC is important for transcriptional regulation of genes that are involved in stress responses and cell-cycle progression

Transcription of Site-specific RNA to be matured by DICER and DROSHA???

Biogenesis of miRNAs and siRNAs



miRNAs are genomically encoded

siRNAs are produced exogenously or from bidirectionally transcribed RNAs

Drosha processes pri-miRNA to pre-miRNA in the nucleus

miRNA is selectively incorporated into the RISC for target recognition

Guide strand of siRNA is incorporated into the RISC for target recognition

miRNAs have imperfect complementarity to their target mRNA and inhibit translation

siRNAs form perfect duplex with their target mRNA and trigger mRNA degradation

from Li and Hannon, Nature Rev. Genet. 5, 522 (2004)



DICER or DROSHA inactivation impairs DDR foci formation in irradiated cells

Francia et al Nature 2012



Site-specific DDR focus formation is RNase A-sensitive and can be restored by site specific RNA in a MRN-dependent manner



A single inducible and detectable DSB



Site-specific DDR focus formation is RNase A-sensitive and can be restored by site specific RNA in a MRN-dependent manner



Mirin prevents MRN-dependent activation of ATM

