**Mathematical modeling**

To model chromatin dynamics in response to UVC laser damage, we considered the damaged chromatin region to have radial symmetry around the focal point of the UVC laser and nucleosomes to be uniformly distributed before damage. We assumed that the fraction of DNA loss () and histone loss () measured 15 min post laser in damaged chromatin were contributed to by a combination of chromatin opening and nucleosome sliding:

The direction of chromatin opening and nucleosome sliding is assumed to be from the focal point of the UVC laser, where the concentration of DNA lesions is the highest, in a radial manner outwards.

Chromatin opening leads to an equal loss of DNA and histones from the damaged region, which we hypothesize is proportional to the amount of UVC damage i.e. to UVC exposure time (noted ):

where is a constant.

Total DNA loss results from chromatin expansion due both to chromatin opening () and to DNA unwrapping during nucleosome sliding (). DNA loss can thus also be expressed as a function of the radial chromatin expansion factor :

The extra histone loss is due to nucleosomes sliding out of the damaged region (and eventually out of the ROI), and is expressed as:

where and are the numbers of nucleosomes in the damaged region beforedamage and 15 min after damage, respectively. Histone and DNA signal intensities before and after damage are measured in a region defined by the presence of DNA damage 15 min post UVC laser micro-irradiation (i.e. after expansion), which contains nucleosomes originally.

The fraction of nucleosomes lost from the damaged region by sliding is:

We assume that the fraction of nucleosomes sliding out of the damaged region is directly proportional to UVC damage:

where is a constant.

Thus, histone loss can be expressed as:

Nucleosome sliding increases chromatin expansion in the damaged region due to DNA unwrapping. The resulting DNA loss can be expressed as:

where is a constant

DNA and histone loss can thus be expressed as functions of UVC exposure time:

, and values were obtained by curve fitting as follows.

Non-linear regression curve fitting was performed with GraphPad Prismusing and data (average values) obtained at different exposure times to UVC laser. and values were constrained to 0 in the absence of DNA damage. Examination of the fraction of nucleosomes sliding out of the damaged region as a function of UVC exposure time indeed revealed a linear dependency to UVC damage with :

up to a saturation point at 30 msec corresponding to the maximum of nucleosomes bearing a UVC lesion in the irradiated region where

We thus considered two phases when fitting the and data as a function of UVC exposure time:

Before sliding saturation, () and () are expressed as:

After sliding saturation, and are expressed as:

The fraction of DNA and histones lost by chromatin opening is thus:

The contribution of chromatin opening to DNA loss was thus calculated as:

**Figure 3 : Parental histone mobilization by chromatin opening and nucleosome sliding**

(**A**) Distribution of parental histones H3.3 (red) and DNA (blue, stained with Hoechst) 15 min after local UVC irradiation (50 msec irradiation time) in U2OS cells stably expressing H3.3-SNAP. Paraformaldehyde-fixed cells were used as a control for photo-bleaching of Hoechst staining by the UVC laser. White arrowheads indicate the irradiated areas. Similar results were obtained by staining parental histones H3.3 in green and DNA in red with NUCLEAR-ID Red DNA Stain (data not shown).

(**B**) Quantifications of fluorescence loss in irradiated areas as a function of UVC exposure time (red fluorescence associated with parental H3.3 and blue fluorescence associated with DNA). Data from n cells scored in two independent experiments.

(**C**) Schematic representation of parental histone mobilization in UVC-damaged regions by chromatin opening (orange arrows) and nucleosome sliding (green arrows).

(**D**) Mathematical modeling of histone and DNA loss in UVC-damaged regions as a function of UVC exposure time. Error bars on experimental points represent S.D. from 30 cells scored in two independent experiments. R2 indicates the goodness-of-fit of non-linear regression.

(**E**) Relative contributions of nucleosome sliding and chromatin opening to chromatin expansion (DNA and histone loss) as a function of UVC damage according to the mathematical model defined in (D).

(**F**) Histone loss by chromatin opening (orange) and nucleosome sliding (green) as a function of UVC damage calculated according to the mathematical model defined in (D).

The dotted line marks the UVC exposure time when nucleosome sliding reaches saturation (maximum of damaged nucleosomes).

See also, Figure S3.

**Figure S3: Mathematical modeling of parental histone mobilization. Related to Figure 3.**

(**A**) Nucleosome sliding fraction as a function of UVC exposure time fitted by non linear regression defines nucleosome sliding saturation (dotted line).

(**B**) Histone and DNA loss as a function of UVC exposure time fitted by non linear regression before and after sliding saturation (dotted line). The equation of the curves are indicated with h: histone loss, d: DNA loss and u: UVC exposure time (msec). After sliding saturation the contribution of nucleosome sliding (green) to histone and DNA loss is constant and the slope of the h and d lines reflects the contribution of chromatin opening as a function of UVC exposure time (orange).