Errata

Title: RNA-related DNA damage and repair: The role of N7-methylguanosine in the cell nucleus exposed to UV light.

Authors: Stixová L, Tichý V, Bártová E.

Journal: Heliyon. 2024 Feb 7;10(4):e25599. doi: 10.1016/j.heliyon.2024.e25599. eCollection 2024 Feb 29.

Erratum 1:

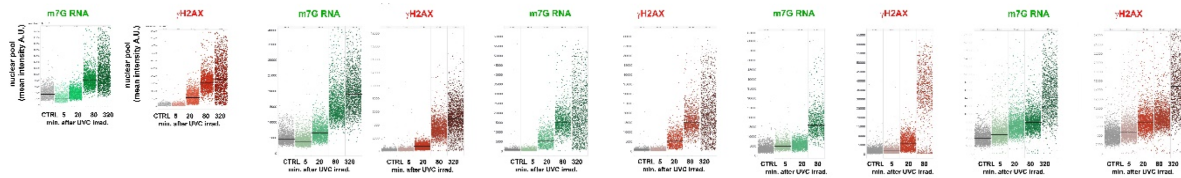
Material and methods – revised version

Quantitative image-based cytometry (QIBC)

QIBC was performed according to Ref. [29]. Images were captured using a ScanR inverted high-content screening station (Evident), equipped with an IX83 inverted microscope frame with wide-field optics, a UPLXAPO dry objective (20×, 0.8 NA), fast excitation and emission filter-wheel devices for DAPI, fluorescein isothiocyanate (FITC), cyanine-3 (Cy3), and cyanine-5 (Cy5) wavelengths, Lumencor Spectra X LED fluorescence light source, and digital monochromatic sCMOS ORCA-Flash 4.0 LT Plus camera. Automated image acquisition was performed using ScanR acquisition software (version 3.4.1, Evident) under non-saturating conditions within a 16-bit dynamic range of the camera. The laser intensity was set to 100%, and exposure times were as follows: for Fig. 4B, C: 5 ms for DAPI, 700 ms for FITC, and 200 ms for Cy5; for Fig. 4D, E: 5 ms for DAPI, 1000 ms for FITC, and 200 ms for Cy5; for Fig. 6D: 5 ms for DAPI, 300 ms for FITC. For each experiment, a minimum of 4000 cells were captured and subsequently analyzed using the ScanR analysis software (version 3.4.1, Evident). Automated dynamic background correction was applied to all images for each fluorescent channel separately, maintaining a threshold at a minimum of 5-fold pixel intensity above background levels for each channel. The background correction parameters were maintained for all treatments within an experiment. The DAPI signal was used to generate an intensity-threshold-based mask to detect individual cell nuclei. This mask was then applied to measure FITC and Cy5 fluorescence intensities in individual nuclei. The multiparameter analysis was exported as a table and further analyzed in Spotfire software (version 11.8.0, TIBCO). Within each experiment, an equivalent number of cells were compared among different conditions. Using quantitative microscopy, we analyzed the nuclear pool of METTL1 (14994-1-AP, Proteintech), WBSCR22 (28192-1-AP, Proteintech) proteins, phospho-Histone H2A.X (Ser139) (#05-636, Sigma-Aldrich) and m7G in RNA (#ab300740, Abcam) in non-irradiated and UVA- or UVC-irradiated HeLa cells. In all cases, the dilution of antibodies was 1:100 in PBS.

Erratum 2:

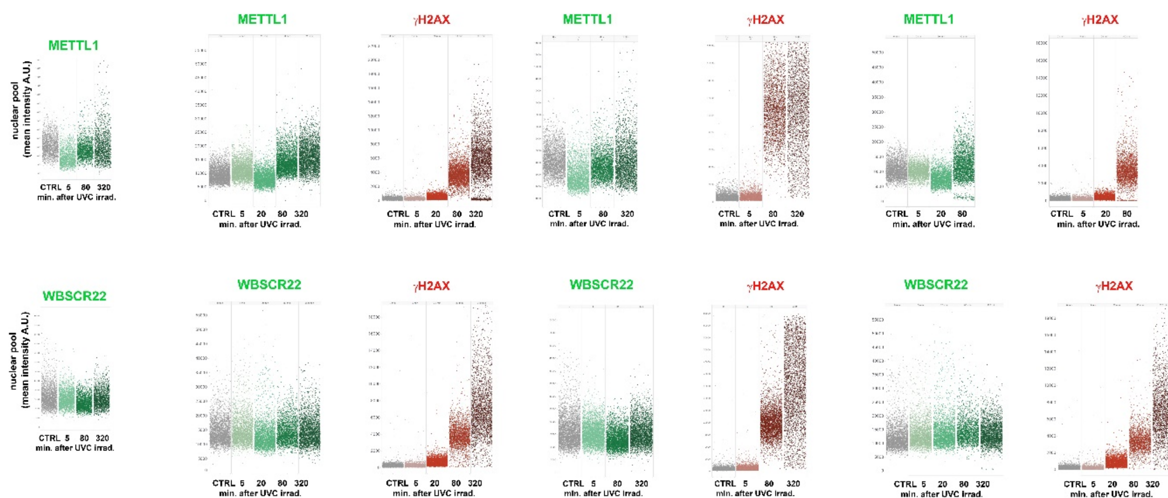
Additional data to Figure 4B, C.



(Note: UVA lamp no longer has the same efficacy as it did last year, and therefore, it causes only slight DNA damage).

Erratum 3:

Additional data to Fig. 6D.



Erratum 4:

We correct the following sentence: Also, we thank Hana Polášek-Sedláčková for help with Scan-R microscopy, analysis, and interpretation, and Jana Krejčí for technical help in the laboratory.

to

Also, we thank Hana Polášek-Sedláčková for training us on how to work with the ScanR microscope, and Jana Krejčí for technical help in the laboratory.