Literature Report

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EDGE ARTICLE

Enhancing biocompatibility of rhodamine fluorescent probes by a neighbouring group effect

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Chromatin Labeling and Imaging

•Creation of new biocompatible fluorescent chromatin probes.

•Application of the newly developed probes for imaging and establishment of image analysis pipelines.

•Elucidation of the chromatin structure and dynamics in living cells during cell cycle or external stimulation









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Fig. 2. Neighbouring group effect in the fluorescent probes. **a**, ^{Dye}D₅₀ values of positional isomers of **TMR-COOH** and ^{probe}D₅₀ of **TMR-LTX**. **b**, DFT optimized geometries of a model 4'regioisomer fluorescent probe in spirolactone and zwitterion forms with truncated linker and targeting moiety. **c**, DFT calculated potential energy differences between spirolactone and zwitterion of model 4'/5'/6'-regiosomer probes in 1,4-dioxane and water environment. **d**, Chemical shifts of the amide proton of **TMR-LTX** regioisomeric probes. **e**, Comparison of retention times of **TMR-LTX** regioisomeric probes in HPLC analysis with SB-C18 column under isocratic elution conditions (75:25 MeOH : H₂O 25mM HCOONH₄ pH = 3.6).











Fig. 3. Imaging performance of fluorescent probes based on rhodamine isomers. a, Wide-field fluorescence microscopy of living primary fibroblasts stained with 100 nM TMR-LTX isomers for 1h at 37°C. Cells were washed once with HBSS and imaged in DMEM growth media. Insets shows zoomed-in images. Scale bars: 100 µm (large field of view), 10 µm (inset). Hoechst staining is shown in cyan and all tubulin probes are in magenta. b, Quantification of fluorescence signal in the cytoplasm of living cells stained with tubulin probes. Data is presented as mean \pm s.e.m., N = 3 independent experiments, each time n > 100 cells were quantified. c, Cytotoxicity of tubulin fluorescent probes presented as half maximal effective concentration (EC50) after 24h incubation at 37°C in growth media. Cytotoxicity was determined as fraction of cells containing less than a single set of genetic material (sub G1 DNA content). Data is presented as mean \pm s.e.m., N = 3 independent experiments, each time n > 100 cells were quantified. d, Wide-field microscopy images of living primary fibroblasts. The cells were stained with 100 nM 4/5/6-580CP-Hoechst (magenta) or 100 nM 4/5/6-610CP-JAS (yellow) for 1h at 37°C, washed once with HBSS and imaged in DMEM media. Inserts show zoomed-in images. Scale bars: 100 µm (large field of view), 10 µm (insets). Overlay with phase contrast (grey) images are shown. e, Quantification of DNA probes fluorescence signal in the nuclei. Data presented as mean ± s.d., N = 3 independent experiments, each n > 100 cells. f, Quantification of 4/5/6-610CP-JAS fluorescence signal in the cytoplasm of living cells. Data presented as mean \pm s.d., N = 3 independent experiments, each n > 100 cells.





Fig. 4. Confocal and Airyscan imaging of living cells stained with rhodamine 4'-isomer probes. **a**, Single microtubule and cytoplasm fluorescence signal ratio in living human fibroblasts stained with 100 nM of indicated probe for 1h at 37°C and imaged without probe removal. Data is presented as mean \pm s.d., N \geq 3 independent fields of view, each time n \geq 20 microtubules. **b**, Zeiss Airyscan images of human primary fibroblasts stained with **5-SiR-Hoechst** and **4-TMR-LTX** for 24 h at 37°C in growth media at indicated concentrations. Images acquired without probe removal. **c**, Cell cycle of human primary fibroblasts stained with **1 nM 4-TMR-LTX** (yellow) and **10 nM 5-610CP-Hoechst** (magenta). Scale bar: 10 µm. Overlay with phase contrast (grey) images are shown. **d**, Three-colour ZEISS Airyscan image of living HeLa cell at metaphase stained with **3 nM 4-TMR-LTX** (yellow), **20 nM 5-SiR-Hoechst** (magenta) and **1000 nM 6-510R-JAS** (cyan). Scale bar: 1 µm.





Fig. 5. STED nanoscopy imaging of living cells stained with rhodamine 4'-isomer probes. **a**, Confocal and STED images of microtubules in human fibroblasts taken with 0.25 AU pinhole. The cells were stained with 100 nM **4-610CP-CTX** for 1h at 37°C. Scale bar: 1 μ m. **b**, Fluorescence intensity profile at the rectangle in panel **a**. Insets show measured (mean ± s.d., N = 20) and predicted diameter from cryo-electron microscopy model of tubulin (orange) bound to paclitaxel (blue). **c**, Apparent microtubule FWHM measured by different microscopy methods. Human fibroblasts stained with 100 nM probes for 1h at 37°C. * - diameter measured between two peaks of fitted intensity profile. Data presented as mean ± s.d., N ≥ 3 independent fields of view, each time n ≥ 10 microtubules. **d**, Nine-fold symmetry of centriole resolved in the deconvolved STED DyMIN²⁵ image of U-2 OS cell stained with 100 nM **4-610CP-CTX** for 1h at 37°C. White dashed lines mark a second centriole. Scale bar: 1 μ m. **e**, Deconvolved STED image of human fibroblast nucleus stained with 100 nM **4-610CP-GTX** for 1h at 37°C. Scale bar: 1 μ m. **e**, Deconvolved STED image of human fibroblast nucleus stained with 100 nM **4-510CP-IAS** and 10 nM **4-TMR-LTX** for 1h at 37°C. Scale bar: 10 μ m.

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