Linker histone H1 functions as a liquid-like glue to organize chromatin

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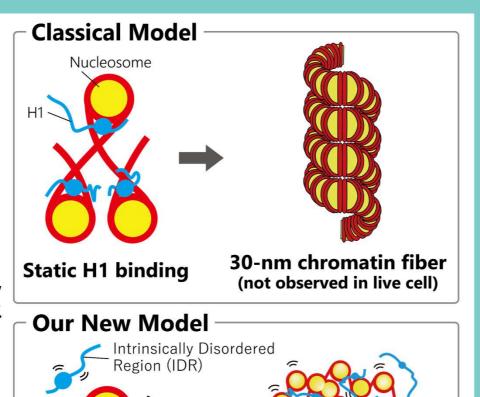


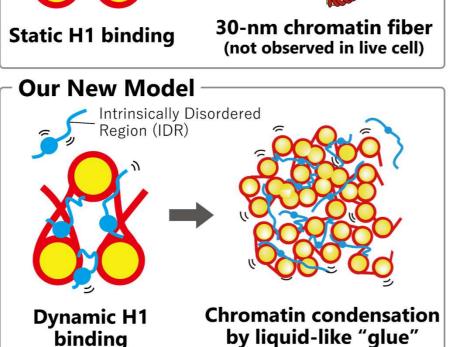


Abstract

- Linker histone H1 makes chromatin condensed.
- H1 helps 30-nm chromatin fiber formation in vitro. (J. Allan et al. Nature (1980))
- In vivo, chromatin folds into irregular "Chromatin domain", but not 30-nm chromatin fiber. (T. Nozaki et al. Molecular Cell (2017))
- H1 has dynamic interaction with chromatin in living higher eukaryotic cells. (T. Misteli et al. Nature (2000))

An alternative model for chromatin condensation by H1 is needed.





Method: Single molecule imaging of H1

'Bound" H1

"Dissociated"

H1

 $D_1 = 0.00720 \, \mu \text{m}^2/\text{s}$

(Persson, Fredrik, et al. Nature methods (2013))

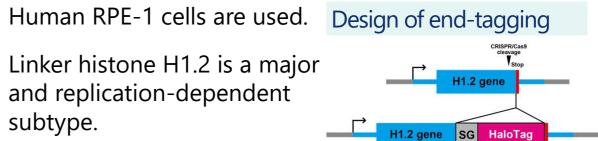
- Linker histone H1.2 is a major and replication-dependent subtype.
- By CRISPR/Cas9 system, HaloTag is inserted into the C-term of endogenous H1.2 with 3x GGGGS linker.
- Sparse labeling by HaloTag ligands and oblique illumination enables single-molecule imaging.
- (J. Tinevez Methods (2017))

Motion classification by vbSPT

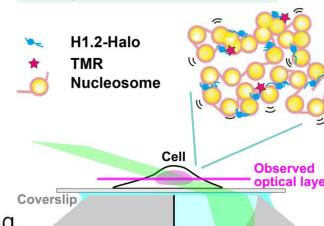
"Liquid-like"

H1

 $D_2 = 0.0262 \, \mu \text{m}^2/\text{s}$

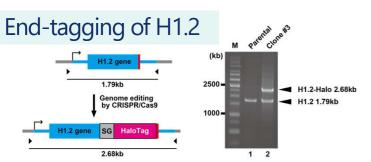




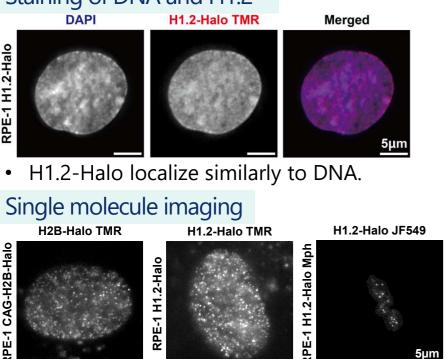


TrackMate is used for tracking.

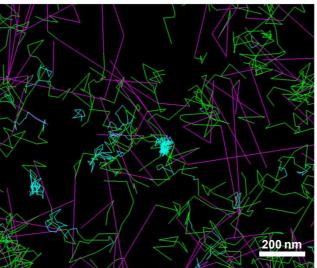
Result 1: Motion of H1





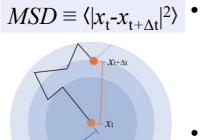


Trajectories of H1



PA-JF549 labeled, 50ms/frame

MSD plot of H1 and H2B



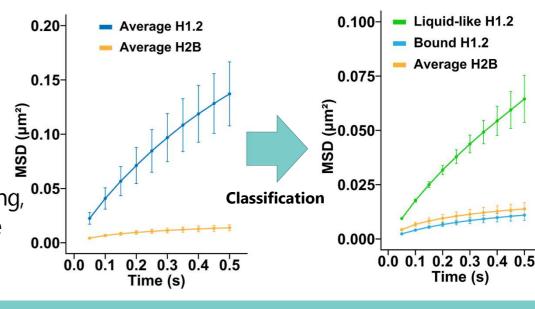
Mean Square Displacement (MSD) indicates how much molecules explored the area during Δt .

If molecules are freely diffusing, that result in a linear increase in the MSD plot.

H1 motion can be classified into 3 states.

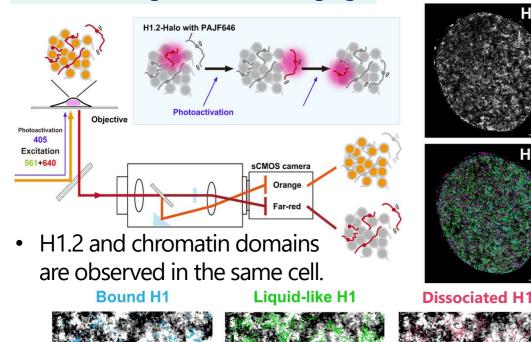
Laser

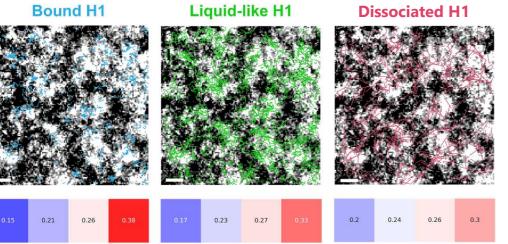
- 30% of H1 behave like nucleosomes ("Bound").
- Major H1 shows dynamic behavior than nucleosome.
- 60% of H1 behave like $D_3 = 0.356 \, \mu \text{m}^2/\text{s}$ liquid (linear MSD plot).
 - H1 rarely shows "Jumps".



Result 2: Liquid-like H1 diffuse within chromatin domains

Dual-color single molecule imaging

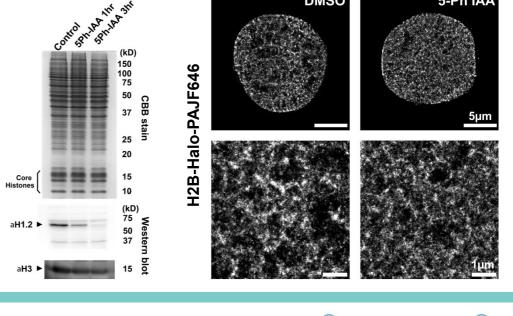




Result 3: H1 depletion decondenses chromatin

PALM imaging of chromatin domain with rapid depletion of H1.2

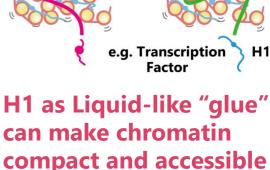
- With AID2* system, mAID-tagged end-H1.2 can be rapidly (~3hrs) depleted by addition of 5-Ph IAA. (*A. Yesbolatova et al. Nat. Comun. (2020))
- Chromatin domain structure get decondensed by H1.2 depletion.



Conclusion & Discussion

"Bound" H1	30%	Nucleosome-bound H1 "Dyad" binding of H1
"Liquid-like" H1	60%	Dynamic binding on nucleosomes Seems to be Liquid-like "glue"
"Dissociated" H1	10%	Temporally dissociated Immediately back to "Liquid"
B. #	6114	101 10 01 041 0 1 40

Major fraction of H1 moves like liquid within chromatin domains, while interact with several nucleosomes.



at the same time!!!