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$SNAP_f$ based pulse labeling for analysis of protein turnover in living cells

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Introduction

SNAP-tag based pulse labeling allows for analysis of protein turnover in living cells (1-3). Since the timing of labeling of a given fusion protein is under experimental control, questions about protein trafficking, protein turnover, organelle dynamics and macromolecular assembly become open to investigation. Sensitivity and temporal resolution of such measurements are limited by reaction kinetics. An improved version of SNAP-tag has been developed, termed $SNAP_f$, that displays better reaction kinetics *in vitro* and *in vivo* (4,5).

Pulse Labeling of SNAP-CENP-A Fusion Protein

To assess $SNAP_f$-tag performance in living cells, both SNAP26m (earlier mutant version) and $SNAP_f$, along with 3 copies of a Haemagglutinin (HA) tag each, were fused to the N-terminus of Centromeric Protein A (CENP-A) (Fig. 1). This histone variant localizes to centromeres producing a unique pattern of nuclear foci (1). HeLa cells were transfected with either fusion protein and labeled with SNAP-Cell TMR-Star (NEB#S9105S) at concentrations ranging from 1-2 µM for 5-15 minutes. Excess substrate was washed away. Cells were fixed and processed for immunofluorescence to detect HA as a measure of SNAP-tag fusion protein expression level. Finally, TMR/HA ratios were obtained as a measurement of SNAP-tag activity per protein amount. $SNAP_f$ outperformed SNAP26m *in vivo* by three-fold across dye concentration and incubation times tested (Fig. 2).

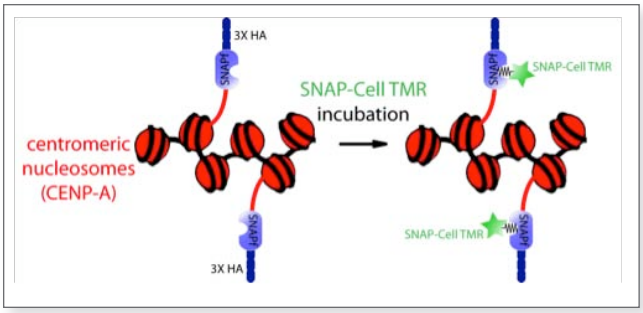

Figure 1. *A proportion of centromeric histones are N-terminally tagged with $SNAP_f$ and an HA epitope tag and incorporated into centromeric chromatin in vivo. Pulse labeling with SNAP-Cell TMR-Star results in specific $SNAP_f$ dependent fluorescence.*

General Protocol

Labeling of SNAP26m and $SNAP_f$-tag fusion proteins

1. Seed cells on a glass coverslip.
2. After 24-48 hours transfect cells with a construct expressing SNAP26m or $SNAP_f$-tag fusion proteins.
3. Incubate for 48 hours at 37°C, 5% CO_2, in a cell culture incubator.

Materials

- Cells expressing SNAP-CENP-A fusion proteins
- SNAP-Cell® TMR-Star (NEB# S9105S)
- HeLa cells
- DMEM medium
- Anti-HA antibody (Covance)
- 4',6-diamidino-2-phenylindole (DAPI)
- Glass coverslips
- Phosphate buffered saline (PBS)

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4. Label cells with 1-2 µM SNAP-Cell TMR-Star (NEB#S9105S) diluted in pre-warmed complete medium.
5. Incubate for 5-15 minutes at 37°C, 5% CO_2, in a cell culture incubator.
6. Wash cells 2x with pre-warmed PBS, followed by incubation in fresh complete medium for 30 minutes.
7. Wash cells 2x with pre-warmed PBS.
8. Fix cells.

Immunofluorescence

9. Perform immunofluorescence using standard procedures to detect the HA-tag (Covance) or protein of interest.
10. Stain with 4',6-diamidino-2-phenylindole (DAPI) before mounting.

Microscopy

11. Image cells using a standard wide field fluorescence microscope using appropriate filters.

Results

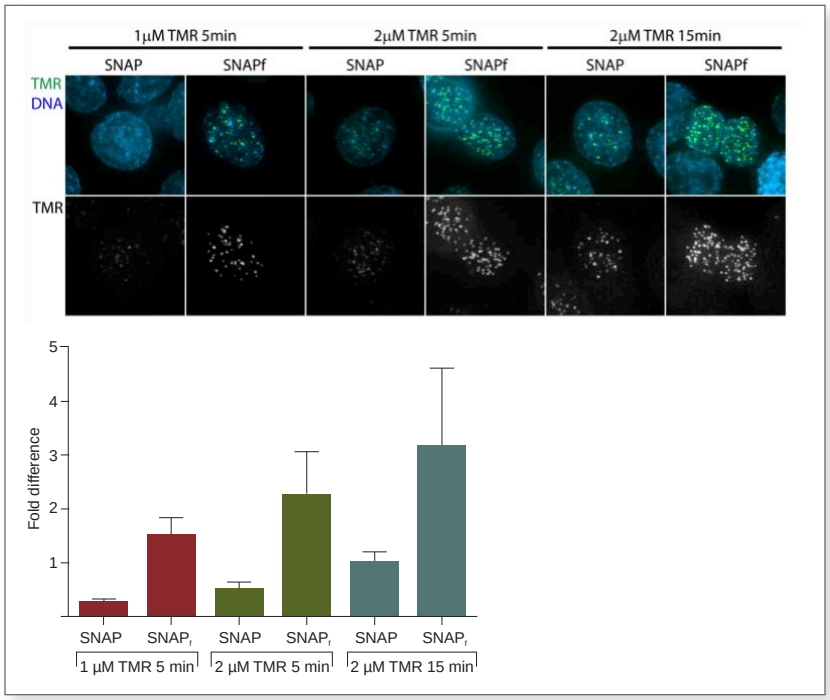

Figure 2. *HeLa cells transiently transfected with centromeric SNAP26m or $SNAP_f$ fusion proteins were labeled with SNAP-Cell TMR-Star at indicated concentrations and incubation times and processed for immunofluorescence with anti-HA. Representative images of cells are shown with SNAP-Cell TMR-Star signals in green and DAPI (DNA) in blue. TMR/HA ratios are used as a measure of $SNAP_f$ activity. Results are plotted as fold difference normalized against signals obtained after incubation with 2 µM SNAP-Cell TMR-Star for 15 minutes.*

Summary

Pulse labeling with SNAP-Cell TMR-Star results in specific $SNAP_f$ dependent fluorescence. The $SNAP_f$ displays a 3-fold better performance in living cells compared to SNAP26m. Faster $SNAP_f$ kinetics allows for reduction of substrate concentration and incubation times. This is a significant improvement that will facilitate sensitivity, better temporal resolution of turnover studies and live cell imaging of $SNAP_f$ pulse labeled cells.

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Development of $SNAP_f$ and $CLIP_f$: Fast-labeling Variants of SNAP and CLIP tags

Introduction

The ability to monitor highly dynamic processes is integral to the understanding of how proteins function in a cellular environment. Processes such as protein synthesis, transport, and degradation can occur on a timescale measured in minutes rather than hours. Additionally, protein expression, localization, and degradation are often rapidly modulated during the course of a variety of cellular processes. In order to effectively study proteins with rapid dynamics or fast turnover rates, researchers need tools to monitor these events in real time.

Results

$SNAP_f$ and $CLIP_f$ tags Fast-labeling Systems

The SNAP- and CLIP-tag are self-labeling tags based on human O6-alkylguanine-DNA-alkyltransferase (hAGT), a DNA repair protein (1-3). New England Biolabs has developed improved versions of these tags, termed $SNAP_f$ and $CLIP_f$. $SNAP_f$ carries 19 amino acid substitutions and a C-terminal deletion compared to wild-type hAGT, and 10 extra mutations compared to SNAP26m (an earlier mutant version). The new polylinker sequences allow expression of $pSNAP_f$ vector (NEB #S9183S) on either the N- or C-terminus of the protein of interest, under control of the CMV promoter. The $CLIP_f$ expression vector $pCLIP_f$ (NEB #S9215S) bears the same backbone and compatible polylinkers. Both vectors contain a neomycin resistance (NeoR) gene for selection of stable transfectants and an IRES element for efficient expression of both the fusion protein and NeoR.

$SNAP_f$ and $CLIP_f$ exhibit faster labeling kinetics than their predecessors in both *in vitro* and in live cell assays (4,5). When comparing the reactivity of $SNAP_f$ and SNAP26m towards several fluorophore conjugates, $SNAP_f$ shows up to 10-fold increased *in vitro* activity relative to SNAP26m (Table 1). The time required for 50% labeling of $SNAP_f$ at 1 µM protein concentration with 5 µM SNAP-Surface 488 (NEB #S9124S), SNAP-Cell TMR-Star (NEB #S9105S), SNAP-Surface 549 (NEB #S9112S), and SNAP-Surface Alexa Fluor 647 (NEB #S9136S) was calculated to be 11, 12, 13, and 34 s, respectively. $SNAP_f$ reacts with a wide range of benzylguanine substrates with efficiencies greater than 90% after a 5 min incubation and greater than 95% and after a 30 min incubation (Table 2).

General Protocol

1. Seed trypsinized U2OS cells stably transfected with $pSNAP_f$-H2B (or pSNAP26m-H2B) in an 8-well Lab-Tek II Chambered Coverglass (Nalgene #155409).
2. Incubate sample for 18-24 hours at 37°C, 5% CO_2.
3. Remove transfection complex media, wash cells twice with complete media, and label cells with 3 µM SNAP-Cell® TMR-Star (NEB #S9105S) labeling media from 0 to 30 minutes at 37°C, 5% CO_2.
4. Lyse cells in 1X SDS loading buffer.
5. Analyze total protein from ~10^5 cells per lane by SDS-PAGE.
6. Transfer samples onto a NC membrane.
7. Scan and visualize using Typhoon 9400 Imager (Ex./Em. filter set: 532/580 nm).
8. Perform Western blot analysis with anti-Tubulin antibody (1:2000) to assess protein level.

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Materials

- $pSNAP_f$-H2B (NEB #N9186S)
- SNAP-Cell® TMR-Star (NEB #S9105S)
- U2OS cells
- DMEM medium
- Anti-Tubulin antibody
- Lab-Tek II Chambered Coverglass (Nalgene)

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Table 1. Kinetics properties of $SNAP_f$ and SNAP26m

SUBSTRATE	MUTANT	$T_{½}$[S]	K_{OBS} [$M^{-1}S^{-1}$]	REL. RATE
SNAP-Surface 488 (NEB #S9124S)	SNAP26m	88	1583	1
	$SNAP_f$	11	12183	7.6
SNAP-Cell 505 (NEB #S9103S)	SNAP26m	28	4945	1
	$SNAP_f$	11	12447	2.5
SNAP-Cell Oregon Green (NEB #S9104S)	SNAP26m	654	212	1
	$SNAP_f$	111	1249	5.9
SNAP-Cell TMR-Star (NEB #S9105S)	SNAP26m	90	1536	1
	$SNAP_f$	12	12033	7.8
SNAP-Surface 549 (NEB #S9112S)	SNAP26m	129	1074	1
	$SNAP_f$	13	11138	10.4
SNAP-Surface Alexa Fluor 647 (NEB #S9136S)	SNAP26m	219	634	1
	$SNAP_f$	34	4768	7.5

Activities of $SNAP_f$ and SNAP26m mutants were measured using proteins isolated with the IMPACT protein expression and purification system. The relative rates are calculated by comparing the k_{obs} value of $SNAP_f$ to that of SNAP26m labeled with the same substrate at 25ºC.

Table 2. Labeling Efficiency of $SNAP_f$ tag

SUBSTRATE	LABELING TIME	
	5 MIN	30 MIN
SNAP-Cell TMR-star (NEB #S9104S)	95%	95%
SNAP-Cell 505 (NEB #S9103S)	93%	95%
SNAP-Cell Fluorescein (NEB #S9107S)	95%	95%
SNAP-Cell Block (NEB #S9106S)	95%	95%
SNAP-Surface 488 (NEB #S9124S)	94%	95%
SNAP-Surface Alexa Fluor 488 (NEB #S9129S)	95%	95%
SNAP-Surface 549 (NEB #S9112S)	92%	95%
SNAP-Surface Alexa Fluor 546 (NEB #S9132S)	95%	95%
SNAP-Surface 647 (NEB #S9137S)	93%	95%
SNAP-Surface Alexa Fluor 647 (NEB #S9136S)	95%	95%
SNAP-Surface Block (NEB #S9143S)	90%	95%
SNAP-Vista Green (NEB #S9147S)	95%	95%
SNAP-Biotin (NEB #S9110S)	95%	95%

The labeling reactions were performed in the presence of 5 µM $SNAP_f$ protein and 10 µM substrate at 25ºC. The reactions were analyzed by mass spectrometry to detect the unlabeled and labeled $SNAP_f$ species.

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Results

$SNAP_f$ Protein Labeling in Living Cells

Time course labeling using SNAP-Cell TMR-Star (NEB #S9105S) exemplifies the superior rate of reaction of $SNAP_f$ over SNAP26m (Fig. 1). The results demonstrate that labeling of $SNAP_f$-H2B can be visualized after an incubation time as short as 5 minutes using 1 µM SNAP-Cell TMR-Star, whereas at least 15 minutes are necessary for the detection of a distinct signal for labeled SNAP26m-H2B. The significantly enhanced labeling of $SNAP_f$ fusion is consistent at every labeling time point from 5–30 minutes.

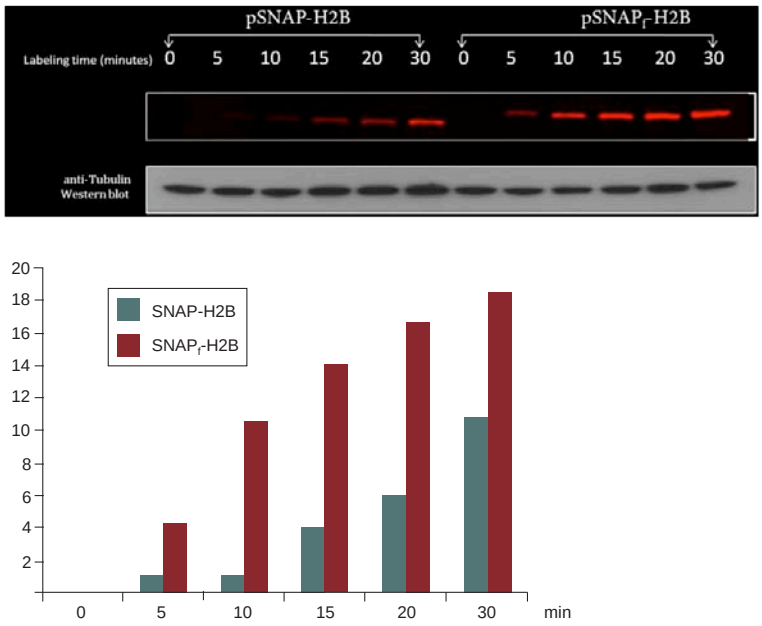

Figure 1. *Improved labeling efficiency of $SNAP_f$ fusion proteins in live U2OS cells. Stable U2OS cells expressing $SNAP_f$-H2B and SNAP-H2B were labeled with 1 µM SNAP-Cell TMR-Star from 0 to 30 min. Labeling efficiency was evaluated by SDS-PAGE and in-gel fluorescence scanning after cell lysis. Tubulin was used as protein expression control.*

Summary

The new generation of fast self-labeling $SNAP_f$ and $CLIP_f$ systems opens new avenues for analysis of highly dynamic processes in living cells with high spatial-temporal resolution. The improved kinetics of $SNAP_f$ and $CLIP_f$ associated with their unique molecular specificity enables the investigation of proteins with regard to their dynamic behavior, including cellular trafficking, stability and interactions in complex biosystems.

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