

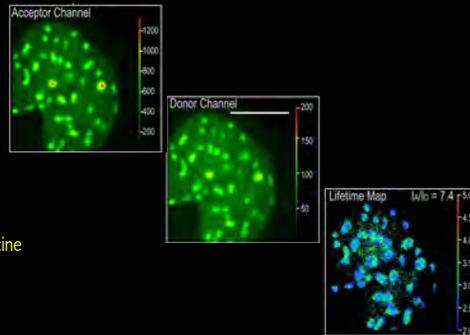
Förster Resonance Energy Transfer: monitoring protein interactions in living cells

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Indiana University School of Medicine
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Overview: Application and limitations of FRET

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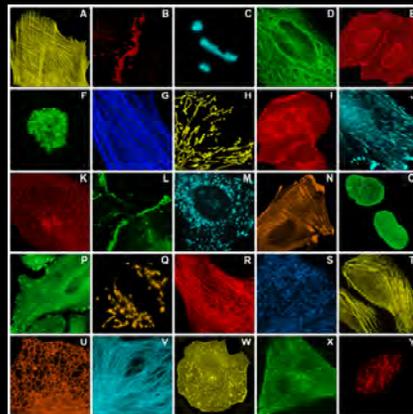
- What is FRET?
- What are the requirements for FRET?
- Problems with spectral crosstalk.
- **FRET by Frequency Domain (FD) FLIM:**
 - Data analysis by phasor plots.
 - Genetically encoded FRET Standards.
 - Biosensor probes.
- **Monitoring nuclear protein interactions with FLIM:**
 - FRET-FLIM measurements of intermolecular interactions: Homologous protein interactions - C/EBP α Bzip domain.
 - Heterologous interactions - HP1 α .

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The expanding fluorescent protein (FP) palette

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- FPs that emit across the visible spectrum are now available.
- Many new FPs have been optimized for expression in a variety of systems.
- Some of the FPs have characteristics suitable for Förster (fluorescence) resonance energy transfer (FRET) microscopy.



Day and Davidson (2009) Chem. Soc. Rev 38:

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The use and abuse of FRET imaging

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- The genetically-encoded FPs led to a dramatic increase in the use of FRET measurements to detect protein interactions in living cells.
- A consequence of this newfound popularity has been the “degradation in the validity of the interpretations” of these experiments.
S. S. Vogel, C. Thaler and S. V. Koushik, *Sci STKE*, 2006, 2006, re2.
- It is often difficult to directly compare the accuracies of different methods.
 - ❖ Use “FRET Standards” to characterize the experimental system.
 - ❖ Use more than one FRET method to verify the results.

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What is FRET and why use it?

- The lateral (x-y) resolution of an optical image: the distance that two objects must be separated by to be resolved as separate objects:

$$r = \frac{(0.61) \lambda}{NA}$$

- Theoretical limit for an ideal specimen - your results may differ.
- Newer optical techniques offer several fold improvement in resolution, but much greater resolution is necessary to detect protein-protein interactions in living cells.
- FRET microscopy can provide measurements of the spatial relationship between fluorophores on the scale of ångströms.

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What is FRET?

- FRET is the direct transfer of excited state energy from a donor fluorophore to a nearby acceptor.
- A fluorophore in the excited-state is an oscillating dipole that creates an electric field (the donor - D).
- If another fluorophore enters the electric field, energy can be transferred directly to that fluorophore (the acceptor - A).
- No intermediate photon!**

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Förster's contribution

- Electric field interactions:

- Theodor Förster recognized the probability of energy transfer would be low, and quantitatively described how FRET efficiency decreased as the inverse of the sixth power of the distance.

"Energiewanderung und Fluoreszenz" Naturwissenschaften (1946) 36:166-175

$$E_{FRET} = \frac{R_0^6}{R_0^6 + r^6}$$

R_0 , the Förster distance

Cerulean-Venus $R_0 = 52 \text{ Å}$

FRET

Distance (Å)

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FRET measures the spatial relationship between the FPs

- The optical resolution of the light microscope is limited to 250 nm.
- The detection of FRET indicates the fluorophores are less than ~ 8 nm (80Å) apart:

Cerulean-Venus $R_0 = 52 \text{ Å}$

EFRET

Distance (Å)

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The spectral overlap requirement

- The donor emission spectrum must significantly overlap the absorption spectrum of the acceptor.

Normalized Intensity vs Wavelength (nm)

--- Excitation
— Emission

A. Quenched emission Sensitized emission
FRET
< 8 nm

- More spectral overlap → more spectral bleedthrough.

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Spectral bleedthrough background signals

- Spectral bleedthrough - the more overlap, the more background.

Normalized Intensity vs Wavelength (nm)

--- Excitation
— Emission

D_{Ex} 436/20x
DM 455
FRET 535/30x

Donor Ex Channel FRET Em Channel

Acceptor crosstalk Donor bleedthrough

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Spectral bleedthrough background signals

- This is still a problem when using LSCM –

Normalized Intensity vs Wavelength (nm)

--- Excitation
— Emission

D_{Ex} 458
DM 505
FRET 535/30x

Donor Ex Channel FRET Em Channel

Acceptor crosstalk Donor bleedthrough

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Spectral bleedthrough background signals

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- This is still a problem when using LSCM – *even with diode lasers:*
- The accurate measurement of FRET by sensitized acceptor emission requires removal of SBT!

Normalized Intensity

Wavelength (nm)

--- Excitation
— Emission

D_{ex} 440
DM 505
FRET 535/30x

Donor Ex Channel
FRET Em Channel

Donor bleedthrough

Acceptor crosstalk

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Spectral bleedthrough background signals

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- This is still a problem when using LSCM – *even with diode lasers:*
- The accurate measurement of FRET by sensitized acceptor emission requires removal of SBT!
- Alternatively, methods that detect changes in donor fluorescence are typically not affected by SBT, and can be most accurate.

Normalized Intensity

Wavelength (nm)

--- Excitation
— Emission

D_{ex} 440
DM 460SP
FRET 480/30 EM

Donor Ex Channel
Donor Em Channel

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Overview: FRET methods

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- Methods for measuring FRET:
 - Sensitized acceptor emission:**
 - $E = \text{FRET} - [\text{Spectral cross-talk}]$
 - Cross-talk algorithms available on most systems;**
 - Relies on data from separate control cells - limits accuracy.
 - Acceptor photobleaching:**
 - $E = 1 - (I_{DA}/I_D)$
 - Simple approach – uses each cell as its own control;**
 - Requires selective acceptor bleaching – end point assay.
 - Donor lifetime measurements:**
 - $E = 1 - (\tau_{DA}/\tau_D)$
 - Detects shortening of donor lifetime – direct measurement.
 - Model independent measurements – most accurate.
 - Complex systems requiring long acquisition times.

Quenched emission
Sensitized emission

FRET

$< 80 \text{ \AA}$

Excited State (S₁)
Internal Conversion (10⁻¹¹ s)

Absorption (10⁻¹⁵ s)
Ground State (S₀)

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Fluorescence Lifetime

- Fluorescence lifetime (τ): the average time a population of fluorophores spend in the excited state before returning to the ground state.
- Every fluorophore has a characteristic lifetime, typically on the order of a few nanoseconds:

Probe	τ_m
Coumarin6 (EtOH)	2.5 ns
Cerulean FP (cells)	3.1
HPTS (Pyranine) (PB)	5.3
Fluorescein (PB)	4.1
mEGFP (cells)	2.9
Alexa 594 (PB)	3.9

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Fluorescence Lifetime Imaging Microscopy (FLIM)

- FRET is a quenching pathway that directly influences the excited state:
- FRET will cause the fluorescence lifetime to shorten - this can be accurately measured microscopically.
- Quantifying FRET efficiency (E_{FRET}) by FLIM requires two measurements:
 - donor lifetime in the absence of acceptor (τ_D).
 - donor lifetime in the presence of acceptor (τ_{DA}).

$$E_{FRET} = 1 - (\tau_{DA}/\tau_D)$$

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FLIM measurements: Frequency domain

- In frequency domain, a continuous light source is modulated at high frequency (1-200 MHz) to excite the fluorophores:
- The emission signal from the fluorophores will also be modulated:

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FLIM measurements: Frequency domain

- Because of the excited state lifetime, there is a delay in the emission relative to the excitation.
- This causes a phase delay (Φ) and a change in modulation (M) of the emission signal relative to the excitation:

Phase delay: Φ

Modulation: $M = \frac{AC}{DC}$

- The Φ and change in M are used to extract the fluorescence lifetime.

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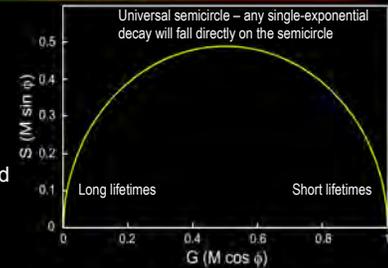
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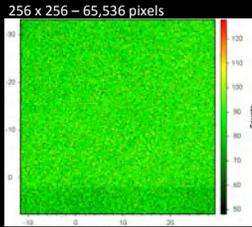
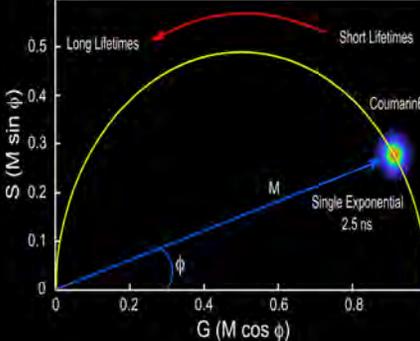
Frequency domain data analysis: the phasor (polar) plot 22

- The phasor plot was developed to analyze and display frequency characteristics.
 - Cole & Cole (1941) J Chem Phys 9:341
 - Jameson et al. (1984) App Spec Rev 20:55
- It is applicable to any system excited with repetitive perturbations.
 - Redford & Clegg (2005) J Fluoresc 15:805
- The phasor plot is a geometric representation of the phase delay (Φ) and relative modulation (M) of the emission signal.
- The frequency characteristics at every image pixel are represented by a vector with the polar coordinates:
 - $G = M \times \cos \Phi$
 - $S = M \times \sin \Phi$



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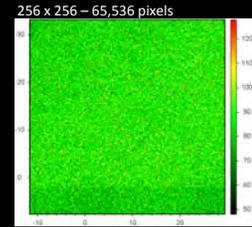
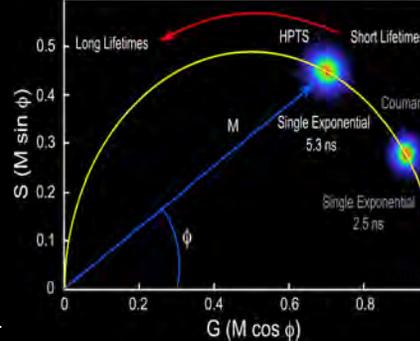
FLIM analysis by phasor plot 23

- Coumarin6 has spectral characteristics similar to the CFPs and a lifetime of 2.5 ns.
- ❖ The phasor plot is made directly from the frequency data at each pixel – there is *no fitting* to determine lifetimes.

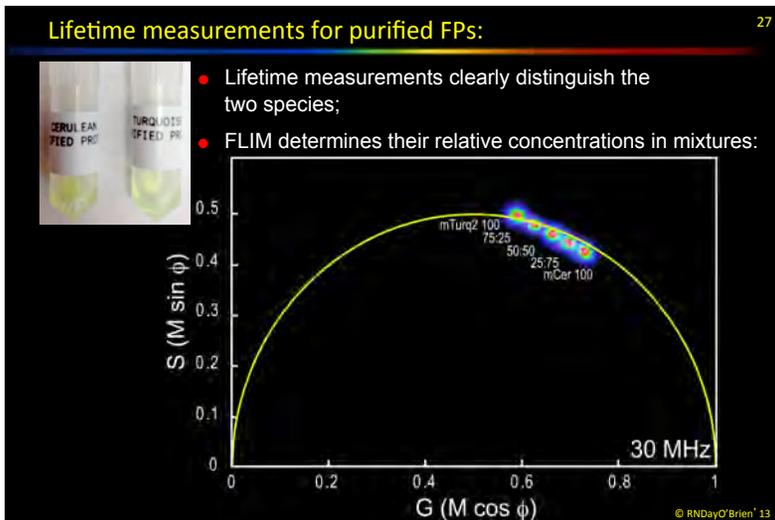
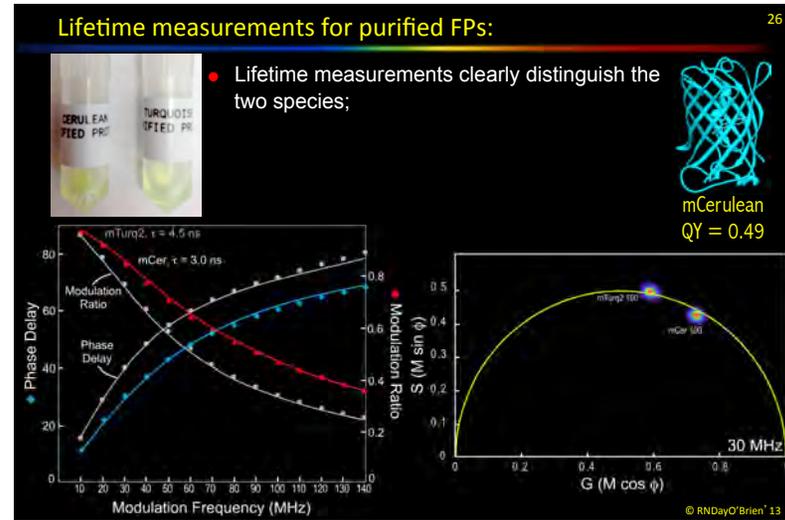
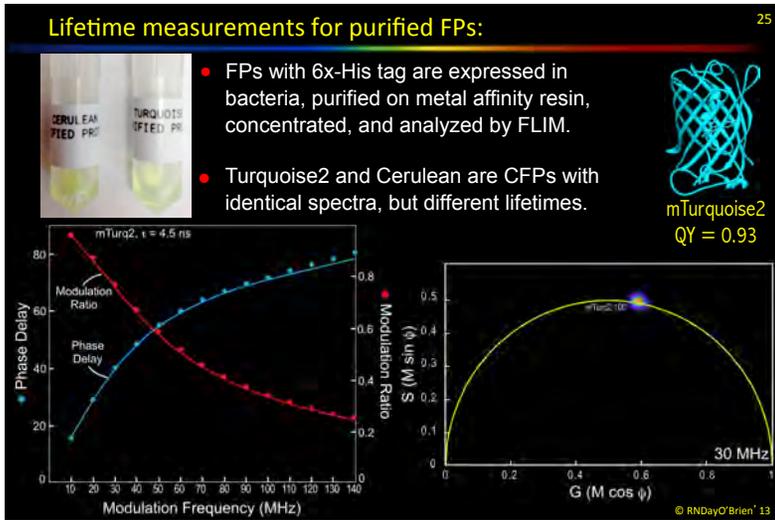
Sun et al. (2012) Meth Enzymol 503:372
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FLIM analysis by phasor plot 24

- HPTS also has spectral characteristics similar to the CFPs, and a lifetime of 5.3 ns.
- ❖ Both of these dyes have only one lifetime component, so the distribution of lifetimes for each population falls directly on the semicircle.

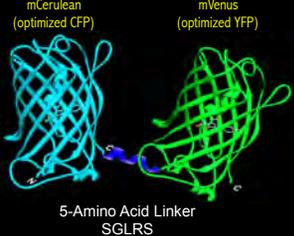
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- © RNDayO'Brien '13

Measurements in living cells: FRET standards

- How do you verify FRET measurements obtained by from living cells by different laboratories?
- A simple solution was to develop genetically encoded FRET reference proteins - "FRET standards".
- The FRET standards have been produced in a variety of cell systems, and measurements by several different methods confirmed their utility.



mCerulean (optimized CFP) mVenus (optimized YFP)

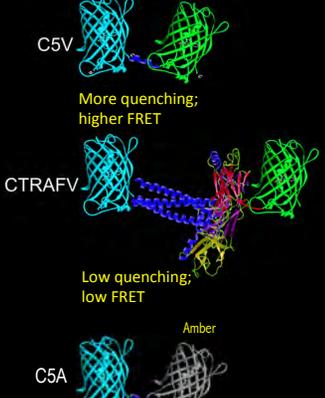
5-Amino Acid Linker SGLRS

Thaler et al. (2005) Biophys. J 89:2736

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Cerulean-Venus FRET standards developed by S. Vogel (NIH)

- The Vogel lab developed a series of fusion proteins based on the optimized Cerulean and Venus FPs.
- The fusions have progressively longer linkers between the Cerulean and Venus.
- Amber** - the Y66C mutant of Venus that folds correctly, but does not act as a FRET acceptor - an important control for donor environment in FLIM.



C5V: More quenching; higher FRET

CTRAFV: Low quenching; low FRET

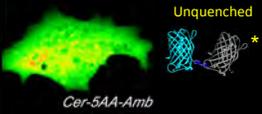
C5A: Unquenched donor; No FRET

Amber

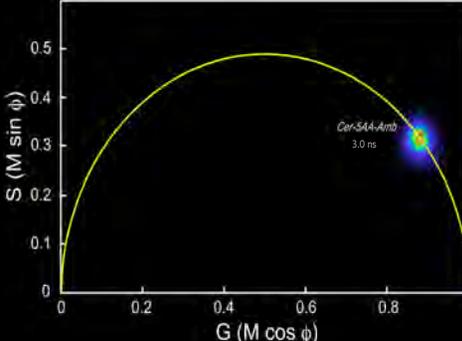
Thaler et al. (2005) Biophys. J 89:2736; Koushik et al. (2006) Biophys. J 91:L99

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FLIM analysis by phasor plot: FRET standards in living cells



Unquenched
Cer-5AA-Amb



$S (M \sin \phi)$

$G (M \cos \phi)$

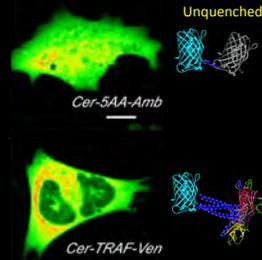
Cer-5AA-Amb 3.0 ns

- Cer-5AA-Amb has a lifetime of ~ 3 ns - unquenched donor.

* Amber (Y66C) folds, but doesn't absorb or emit - control for probe environment

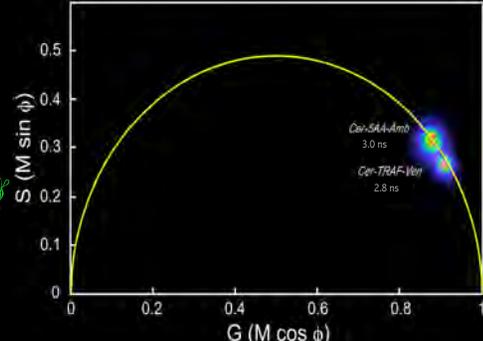
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FLIM analysis by phasor plot: FRET standards in living cells



Unquenched
Cer-5AA-Amb

Cer-TRAF-Ven



$S (M \sin \phi)$

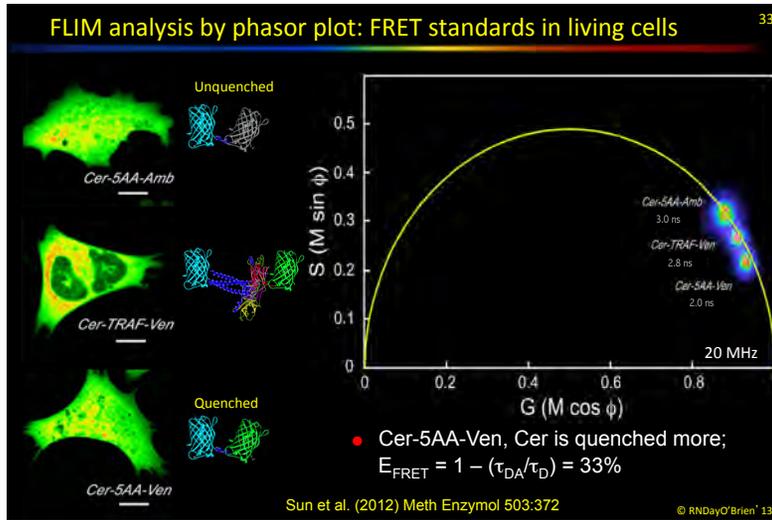
$G (M \cos \phi)$

Cer-5AA-Amb 3.0 ns

Cer-TRAF-Ven 2.8 ns

- For Cer-TRAF-Ven, Cer is quenched; $E_{FRET} = 1 - (\tau_{DA}/\tau_D) = 7\%$

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FRET-based biosensor probes

- The genetically encoded biosensor probes consist of donor and acceptor FPs connected by sensing unit:
 - The sensing unit includes an element that is modified by the biological event,
 - and a binding motif that recognizes the modification.
- The biological event causes the sensing unit to change conformation, altering the distance between the FRET pair.
- The changing intramolecular FRET signal reports the spatiotemporal dynamics of protein activity inside living cells.

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Detecting Src kinase activity

- The sensing unit of the Src biosensor consists of the c-Src substrate peptide from p130 cas, and the c-Src SH2 domain:
 - The probe is in a “closed conformation” before phosphorylation → high FRET.
 - Phosphorylation by c-Src induces a conformational change → low FRET.
 - Ratiometric imaging reports the changes in biosensor conformation on the time scale of seconds.

Wang et al. (2005) Nature 434:1041 © RNDayO'Brien '13

Lifetime imaging of biosensor probe activities

- Lifetime imaging maps the subcellular distribution of probe activities:

Julia Hum
Fred Pavalko

Hum et al. (2012) Int J Mol Sci 13:14385 © RNDayO'Brien '13

Measuring FRET using FLIM

- Strength -
 - Measurements are not influenced by intensity or probe concentration;
 - Quenched (bound) and unquenched donor populations can be quantified.
 - Independent method to verify intensity measurements.
- Weakness -
 - System and analysis are complex;
 - Photon-intensive - measurements can take many seconds to acquire.

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- Monitoring nuclear protein interactions with FLIM:

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Heterochromatin maintains genome integrity

- We're using live cell imaging approaches to determine how networks of protein interactions are coordinated inside the cell nucleus.
- Pericentric heterochromatin provides a structural scaffold that maintains genome integrity.
- The formation of heterochromatin requires heterochromatin protein 1 (HP1 α) through its direct interactions with histones and chromatin modifying proteins.
- There is increasing evidence that HP1 α plays roles in the regulation of gene transcription, DNA replication, and repair.

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HP1 α coordinates networks of protein interactions

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- Recent studies indicate that HP1 α interacts with sequence-specific transcription factors (TF).

Bulut-Karslioglu et al. (2012) Nat Struct Mol Biol 19:1023

- Our studies demonstrated that the transcription factor **CCAAT/enhancer binding protein alpha (C/EBP α)** interacts with HP1 α .
- C/EBP α directs programs of cell differentiation, regulates genes involved in energy metabolism, and localizes to methylated promoters in regions of heterochromatin.

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The intranuclear distribution of C/EBP α

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- C/EBP α localizes to regions of heterochromatin in 3T3-L1 adipocyte cells (ICC staining):

Induced 3T3-L1

- GFP-tagged C/EBP α localizes to regions of heterochromatin in mouse cells:

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C/EBP α localizes to heterochromatin

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Pituitary GHFT1 cell

Heterochromatin

- Does C/EBP α specifically interact with HP1 α in regions of heterochromatin?
- If so, what protein domains are involved, and what is the functional significance?

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Heterochromatin protein 1 (HP1 α)

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- HP1 α binds to methylated K9 of H3 in heterochromatin where it functions to assemble macromolecular complexes.

YFP-HP1 α CFP-C/EBP α Merge

C		5% INPUT		IP:α-HA	
HA-C/EBP α	-	+	-	-	+
YFP-HP1 α	+	+	+	+	+
WB:α-GFP					

- How dynamic is HP1 α ?

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PA-GFP: an optical marker 45

- Intense 405 nm illumination is thought to cause decarboxylation of the glutamic acid at position 222 near the chromophore;
- this converts the chromophore from a neutral to an anionic state:

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PA-GFP: an optical marker to measure protein mobility 46

- Photoactivate PA-GFP in a region of interest in the cell.
- Monitor the diffusion of the newly fluorescent protein over time.

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HP1 α is highly mobile within the cell nucleus 47

Normalized Intensity vs Time (s) for PA-GFP: $\tau_{1/2} = 4.5 \pm 0.1 \text{ s}$

Normalized Intensity vs Time (s) for CFP-HP1 α : $\tau_{1/2} = 4.2 \pm 0.4 \text{ s}$

❖ Do C/EBP α and HP1 α interact in living cells?
Demarco et al. (2006) Mol. Cell. Biol. 26:8087

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The intranuclear distribution of C/EBP α

- C/EBP α localizes to regions of heterochromatin in 3T3-L1 adipocyte cells (ICC staining):
- GFP-tagged C/EBP α localizes to regions of heterochromatin in mouse cells:

The C/EBP α BZip domain binds to DNA as an obligate dimer.

FRET-FLIM: measuring intermolecular protein interactions

- Because the Acceptor- and Donor-labeled proteins are encoded by different plasmids, every transfected cell will have a different A:D ratio.
 - The A:D ratio influences the FRET efficiency (E_{FRET}).
 - To detect FRET, FLIM measurements need only made in the donor channel:

- Changing the input ratio influences D:A levels.

BZip domain interactions analyzed in cell populations

- The lifetime map shows the probe lifetime in specific regions:
- The phasor plot represents the lifetime distribution in the entire image:

The lifetime information can be acquired from individual regions of interest (ROI).

BZip domain interactions analyzed in cell populations

- Because the D- and A-labeled proteins were expressed independently, each cell has a different A:D ratio, and this affects the FRET efficiency ($E\%$).
 - “Variation is your friend” - FS

$E_{FRET}^{max} = 19.2 \pm 1.5 \%$

- FLIM-FRET was used to measure the interactions of the Turquoise- and Venus-labeled BZip domains:
 - The $E\%$ and mean lifetime for 16 different cells (~10 ROI per cell) are plotted as a function of the A/D intensity ratio.

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Intermolecular FRET measurements in living cells

- FLIM was used to measure the interactions of Cer3-C/EBP α and Venus-HP1 α :

- The average E_{FRET} and the acceptor to donor intensity ratio (I_A/I_D) was determined in 5-10 different ROI for each cell (n=23).
- The results are plotted as a function of the I_A/I_D for each cell:

Siegel et al. (2013) J Biomed Optics 18:0250

The interactions between HP1 α and the BZip domain

- Does the BZip domain of C/EBP α interact with HP1 α ?

- The BZip domain is sufficient for the interaction in regions of heterochromatin.

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The interactions between HP1 α and the BZip domain

- Many proteins interacting with HP1 α have a common PxVxL motif – the HP1 α ^{W174A} disrupts these interactions:

- There are two PxVxL-like sequences in the BZip domain;
- they do not appear to mediate the interaction.

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