

## SIGNIFICANCE

RNA lies at the center of cellular function. Its most appreciated function is to carry protein blueprints to the ribosome for manufacture. Only recently have researchers begun to appreciate its myriad of other functions, many of which also lie at the center of important cellular processes.[1] Long, noncoding RNA (lncRNA) comprise one such important class of RNA that does not participate in the central dogma.[2] Alarming, the human genome encodes for as many lncRNA as proteins.[3] These biomolecules regulate localization of protein complexes within chromatin *X, Y, and Z (maybe the proposed test systems??)* have been recently found to have crucial RNA components. *Need more on these systems here. Talk about how localization is important.* This importance for cellular function necessitates a toolset of probes to study these RNAs as they traverse the cell.

## BACKGROUND

Protein studies benefit from a large imaging toolkit that has been developed over the last 25 years. Genetically encodable fluorescent proteins are now ubiquitous for the study of the localization of any translated target in the cell. While fluorescent proteins are a mature, well-understood technology, tools for imaging the localization of individual RNA transcripts in living cells remain limited. The most popular systems to date include dye-binding aptamers (Spinach[4], Broccoli[5], and Mango[6, 7]), and RNA-binding protein fusions (MS2-FPs).[8]

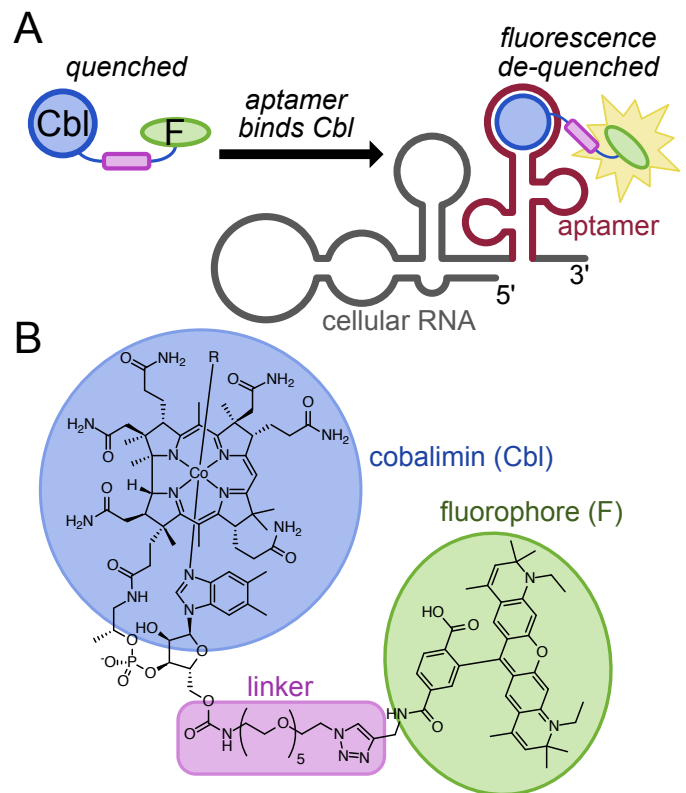
The most analogous to fluorescent proteins, dye-binding aptamers utilize exogenously administered dyes that give fluorescence induction upon binding their RNA partner.[4–7] This sequence is encoded downstream of an RNA of interest to track its location in the cell. Though excellent binders for their dyes, the aptamers utilized by this technology are unstable in mammalian cells due to their non-native structure.[9] Additionally, though fluorescence turn-on is excellent *in vitro*, often reaching 1,000 fold, signal induction in cells is typically two to four fold, most likely due to nonspecific binding of the dye.

RNA-binding protein fusions are a much more robust technique for imaging RNA transcripts.[8] This method often utilizes the MS2 bacteriophage coat protein that binds an encoded stem loop of RNA. When MS2 is fused to a fluorescent protein, transcripts can be visualized in the cell. In order to concentrate the fluorescence signal above background, multiple stem loops are placed in series (up to 24 in a row). Though this technique has enabled imaging of single transcripts in the cell,[8, 10] the resulting protein-RNA complex is prohibitively large for many studies.

Riboglow is a recently developed platform in the Palmer

lab that solves many of the drawbacks of current RNA imaging techniques (Fig. 1).[11] The two-component system utilizes a synthetic fluorophore-quencher pair, and a genetically-encoded riboswitch. A transcript of interest is first tagged within the cell, and the probe construct is administered via bead loading.[10, 12, 13] When the construct binds the transcribed riboswitch, the fluorophore is dequenched, giving fluorescent signal. Like the dye-binding aptamers, Riboglow utilizes a riboswitch receptor domain that natively binds vitamin B<sub>12</sub> (cobalamin, Cbl, Fig. 1B).[14] Conveniently, cobalamin is known to act as a fluorescence quencher for a variety of fluorophores.[15–17] The cobalamin center is conjugated to the fluorophore through a flexible linker that promotes quenching in the unbound state, but enables the fluorophore to reside at a distance in the bound state (Fig. 1B).

The Palmer lab found that this initial generation of Riboglow has the potential to outperform the existing tools in the field. Its use of a naturally occurring riboswitch imparts stability to the construct that is not present in aptamer-based techniques. Additionally, the use of a donor-quencher pair reduces nonspecific fluorescence in the unbound state. Such signal induction is low in the aptamer-binding dyes, and cannot be obtained at all with



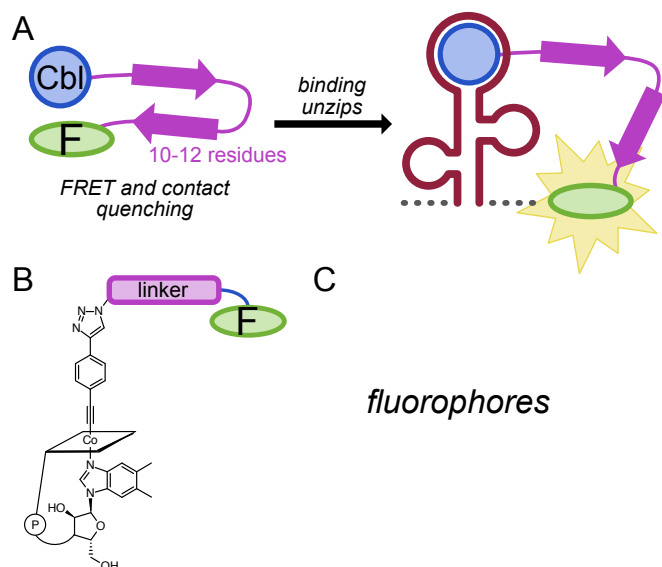
**Figure 1.** A) Cobalamin acts as a quenching and localization moiety to guide a fluorescent probe to an RNA transcript of interest. When unbound, fluorescence is quenched. In the presence of RNA tagged with the cobalamin riboswitch, fluorescence is restored. B) Structure of the generation 1 Riboglow probe. A polyethylene glycol linker of five units (5xPEG) connected to the 5' hydroxyl of the cobalamin ribose was used to tether an ATTO 590 fluorophore to the construct.

the MS2-fluorescent protein fusions. Due to these advantages, Riboglow outperformed Broccoli and the MS2 system in initial studies of stress granule (SG) detection in mammalian cells.

Though promising, the initial iteration of Riboglow has significant room for improvement. With initial constructs, signal induction upon riboswitch binding never exceeded seven fold *in vitro*, and the pendant dye was never fully quenched (with 10-20% residual fluorescence). Additionally, to effectively detect stress granules, four riboswitches had to be placed in series to concentrate fluorescence signal. This high background precluded single-molecule imaging. Finally, the strategy cannot currently be used to monitor the location of multiple transcripts in tandem. Herein, I will propose strategies to overcome these limitations through simultaneous modulation of the small molecule construct and riboswitch sequence. This is an undertaking for which I am uniquely suited, due to my experience of tandem modification of small molecule-protein interactions during my graduate studies. First, I will synthesize a variety of new Riboglow probes to optimize fluorescence quenching (Aim 1). Next, I will turn to the sequence of the riboswitch itself. I'll design a screen for brightness that will select the best riboswitch sequence to match the optimized probe structure (Aim 2). This new, brighter pair will be tested for single-molecule detection. Finally, I will use SELEX to identify mutually orthogonal probe-riboswitch pairs for multicomponent RNA imaging (Aim 3).

### **APPROACH Aim 1. Synthesize improved Riboglow probes.**

The main drawback of Riboglow is the poor turn-on that is observed upon probe binding. In this aim, I intend to leverage my background in synthetic chemistry to produce a panel of diverse probe structures that improve fluorescence quenching (and thus signal induction). In previous studies in collaboration with Professor Dorota Gryko (see Gryko letter of support) a small number of linkers and fluorophores were evaluated for quenching and fluorescence turn-on. Linker length and fluorophore wavelength were varied to gauge the quenching ability of cobalamin. Remarkably, some degree of quenching occurred in all of the constructs synthesized, regardless of the spectral overlap of the fluorophore and the cobalamin. However, most retained 10-20% residual fluorescence, which increased background signal significantly. *To optimize probe function, I will vary linker composition, attachment point, and pendant fluorophore.*



**Figure 2:** A) Linkers. B) Conjugation sites. C) Fluorophores.

solid phase peptide synthesis.[20–22] Cobalamin and a fluorophore will then be coupled to each terminus of the linker via additional amide couplings.[23] If the fold proves to be too stable (dequenching is not observed), the amino acids of the peptide linker will be varied to tune the melting temperature. Or, if adequate quenching is not observed, the relative positions of the N and C termini will be adjusted based upon structural data available on these beta turns, available in the Protein Data Bank (PDB). Each new construct will be tested for their ability to quench fluorescence *in vitro* by comparing the fluorescence of the construct with that of the free fluorophore in solution. Fluorescence signal in the presence of the Riboglow riboswitch will also be measured to calculate fluorescence turn-on.

Another underexplored variable of the original Riboglow probes is the linker attachment point. Though the 5' hydroxyl of the cobalamin ribose is the most accessible nucleophile on the structure, there exist several other

Ideally, in the unbound state, the cobalamin and fluorophore would be closely associated to maximize FRET and contact quenching.[15, 18, 19] In the RNA-bound state, the molecules would reside at their maximal distance to promote fluorescence.[16] To strike this balance, I will use a synthetic beta turn as the linker between cobalamin and the fluorophore (Fig. 2A). Such a linker would hold the molecules close in solution, but would be linearized upon binding to the riboswitch. A number of such beta turns have been developed, and are referred to as tryptophan zippers (trpzip).[20] These motifs are as small as twelve amino acids and many are stable to denaturation up to 85 °C. In the unbound state, such a linker would hold the quencher and fluorophore in close proximity (due to the short distance between the N and C termini of the peptide, Fig. 2A). When the cobalamin is bound by the riboswitch, steric occlusion would force the beta turn to unfold to place the fluorophore-quencher pair at a larger distance. A wide range of tryptophan zippers have been developed with a variety of structures and stabilities, enabling easy synthesis of a range of different linkers via

possible sites of conjugation. Perhaps the second most common site is the axial ligand of the cobalt metal itself. Though many studies have taken advantage of the labile nature of certain alkyl modifications at this position,[18] others have found alkynyl modifications to be stable to air and light.[24, 25] Following this precedent, I will synthesize a cobalamin with an alkyne handle attached to the cobalt metal center (Fig. 2B). Such a molecule has already been synthesized in the lab of Dorota Gryko (see Gryko letter of support), and shown to be amenable to functionalization via dipolar azide-alkyne cycloaddition (AAC).[26] The alkyne handle will be readily conjugated to a variety of linkers with terminal azides.[27, 28] These constructs will also be evaluated for degree of fluorescence quenching, and brightness in the presence and absence of the cobalamin riboswitch. It is possible that incorporation of a ligand at this site on the metal center will abolish binding to the native riboswitch due to its positioning in the binding pocket.[14] If this is the case, these probes could serve as excellent starting points for directed evolution of orthogonal aptamer-probe pairs (see Aim 3). Additionally, perturbations to the native binding mode of cobalamin could reduce off-target association with native B<sub>12</sub> machinery,[29] further reducing fluorescence background.

The final variable in the molecular structure of the Riboglow probe is the fluorophore itself. The ideal probe would minimize cellular autofluorescence through the use of a red fluorophore with a high extinction coefficient. I believe that the Janelia Fluor series of dyes is well suited for our application (see Lavis support letter).[30] Through minor modifications to the rhodamine scaffold, the Lavis lab has developed a range of fluorophores with varying excitation and emission spectra, and excellent photophysical properties. Table XXX includes a subset of the probes that will be explored. Emphasis will be placed on fluorophores with high extinction coefficients and quantum yields, with the intent for these probes to be used in single-molecule imaging (Aim 2). *Highlight JF585 and 635, as it might give a greater increase in fluorescence with binding.*[31]

Summary and alternate approaches:

Aim 2. Adapt Riboglow for single-molecule imaging.

Visualization of the lifecycle of single RNA transcripts as they move throughout the cell remains a holy grail of RNA imaging.[Cite] Such a goal is possible via single-molecule imaging and a probe with adequate photostability, and should be achievable with the Riboglow platform. With the wide variety of new probe constructs developed in Aim 1, changes will be made to the sequence of the cobalamin riboswitch to increase fluorescence turn-on. *A directed evolution screen for fluorescence brightness will identify optimal riboswitch sequences that promote fluorescence signal induction.*

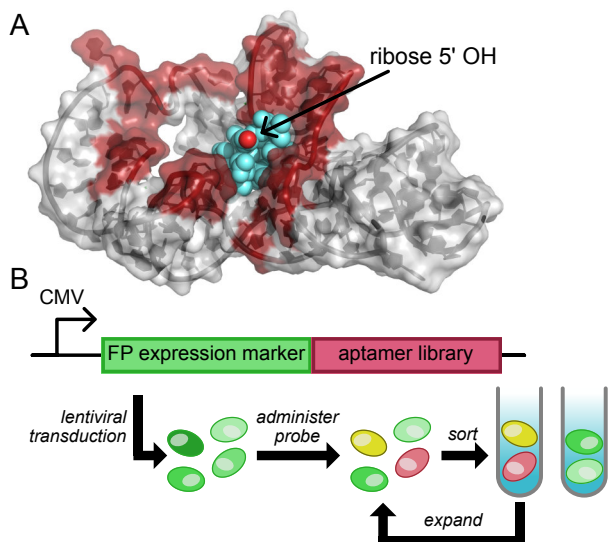
First, a library will be designed that varies the environment surrounding the binding pocket of the cobalamin riboswitch (Fig. 3A). Though the guidance of Robert Batey (see Batey support letter), sites will be chosen to retain binding of the cobalamin, yet maximize the distance between the quencher and the fluorophore upon binding.[14] The Palmer lab is a leader in technologies for tool development in mammalian cells.[32, 33] This expertise will be leveraged for screening libraries of cobalamin riboswitches (Fig. 3B). Libraries of transcripts will be transduced into mammalian cells, the probe of interest will be administered, and cells will be sorted via flow cytometry. Cells that show elevated brightness relative to a fluorescent protein expression control will be sorted. In this way, libraries of up to one million members will be screened. Bright variants will be collected, cultured, and resubjected to sorting until only bright variants remain. Sequences will be evaluated through deep sequencing.

Candidate probes found through cell sorting will be verified in single molecule imaging experiments under the guidance of Professor John Rinn... *Not sure what I should propose to image here, especially with respect to proving that single molecules can be visualized.*

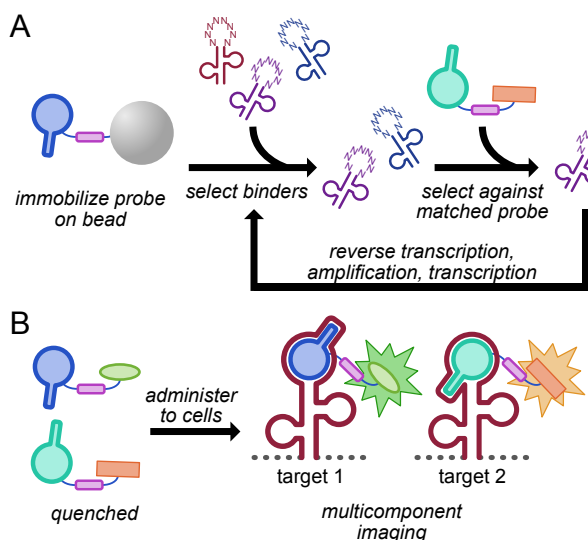
Summary and alternate approaches:

Dye	$\lambda_{\text{ex}}$ (nm)	$\lambda_{\text{em}}$ (nm)	$\epsilon$ (M <sup>-1</sup> cm <sup>-1</sup> )	$\phi$
Cy5	646	662	271,000	0.2
ATTO 488	501	523	90,000	0.8
ATTO 590	594	624	120,000	0.8
ATTO 633	629	657	130,000	0.6
JF <sub>549</sub>	549	571	101,000	0.88
JF <sub>585</sub>	585	609	156,000	0.78
JF <sub>635</sub>	635	652	167,000	0.56
x	x	x	x	x

Table 1: A wrapped table going nicely inside the text.



**Figure 3.** A) Riboswitch sites for mutation will be targeted based on potential contact with the linker and fluorophore. PDB: 4FRN[14] B) RNA sequences will be screened for brightness relative to a fluorescent protein control.



**Figure 4.** A) SELEX will be used to screen for riboswitches that bind each cobalamin in a mutually-exclusive manner. B) Mutually orthogonal cobalamin analogs will enable multicomponent RNA imaging. Signal turn-on will only be observed in the presence of the matched pair.

### Aim 3. Develop mutually orthogonal Riboglow probes for multicomponent imaging.

The ability to track multiple RNA transcripts simultaneously would enable study of the interactions of RNA as they move through the cell. *Independent RNA transcripts are implicated to interact in X and Y ways.* The modularity of the Riboglow platform is well suited to enable such an experiment. Probes will be distinguished through the use of different fluorophores, and different riboswitch sequences will be used to bind each structurally different probe in a mutually exclusive manner (Fig. 4B).

Fortunately, screening for substrate selectivity is well-precedented in RNA engineering through systematic evolution of ligands by exponential enrichment (SELEX).[34, 35] In fact, *de novo* riboswitches have already been developed for cobalamin and a few of its analogs via SELEX.[36] This important precedent shows that even small changes to the structure of the cobalamin can be distinguished by engineered RNA, and implies that no additional changes will need to be made to the cobalamin structure apart from those constructs already proposed above.

Importantly, for our selection experiments, we will not be starting from a completely randomized sequence of nucleic acids. It will be crucial to retain the original fold (and thus *in cellulo* stability)

of the native riboswitch. The design of the starting RNA libraries, and subsequent selection experiments will be carried out under the supervision of Professor Robert Batey (see Batey letter of support), an expert in SELEX and RNA engineering.[37] The selection will be carried out as shown in Figure 4A. Briefly, cobalamin probe of interest will be immobilized on a bead via the same linker that will be used in the final construct. The synthetic library of riboswitches will be incubated with the beads, and unbound sequences will be rinsed away. In a second rinsing step, the probe (or probes) intended to be orthogonal to the construct under selection will be incubated with the beads to wash away any riboswitches that do not bind selectively. *Is this kind of negative screen known?* Riboswitches that bind selectively will be collected off the beads and amplified (via reverse transcription, PCR amplification, and transcription) to undergo another round of selection. Riboswitches will be deep sequenced to identify library convergence and optimal clones. This process will be repeated for each probe of interest, with negative screens against each other probe that is intended for multiplexed use.

Once mutually-selective Riboglow probes are identified, they will be tested in mammalian cells... *Maybe look at two differently localized RNAs that both migrate to SGs upon arsenite addition?*

**Summary and alternate approaches:**



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