Resource

Cell Chemical Biology

Rational Design of a GFP-Based Fluorogenic Caspase Reporter for Imaging Apoptosis In Vivo

Highlights

- Split GFP is "zipped" or redesigned to sense protease activity
- ZipGFP-based caspase reporter detects apoptosis in human cells
- ZipGFP caspase reporter enables imaging physiological apoptosis in zebrafish

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In Brief

Shu et al. develop a fluorogenic protease reporter by "zipping up" each fragment of split GFP in a manner that prevents their associate and fluorophore formation until release by specific proteolytic cleavage. The large signal enables imaging of protease activity in vivo.

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Rational Design of a GFP-Based Fluorogenic Caspase Reporter for Imaging Apoptosis In Vivo

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SUMMARY

Fluorescence resonance energy transfer-based executioner caspase reporters using GFP are important tools for imaging apoptosis. While these reporters are useful for imaging apoptosis in cultured cells, their in vivo application has been handicapped by poor signal to noise. Here, we report the design and characterization of a GFP-based fluorogenic protease reporter, dubbed ZipGFP. ZipGFP-based TEV protease reporter increased fluorescence 10-fold after activation by protease. A ZipGFP-based executioner caspase reporter visualized apoptosis in live zebrafish embryos with spatiotemporal resolution. Thus, the ZipGFP-based caspase reporter may be useful for monitoring apoptosis during animal development and for designing reporters of proteases beyond the executioner caspases.

INTRODUCTION

Förster resonance energy transfer (FRET)-based reporters using GFP are valuable tools in dissecting signaling pathways in living cells. Further understanding of molecular and cell biology requires investigation of cell signaling in living animals. However, in vivo use of FRET reporters is difficult for two main reasons (Kardash et al., 2011). First, the signal of FRET reporters is weak due to small fluorescence change in the donor and acceptor fluorophores. Second, fluorescence imaging of living animals is challenging because of tissue autofluorescence, cell heterogeneity, and rapid shape and position changes. It is thus not surprising that use of FRET-based executioner caspase reporters in animals is limited (Campbell and Okamoto, 2013; Takemoto, 2003; Takemoto et al., 2007; Yamaguchi et al., 2011).

To overcome the limitations of FRET-based executioner caspase reporters, we sought to design a GFP-based fluorogenic protease reporter that achieves several-fold fluorescence increase upon caspase activation. Very recently, an infrared fluorogenic caspase reporter (iCasper) based on an infrared fluorescent protein (mIFP) was reported for imaging apoptosis in *Drosophila* (To et al., 2015). However, the bacterial phytochrome-based iCasper requires the cofactor biliverdin, which seems to be limiting in *Drosophila* and zebrafish (Yu et al., 2015). Although expression of heme oxygenase, which converts heme into biliverdin, overcomes this problem, a GFP-based fluorogenic reporter would be preferred since its fluorescence requires no cofactor in animals. Two GFP-based fluorogenic reporters, CA-GFP (Nicholls et al., 2011) and VC3AI (Zhang et al., 2013), have been used to image apoptosis in cultured cells. However, neither has been shown to detect apoptosis in animals such as zebrafish. Here we report the rational design of a GFP-based fluorogenic caspase reporter and its application to imaging apoptosis in the zebrafish embryo with spatiotemporal resolution.

RESULTS AND DISCUSSION

Design of a Protease Reporter by Caging GFP with mIFP

To design a GFP-based fluorogenic protease reporter, we modified self-assembling split GFP so that its self-assembly is regulated by protease activity. GFP contains 11 β strands (Movie S1) (Ormö et al., 1996; Yang et al., 1996). One part of split GFP contains ten β strands (β1–10); the other part contains the 11th β strand (β11) (Cabantous et al., 2005). β1–10 contain three amino acids that form the chromophore (Tsien, 1998, 2009), whereas β11 contains the highly conserved Glu222 that catalyzes chromophore maturation (Sniegowski, 2005). It has been shown that β11 rapidly binds to β1–10 and green fluorescence develops within several tens of minutes (Cabantous et al., 2005). The crystal structure of GFP suggests a compact fit of β1–10 and β11, which presumably provides the structural basis of the high binding affinity between the two parts (Movie S2). Based on this, we sought to prevent β11 binding to β1–10 by inserting β11, a short peptide (16 residues), into another protein in a manner such that β11 could be hidden until made available by proteolysis.

To achieve this, we first used iProtease (the protein scaffold of iCasper) as a vehicle to cage β11 rather than as a fluorogenic reporter (Figure S1A). We inserted β11 between the PAS and GAF domains of iProtease together with a TEV protease cleavage sequence (TevS) at a location previously suggested to be constrained until released by protease (Figure S1A) (To et al., 2015). The length of the insert plus TevS was 23 amino acids.

Because insertions of >11 residues at this site led to potentially decreased constraint based on the appearance of weak infrared fluorescence of the iProtease reporter in the absence of the protease activity, we truncated the PAS domain so that β11 would likely be tightened or distorted. We made four constructs with various truncations of the PAS domain (Figure S1A). In addition, we used heterodimerizing coiled coils (E5 and K5) (De Crescenzo et al., 2003) to lock the PAS and GAF domains together. In the original iProtease design, the self-assembling split GFP was used to lock the PAS and GAF domains together. We next co-expressed the β11-mIFP and β1–10 in HEK293 cells (and mCherry as a reference), with or without the TEV protease (Figures S1B and S1C). However, we observed constitutive fluorescence without TEV dependence. We hypothesized that this might be due to β1–10 binding to β11 before the translation or folding of the PAS domain and/or that β11 was not sufficiently constrained in the fully folded β11-mIFP.

To solve this problem, we decided to occlude the binding cavity of β1–10 so that it would not accommodate β11, with the occlusion being released by protease activity. We flanked the N and C termini of β1–10 with the heterodimerizing E5 and K5 coiled coils (Figure S1B), such that the leucine zipper-like E5/K5 coiled coils might block or "zip" the binding cavity and prevent β11 binding. Indeed, the new design obtained ~5-fold fluorescence increase upon TEV protease cleavage (Figure S1D). However, we noticed punctate structures of green fluorescence when employing β11-mIFP with truncations to Cys18 and Ile23, both in the absence and presence of TEV protease. The number of punctate structures was significantly reduced for β11-mIFP with truncations to Gly27 and Ile29. We considered further truncating the PAS domain to possibly reduce this potential aggregation problem and increase the signal gain to >5-fold. However, Ile29 is already at the knot region of mIFP (Figure S1A and Movie S3) and further truncations would be expected to either prevent protease cleaving or block β11 from binding to β1–10 after protease cleavage by pulling β11 into the knot region. Therefore, the mIFP caging approach was abandoned, but the principle of caging both β11 and β1–10 was applied and turned out to be important (see below).

Design of a Protease Reporter by Zipping GFP with Coiled Coils

In order to solve the aggregation problem and to further increase the signal, we decided to simply flank β11 with E5 and K5 since the coiled coils appear to successfully block β1–10. Based on this new design, the E5/K5 heterodimer (with protease cleavage sequence) zips both β11 and β1–10 in order to prevent self-assembly of the split GFP (Figure 1A). Upon protease cleavage, both β11 and β1–10 are unzipped, which enables self-assembly and leads to an increase in fluorescence. We named this reporter ZipGFP. As a proof of concept, we designed a TEV protease reporter by inserting a TEV cleavage sequence into ZipGFP (both the zipped β11 and β1–10). This ZipGFP-based TEV reporter achieved 10-fold fluorescence increase upon TEV cleavage in HEK293 cells with no punctate structures of green fluorescence (Figures 1B and 1C). The fluorescence quantum yield of the reassembled ZipGFP was determined to be 0.25. Zipping either β11 or β1–10 alone led to bright fluorescence even in the absence of TEV protease, and the fluorescence did not increase upon protease cleavage (Figure 1B). Thus, zipping of both β11 and β1–10 was required to adequately prevent reconstitution of split GFP in this system.

We next measured the kinetics of the ZipGFP-based protease reporter to determine its temporal resolution. First, we separately purified two parts of ZipGFP in the presence of TEV protease. Then we mixed the cleaved ZipGFP and monitored green fluorescence over time. The green fluorescence increased over time with time to half-maximal fluorescence ($T_{1/2}$) of ~40 min (Figures 1D and 1E), which is similar to the previously reported kinetics for split GFP self-assembly (Cabantous et al., 2005). We also measured the kinetics of ZipGFP in cells with a rapamycin-activatable TEV system, in which the two parts of split TEV were fused to FKBP and Frb (Gray et al., 2010; Wehr et al., 2006). The addition of rapamycin induces a strong interaction between FKBP and Frb, which leads to reconstitution of split TEV. We co-expressed ZipGFP, mCherry, and the rapamycin-activatable TEV system in HEK293 cells and monitored green and red fluorescence over time upon addition of rapamycin, which revealed $T_{1/2}$ of ~100 min (Figure S2 and Movie S4).

ZipGFP Caspase Reporter Detects Apoptosis in Mammalian Cells

To design a ZipGFP-based caspase reporter for imaging apoptosis, we inserted the consensus cleavage sequence (DEVD) of caspase-3 into both parts of ZipGFP. The well-characterized signaling pathways of apoptosis are composed of extrinsic and intrinsic pathways, both of which lead to activation of the executioner caspases that include caspase-3 (Crawford and Wells, 2011). Detection of activated caspase-3 using antibody has been proved to be useful in identifying apoptotic cells in animals including zebrafish (Sorrells et al., 2013). And the conserved cleavage sequence (DEVD) of caspase-3 has been used previously in caspase reporters (Ding et al., 2015; Nicholls et al., 2011; Takemoto, 2003; To et al., 2015; Zhang et al., 2013).

We expressed ZipGFP in human glioblastoma LN229 cells. Upon addition of staurosporine, which induces apoptosis by activating caspase-3 (Tee and Proud, 2001), ZipGFP's green fluorescence increased significantly in cells treated with staurosporine (Figure 2A and Movie S5), whereas the fluorescence signal of ZipGFP showed no or little change in cells not treated with staurosporine (Movie S6). To account for a potential increase in the concentration of reporter with time after transient transfection, we co-expressed mCherry. The ratio of green fluorescence to mCherry's red fluorescence revealed a 5- to 10-fold increase in ZipGFP's fluorescence upon apoptosis. Activation of caspase-3 in ZipGFP fluorescing cells was confirmed using a commercially available small-molecule active-site modifier for far-red fluorescent imaging of caspase-3 activity (Figure 2B). And the onset of apoptosis in single cells as detected by ZipGFP varied between 2 and 5 hr after addition of staurosporine (Figure 2C), consistent with previous results (Albeck et al., 2008). In addition, replacing the caspase cleavage site in ZipGFP β11 with TevS abolished the increase in fluorescence upon apoptosis (Figure S3), suggesting that the increased fluorescence requires caspase cleavage.

We next compared ZipGFP with a previous GFP-based fluorogenic caspase reporter CA-GFP. CA-GFP was reported to show

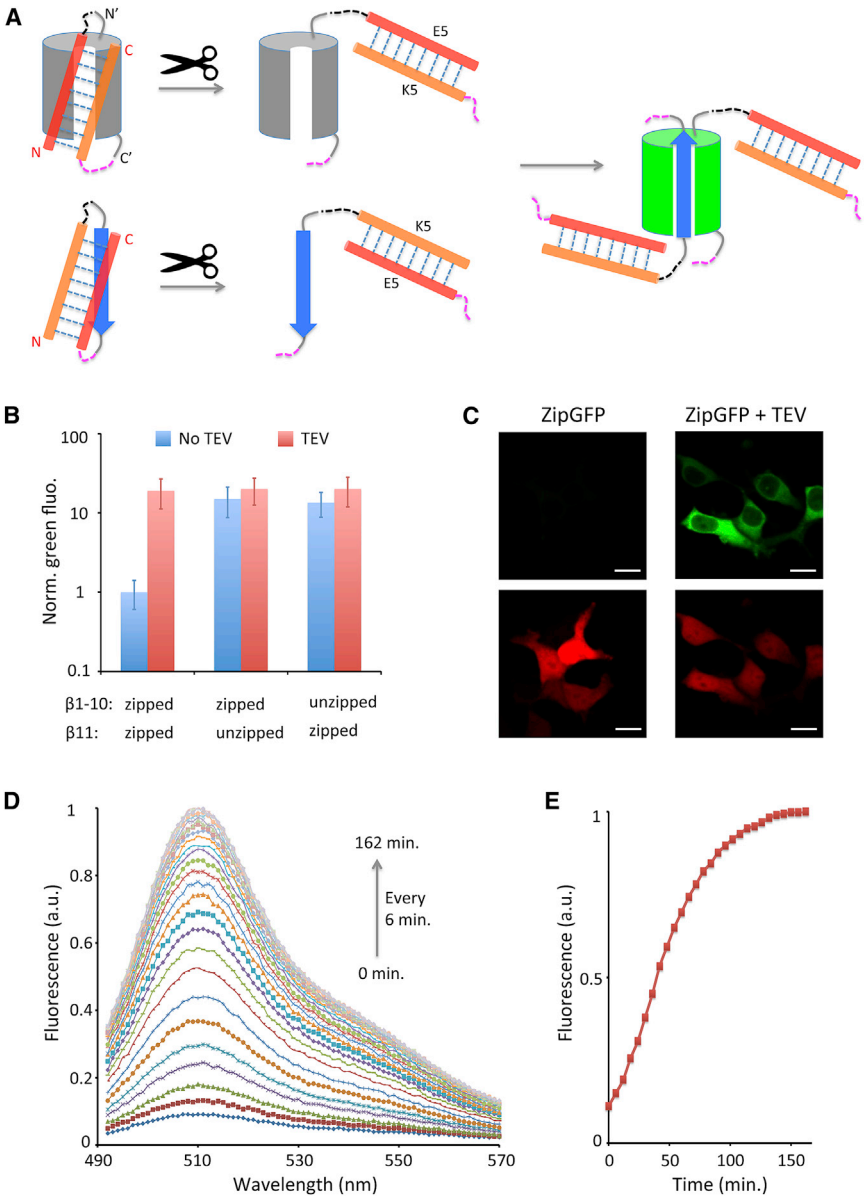

Figure 1. Rational Design and Characterization of a ZipGFP Protease Reporter

(A) Schematic diagram of ZipGFP (see Movies S1 and S2). β1–10 (in gray) is flanked with E5 and K5 (in red and orange, respectively) at the N terminus and C terminus, respectively. β11 (in blue) is flanked with K5 and E5 (in orange and red, respectively) at the N terminus and C terminus, respectively. The protease cleavage sequence is shown in pink. The black dashed line represents an amino acid linker. The green color indicates restored green fluorescence.

(B) The green fluorescence normalized by co-expressed mCherry for unmodified (i.e., unzipped) or modified (i.e., zipped) β1–10 and β11 as in (A). The error bars are standard deviations based on analysis of ~50 cells.

(C) Fluorescence images of ZipGFP with the TEV cleavage sequence expressed in HEK293 cells. Scale bar, 10 μm.

(D) Emission spectra of ZipGFP over time. The two parts of cleaved ZipGFP were purified and mixed (β1–10, 2.7 μM; β11, 6.3 μM). The fluorescence spectra were then taken every 6 min.

(E) The green fluorescence intensity over time after mixing the two cleaved parts of ZipGFP as in (D). The fluorescence intensity was calculated based on the emission spectra by integrating emission from 490 to 550 nm.

a 45-fold fluorescence increase after caspase activation in bacteria and a 3-fold increase in mammalian cells upon staurosporine-induced apoptosis (Nicholls et al., 2011). However, we observed less than 1-fold fluorescence increase after normalization by a co-expressed red fluorescent protein in LN229 cells upon addition of staurosporine (Figure 2D). We also compared ZipGFP with VC3AI, another previous GFP-based caspase reporter. Green fluorescence of VC3AI normalized to co-expressed mCherry in LN229 cells showed 2- to 6-fold fluorescence increase upon addition of staurosporine (Figure 2E), which is slightly smaller than ZipGFP. Together, these data suggest that the newly designed ZipGFP is one of the best choices for genetically encoded caspase detection in mammalian cells.

It should be pointed out that compared with iCasper, the fluorescence increase of ZipGFP is slower after triggering apoptosis. This is consistent with the fact that the in vitro $T_{1/2}$ of ZipGFP (~40 min) is significantly slower than that of iCasper (<10 s). The different kinetics is likely due to different mechanisms of fluorescence development: for iCasper; the chromophore is an endogenous molecule and rapidly binds to the activated reporter, and thus quickly becomes fluorescent (To et al., 2015). On the other hand, the chromophore of GFP is formed from three amino acids in a reaction that requires tens of minutes (Tsien, 1998). Nevertheless, our results demonstrated that ZipGFP develops fluorescence sufficiently fast to visualize caspase-3 activity and apoptosis in cultured mammalian cells.

ZipGFP Visualizes Caspase Activity and Apoptosis in Live Zebrafish

To determine whether the fluorescence signal and the temporal resolution of ZipGFP are sufficient for imaging apoptosis in animals, we expressed the ZipGFP-based caspase reporter in zebrafish. Zebrafish was chosen based on optical transparency and its importance as a model organism among vertebrate animals (Grunwald and Eisen, 2002). We injected mRNA encoding ZipGFP caspase reporter and mCherry linked via a T2A site into the embryo at the one-cell stage. T2A is a self-cleaving peptide used in co-expression of multiple genes (Szymczak et al., 2004).

We exposed the zebrafish embryo at the 50% epiboly stage (i.e., the blastoderm covers 50% of the entire distance between

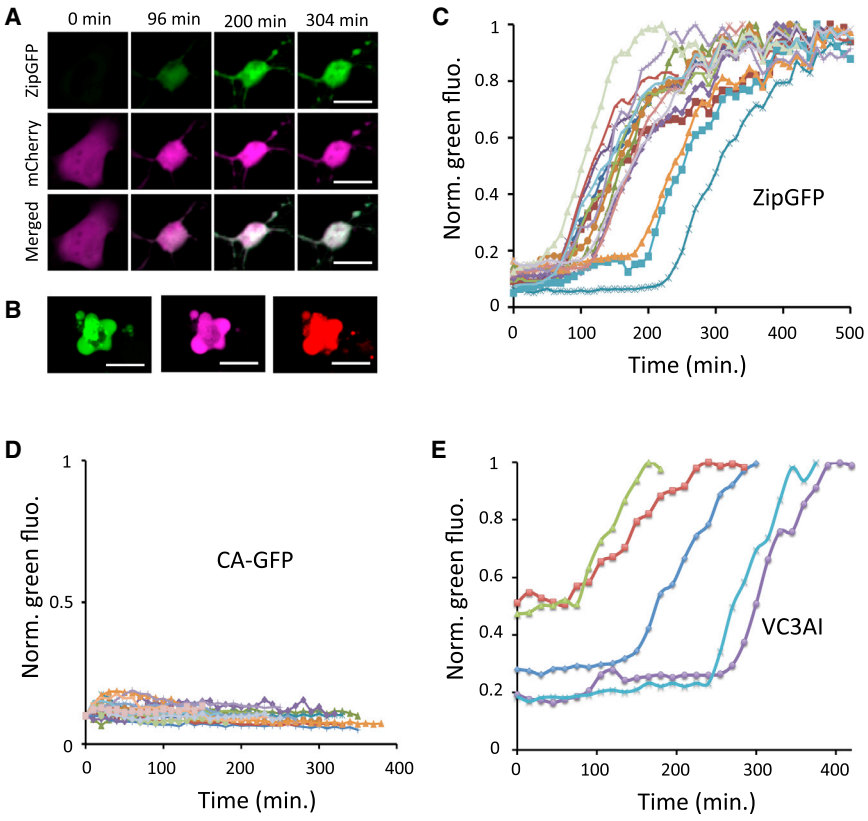

Figure 2. Characterization and Comparison of ZipGFP Caspase Reporter in Mammalian Cells

(A) Time-lapse confocal images of human glioblastoma cells LN229 expressing ZipGFP caspase reporter upon treatment with 1 μM staurosporine (see Movie S5). mCherry was co-expressed.

(B) Confocal image of the LN229 cell expressing ZipGFP caspase reporter and stained with caspase imaging agent FLICA after addition of staurosporine. Left, green fluorescence from GFP; middle, red fluorescence from co-expressed mCherry; right, far-red fluorescence from FLICA 660 caspase-3/-7 reagent.

(C) Normalized green fluorescence of LN229 cells expressing ZipGFP caspase reporter reveals 5- to 10-fold fluorescence increase and cell-to-cell heterogeneity of caspase activation upon addition of staurosporine. The green fluorescence was normalized by co-expressed mCherry red fluorescence based on confocal images of live cells, which were collected every 10 min, after treatment with 1 μM staurosporine.

(D) Normalized green fluorescence of LN229 cells expressing CA-GFP caspase reporter reveals <1-fold fluorescence increase upon addition of staurosporine. mLumin, a red fluorescent protein, was co-expressed and used to normalize the CA-GFP fluorescence.

(E) Normalized green fluorescence of LN229 cells expressing VC3AI caspase reporter reveals 2- to 6-fold fluorescence increase upon addition of staurosporine. The red fluorescent protein mCherry was co-expressed and used to normalize the VC3AI fluorescence.

Scale bars, 20 μm (A); 15 μm (B).

the animal and vegetal poles) to 100 μg/ml cycloheximide (Figure 3A), which was previously shown to induce apoptosis in the early zebrafish embryo (Negron and Lockshin, 2004). The embryo continued to develop with epiboly continuing for 2 hr after exposure to cycloheximide (Figure 3B and Movie S7), but cell movement became arrested at 2 hr and cells started to retract at 3 hr. During this time, the embryo showed bright mCherry fluorescence, indicating that the reporter was well expressed, but green fluorescence was absent or dim, suggesting that the caspase was inactive in the embryo. However, by 4 hr, green fluorescence became obvious in a few cells, and after 5–6 hr of treatment, many cells showed strong green fluorescence, suggesting caspase activation and apoptosis. Indeed, many of these cells were also fragmented or were round in shape, consistent with cellular morphological change during apoptosis. In the absence of cycloheximide treatment, embryonic development continued normally with evident somite formation as expected; red fluorescence was easily detected but green fluorescence was negligible, consistent with little apoptosis occurring during this early stage of development (Figure 3C). Caspase activation using antibody staining against the cleaved caspase-3 was confirmed in the zebrafish embryo treated with cycloheximide (Figure S4), and the observed effects of cycloheximide treatment on the zebrafish embryo are consistent with a previous demonstration of cycloheximide-induced apoptosis in this setting (Negron and Lockshin, 2004).

After demonstrating that the ZipGFP caspase reporter could be used to image cycloheximide-induced apoptosis in early zebrafish embryo during the gastrulation stage, we next demonstrated that this system could be used to visualize the spatiotemporal dynamics of apoptosis during normal embryo development after the gastrulation stage. We again expressed the ZipGFP caspase reporter (and mCherry) in zebrafish embryos by injection of mRNA at the one-cell stage. Time-lapse imaging of the head was started at 24 hr postfertilization (hpf) (Figure 3D). At this time, little green fluorescence was observed (Figure 3D and Movie S8). Ten hours later, green fluorescence was detected in a couple of cells. After 15–20 hr, more cells showed strong green fluorescence. By contrast, mCherry fluorescence was weak and decreased over time (Movie S8), presumably because its mRNA injected at the one-cell stage was degraded over time and/or diluted as development progressed. Green, presumed apoptotic cells were distributed around the developing retina and the forebrain. In particular, time-lapse imaging first detected green fluorescence on the rostral aspect of the forebrain. The number of green cells increased over time, and they appeared to form clusters. These cells appeared to have neuron-like long extensions or processes (Figure 3D, inset). Z section imaging indicated that many of them appeared to be located on the outer layer of the forebrain and the retina (Movie S9). Caspase activation in the brain region of zebrafish embryo at 48 hpf was confirmed using antibody staining against the cleaved

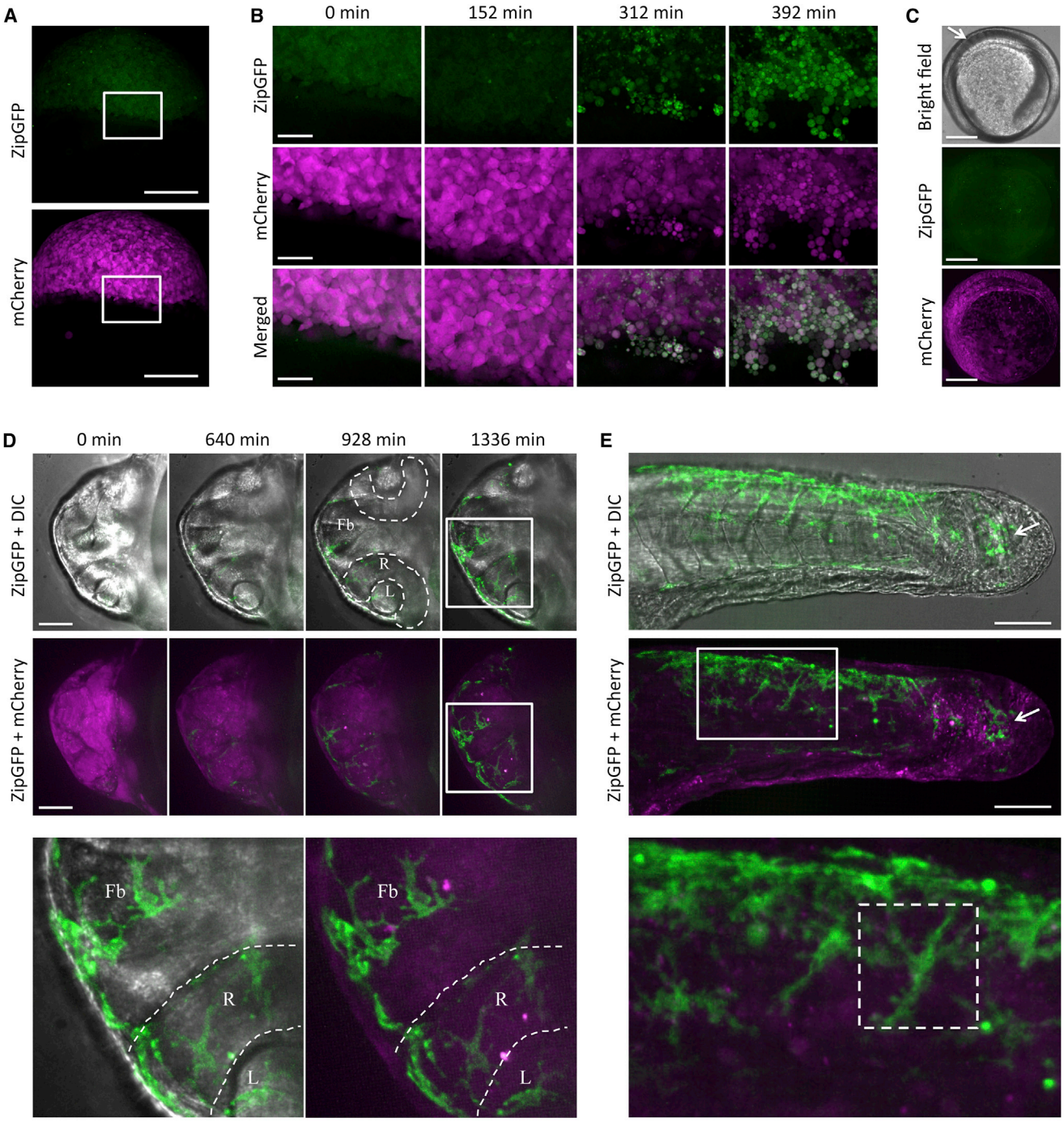

Figure 3. ZipGFP Caspase Reporter in Imaging Apoptosis in Zebrafish

(A) Confocal images of the zebrafish embryo at the 50% epiboly stage expressing ZipGFP caspase reporter and mCherry (see Movie S7).

(B) Time-lapse fluorescence images of zebrafish embryo in the zoomed area in (A) after addition of cycloheximide.

(C) Confocal images of the control zebrafish embryo (no addition of cycloheximide) expressing ZipGFP caspase reporter at 12 hpf. Arrow points to one of the somites.

(D) Time-lapse images of the brain of the zebrafish embryo expressing ZipGFP caspase reporter and mCherry. Imaging started at 24 hpf (see Movies S8, S9, and S10). Fb, forebrain; R, retina; L, lens. The dashed lines outline the retina.

(E) Images around the trunk of the zebrafish embryo expressing ZipGFP caspase reporter and mCherry at 48 hpf. Arrow points to the tail bud.

Scale bars, 200 μm (A); 50 μm (B); 200 μm (C); 80 μm (D and E).

caspase-3, which overlapped with ZipGFP fluorescence (Figure S5). Imaging of the trunk region of the zebrafish embryo also revealed green cells around the dorsal part of the somites and in the tail bud (Figure 3E). Some of them extended into the intersomitic regions (inset of Figure 3E and Movie S10).

The spatial pattern of ZipGFP fluorescence that we observed in the zebrafish embryo is consistent with a previous study based on TUNEL staining that showed clusters of apoptotic cells in the developing brain as well as in the trunk, including the tail bud (Cole, 2001). While TUNEL staining lacks temporal resolution, the temporal pattern revealed by ZipGFP indicated that apoptosis first occurred at the rostral part of the forebrain (Movie S6). It has been suggested that apoptosis provides a mechanism of removing neurons that failed to form appropriate connections during early neural circuit formation. Although our data suggest that the apoptotic cells in the brain are morphologically like neurons, detailed studies will be required to identify the cell type(s) and to reveal the molecular mechanisms. For example, specific promoters may be used to express the ZipGFP caspase reporter in the neurons or other cell types in the transgenic zebrafish, or zebrafish that express ZipGFP ubiquitously may be bred with existing lines that express fluorescent markers specifically in cell types of interest. And genetic manipulation can be used to investigate specific mechanisms of apoptosis.

SIGNIFICANCE

We have designed a fluorogenic protease reporter by "zipping" both parts of the self-assembling split GFP. ZipGFP-based protease reporter achieves ~10-fold fluorescence increase upon proteolytic cleavage, which is significantly larger than FRET-based fluorescence changes in donor and acceptor fluorophores and is thus ideal for imaging apoptosis in vivo. We have demonstrated that ZipGFP-based executioner caspase reporter is able to visualize apoptosis in the living embryos of zebrafish, which is an important model vertebrate for understanding embryonic development (Grunwald and Eisen, 2002). The ZipGFP caspase reporter will thus be an important tool in imaging apoptosis in vivo, which plays essential roles in animal development, maintenance of tissue homeostasis, and disease (Fuchs and Steller, 2011; Jacobson et al., 1997). It will be useful to dissect signaling networks that lead to apoptosis by hypothesis-driven studies as well as unbiased high-throughput screening in live animals such as zebrafish. ZipGFP may be further used to design reporters of many other proteases, which are essential for many biological processes (Lopez-Otin and Bond, 2008). These fluorogenic reporters overcome the sensitivity limitation of FRET-based reporters and will be suitable for imaging protease activity in physiological environments.

EXPERIMENTAL PROCEDURES

DNA Constructs

The details of all constructs in this study are listed in Table S1. All plasmid constructs were created by standard molecular biology techniques and confirmed by exhaustively sequencing the cloned fragments. To create the ZipGFP, we flanked split GFP 1–10 (β1–10) and split GFP 11 (β11) with the K5/E5 heterodimerizing coiled-coil system. Both K5 and E5 coils are 35 amino acids in length. In earlier designs, the PAS and GAF domains from mIFP were also incorporated as scaffolding elements. In the original design, the E5-mIFP(GAF)-protease cleavage sequence was fused to the N terminus of the split GFP 11, whereas mIFP(PAS)-K5 was fused to the C terminus. In the later design, K5 was fused to the N terminus of split GFP 11, and protease cleavage sequence E5 to the C terminus. For split GFP 1–10, E5 was fused to the N terminus, whereas protease cleavage sequence-K5 was fused to the C terminus. To create a TEV protease reporter, we used the TEV consensus cleavage sequence ENLYFQS in both zipped split GFP 1–10 and split GFP 11. To create a caspase-3 reporter, we used the Caspase-3/7 cleavage sequence DEVDG (an additional glycine was added before the cleavage sequence as a flexible linker) in a manner similar to the TEV reporter. The two parts of the ZipGFP were cloned into the pcDNA3.1 vector (Life Technologies) for mammalian cell expression. The part containing the split GFP 1–10 was co-expressed with the mCherry fluorescent marker using a Thosea asigna virus 2A cleavage site (T2A). The two parts of the ZipGFP were either co-transfected as two plasmids (e.g., TEV reporter) or co-expressed in a single plasmid using an additional T2A (e.g., caspase-3 reporter). We also created unzipped controls in which either split GFP 1–10 or split GFP 11 was not zipped by K5/E5. As unzipped control, the split GFP 11 was fused to the C terminus of the FKBP protein. The CA-GFP construct pT-CA-GFP-IRES-mLumin was a gift from Jeanne Hardy at UMass Amherst (Addgene plasmid no. 32749). To create the construct for in vitro transcription of mRNA, ZipGFP caspase reporter (with T2A mCherry) was cloned into the pCS+ vector. DNA of VC3AI was synthesized with codon optimization for expression in mammalian cells.

Protein Purification and Characterization

Zipped split GFP 1–10 and split GFP 11 containing the TEV cleavage sequence (ENYLFQS) were individually expressed with a C-terminal polyhistidine tag on pBAD expression vector (Invitrogen). The TEV protease was co-expressed with each ZipGFP subunit using a ribosomal binding site in order to generate the cleaved form of each subunit in *Escherichia coli*. The pBAD constructs used for protein expression in *E. coli* are listed in Table S1. Proteins were purified with the Ni-NTA purification system (QIAGEN). Protein concentration was measured by the BCA method (Pierce). The protein solutions were assayed by LDS-PAGE using NuPAGE Novex 4%–12% Bis-Tris protein gels (Life Technologies). All spectroscopic and kinetic measurements of the protein solutions were performed in protein elution buffer (50 mM Tris, 300 mM NaCl, 350 mM imidazole [pH 7.9]). For the absorbance and fluorescence measurements, 35 μl of 0.25 mg/ml spGFP1–10 was mixed with 65 μl of 0.10 mg/ml spGFP11. The absorbance and fluorescence emission spectra were obtained using the Tecan Infinite M1000 microplate reader. Measurement of complementation kinetics was done in protein elution buffer in a total volume of 100 μl (spGFP1–10, 2.7 μM; spGFP11, 6.3 μM) at 37°C as maintained by the Tecan microplate reader. The quantum yield of re-assembled ZipGFP was measured using a fluorometer LS-55 (PerkinElmer) with fluorescein as the standard. The two parts of ZipGFP were purified in the presence of TEV and were then mixed. The absorbance of fluorescein and the re-assembled ZipGFP was matched and their fluorescence spectra were taken by the fluorometer. The areas of the emission spectra of both samples were then compared, and the quantum yield was calculated.

Mammalian Cell Cultures

The HEK293T/17 (ATCC CRL-11268) and LN229 (ATCC CRL-2611) were obtained from ATCC. Cells were passaged in DMEM supplemented with 10% fetal bovine serum, non-essential amino acids, penicillin (100 units/ml), and streptomycin (100 μg/ml). All culture supplies were obtained from the UCSF Cell-Culture Facility.

HEK293T/17 and LN229 cells were transiently transfected with the protease reporter (and the protease of interest if applicable) with the calcium phosphate method. Cells were grown in 35 mm glass-bottom microwell (14 mm) dishes (MatTek Corporation). Transfection was performed when cells were cultured to ~50% confluence. For each transfection, 4.3 μg of plasmid DNA was mixed with 71 μl of 1× Hanks' balanced salts buffer and 4.3 μl of 2.5 M $CaCl_2$. Cells were imaged 24 hr after transient transfection.

Confocal Microscopy

For characterization of the protease reporters in cultured mammalian cells, transfected HEK293T/17 or LN229 cells were imaged in 35 mm glass-bottom

microwell dishes on a Nikon Eclipse Ti inverted microscope equipped with a Yokogawa CSU-W1 confocal scanner unit (Andor), a digital CMOS camera ORCA-Flash4.0 (Hamamatsu), an ASI MS-2000 XYZ automated stage (Applied Scientific Instrumentation), and a Nikon Plan Apo λ 20X air (NA 0.75) objective. Laser inputs were provided by an integrated laser engine (Spectral Applied Research) equipped with laser lines (Coherent) 488 nm (6.3 mW) for GFP imaging and 561 nm (3.5 mW) for mCherry/mLumin imaging. The confocal scanning unit was equipped with the following emission filters: 525/50 nm for GFP imaging and 610/60 nm for mCherry/mLumin imaging. For the characterization of ZipGFP-based reporters in mammalian cells, images were acquired with an exposure time of 100 ms for both GFP and mCherry. For CA-GFP, an exposure time of 500 ms was used for both GFP and mLumin. For the characterization of ZipGFP caspase-3 reporter in zebrafish embryos, images were acquired with an exposure time of 500 ms for GFP and 500 ms (for embryo at the 50% epiboly stage) or 1 s (for embryo at 24 hpf) for mCherry. For the time-lapse imaging of embryo at the 50% epiboly stage, a z stack spanning 115 μm at an interval 5 μm was acquired every 8 min for ~7 hr. For the time-lapse imaging of embryo at 24 hpf, a z stack spanning 225 μm at an interval 5 μm was acquired every 8 min for ~24 hr. Image acquisition was controlled by the NIS-Elements Ar microscope imaging software (Nikon). Images were processed using NIS-Elements and ImageJ (NIH).

Characterization in Cultured Mammalian Cells

HEK293T/17 cells transiently transfected with TEV reporter or TEV reporter + TEV were imaged in 35 mm glass-bottom dishes ~24 hr after transfection. For time-lapse imaging of the caspase-3 reporter during apoptosis, LN229 cells at ~24 hr after transient transfection with the reporter were grown to ~90% confluence in 35 mm glass-bottom dishes. Time-lapse microscopy was performed using the confocal microscope described above with the aid of an environmental control unit incubation chamber (InVivo Scientific), which was maintained at 37°C and 5% CO_2. To induce apoptosis, 1 μM of staurosporine was added to cells in PBS. The imaging dish was then quickly transferred to the incubation chamber for imaging. The time-lapse imaging continued for 6–8 hr with image acquisition every 8 min. For caspase-3 staining of cells treated with staurosporine, the 1× FLICA reagent from the FLICA 660 caspase-3/-7 assay kit (Immunochemistry Technologies) was added to the cell-culture medium. Cells were incubated for 60 min under existing culture conditions. Afterward, cells were washed twice with the apoptosis wash buffer provided in the detection kit and imaged in PBS (without fixation) using the confocal microscope describe above. For characterization of the kinetics of ZipGFP in HEK293 cells, the cells expressing ZipGFP, mCherry, and the split TEV system were treated with 10 nM rapamycin.

Characterization in Zebrafish Embryos

Zebrafish were handled in compliance with local animal welfare regulations and were maintained according to standard protocols (http://zfin.org). The culture was conducted in conformity with UCSF IACUC and AAALAC guidelines. In order to make mRNA for injection, the plasmid pCS2+ ZipGFP-T2a-mCherry was linearized with KpnI. In vitro transcription was performed using the mMachine mMessage Kit (Ambion). mRNA (100 pg) was injected at the one-cell stage. To perform live imaging, embryos at the 50% epiboly stage were manually dechorionated and mounted in 0.5% agar; 100 μg/ml cycloheximide in embryo medium was added shortly before recording. For the normal embryonic development experiment, embryos at 24 hpf were mounted in 1% agar. Time-lapse microscopy was performed using the confocal microscope described above with the aid of an environmental control unit incubation chamber (InVivo Scientific), which was maintained at 28°C. For whole-mount immunostaining, embryos were fixed at 12 hpf with 4% paraformaldehyde (PFA) in 1× PBS. After several washes with PBS, the embryos were permeabilized with 0.5% Triton for 1 hr and then incubated in blocking solution (PBS, 10% goat serum, 1% DMSO, 0.1% Triton) for 2 hr. The embryos were then incubated with anti-activated caspase-3 antibody (1:100; BD Pharmingen, catalog no. 559565), followed by several washes in PBS 0.1% Triton and incubation with secondary Alexa Fluor 647 conjugated antibody (1:500; Invitrogen) in blocking solution. Finally, the embryos were mounted in agar and imaged with a Zeiss 710 confocal microscope. For antibody staining of the zebrafish brain, embryos at 48 hpf were fixed with 4% PFA in PBS for 2 days and post-fixed in 100% methanol for 2 hr. The embryos were then treated with 1% Triton in PBS for 1 hr and incubated in the blocking solution. The embryos were then incubated with anti-activated caspase-3 antibody (1:100; BD Pharmingen, catalog no. 559565), followed by several washes in PBS 0.1% Triton and incubation with secondary Alexa Fluor 647 conjugated antibody (1:500; Invitrogen) in blocking solution. Embryos were mounted in agar and imaged with the confocal microscope.

SUPPLEMENTAL INFORMATION

Supplemental Information includes five figures, one table, and ten movies and can be found with this article online at http://dx.doi.org/10.1016/j.chembiol.2016.06.007.

AUTHOR CONTRIBUTIONS

X.S. and S.R.C. initiated the project. X.S. and T.-L.T designed the reporters. S.R.C. and A.S. designed the zebrafish experiments. T.-L.T., A.S., R.R., Q.Z., D.Y., and Z.D. performed the experiments. X.S. and T.-L.T. wrote the manuscript. All the authors contributed to the final draft.

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