Technical Reports

Simultaneous observation of Pol II and potato spindle tuber viroid RNA in the

nucleus by combining immunofluorescence and RNA in situ hybridization

Junfei Ma[1†*], Yunhan Wang[2†], Svetlana Y. Folimonova[1,2], Bin Liu[3], Ying Wang[1,2*]

1 Department of Plant Pathology, University of Florida, Gainesville, FL 32611, USA

2 Plant Molecular and Cell Biology Program, University of Florida, Gainesville, FL, USA

3 Food Science and Human Nutrition Department, University of Florida, FL, USA

[†] These authors contributed equally to the work.
*Correspondence: Junfei Ma and Ying Wang

Email: junfeima@ufl.edu (JM) and ying.wang1@ufl.edu (YW)

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protein co-localization, RNA polymerase II (Pol II)

Abstract

RNA comprises a versatile group of biomolecules that play diverse roles in a wide

range of biological processes. From synthesis to degradation, RNAs interact with cognate

proteins that assist in processes such as transcription, splicing, modification, trafficking,

and the execution of their functions. While numerous valuable techniques exist to study

RNA-protein interactions, observing RNAs and their associated proteins simultaneously

within cells remains a challenge, despite its potential to provide deeper insights into RNA-

protein interactions. In this study, we adapted a modified immunofluorescence (IF) assay

combined with RNA fluorescence in situ hybridization (FISH) to successfully visualize the

colocalization of potato spindle tuber viroid with RNA polymerase II in the nucleus. This

new method that combines IF and FISH will facilitate future studies on RNA and protein

colocalization in various plant systems.

Introduction

Mounting evidence has highlighted the essential roles of diverse classes of RNAs across a wide range of biological processes (Sharp, 2009). From transcription to decay, RNAs interact with specific RNA-binding proteins, and these interactions often correlate with distinct biological functions (Street et al., 2024). In certain cases, RNA-protein complexes organize into membrane-less organelles via liquid-liquid phase separation (Miao, Chodasiewicz, & Fang, 2024). Examples include Processing bodies and Stress Granules involved in mRNA turnover or storage (Chantarachot & Bailey-Serres, 2018), SERRATE-driven dicing bodies in microRNA processing (Xie et al., 2021), and FLL2-promoted phase separation of polyadenylation complexes for mRNA 3' end processing (Fang et al., 2019). Although tools such as RNA immunoprecipitation and gel electrophoresis mobility shift assays are valuable for studying RNA-protein interactions, observing RNA subcellular localization or simultaneously visualizing specific RNAs with their associated proteins in cells remains challenging, hindering the understanding of RNA-protein dynamics in the context of cell biology.

The MS2-MCP system enables live-cell imaging of RNAs by using MS2-binding coat proteins (MCP) tagged with green fluorescent protein (GFP) to recognize RNAs fused with MS2 hairpins (Syed & Lim, 2024). By tracking MSP-fused GFP fluorescence, RNA subcellular localization can be observed in living cells with high specificity and temporal resolution. RNA-binding proteins can be co-visualized by tagging them with fluorescent proteins other than GFP. In addition to the MS2-MCP system, RNA fluorescence aptamers also allow visualization of fusion RNAs in living cells (Sachdeva, Garg, Godding, Way, & Silver, 2014). However, both systems pose a risk of disrupting RNA overall structures and functions. For example, any insertion in the viroid RNA genome can lead to a loss of infectivity, limiting the applications of these methods to certain RNAs.

Observing proteins and RNAs in chemically fixed cells can provide insights into their subcellular dynamics. Immunofluorescence (IF) detects specific proteins, while RNA in situ hybridization (FISH) reveals RNA subcellular localization patterns. The development of single-molecule RNA FISH (smFISH) enables the quantitative observation of mRNAs, but it requires dozens of short, specific oligos (17-22 nt) and may not be suitable for short RNAs or those with limited unique sequences (Duncan, Johansson, & Ding, 2023).

Traditional IF and FISH are often incompatible, as the high-temperature treatment and
formamide used in FISH denature antibodies, hindering protein detection (Meyer, Garzia,
& Tuschl, 2017). Recent protocols offer modifications to address this issue by adjusting
formamide concentration and other conditions (B. Ma & Tanese, 2013; Meng, Zhao, &
Lao, 2018; Meyer et al., 2017), but performing IF after FISH or smFISH still remains
difficult. In some cases, fluorescent proteins (FPs) can retain fluorescence to outline
protein subcellular localization after RNA FISH steps (Duncan et al., 2023; Huang,
Guillotin, Rahni, Birnbaum, & Wagner, 2023; Zhao, Fonseca, Meschichi, Sicard, & Rosa,
2023), but this approach is mostly limited to observing protein colocalized with cytosolic
RNAs. For nuclear RNAs, high temperatures and stringent treatments in the
corresponding FISH protocols can cause FPs to lose fluorescence (Jolly, Mongelard,
Robert-Nicoud, & Vourc'h, 1997; Qi & Ding, 2003; Yokoyama, Ogawa, Nozu, &
Hashimoto, 1990).

Our goal is to understand viroid-host interactions at cellular and subcellular levels.
Viroids are single-stranded, circular noncoding RNA pathogens that primarily infect crops
(J. Ma, Dissanayaka Mudiyanselage, Hao, & Wang, 2023; Ortola & Daros, 2023). There
are two viroid families, *Pospiviroidae* and *Avsunviroidae*. Members of *Pospiviroidae*
replicate in the nucleus using RNA polymerase II (Pol II)(Wang, 2021). Unlike the well-
known 12-subunit Pol II, a modified Pol II with 6-7 subunits transcribes the potato spindle
tuber viroid (PSTVd) RNA (Dissanayaka Mudiyanselage et al., 2022), assisted by an
RNA-specific transcription factor (TFIIIA-7ZF)(Dissanayaka Mudiyanselage et al., 2022;
Wang et al., 2016). Despite the progress, the detailed subcellular localization and pattern
of Pol II transcription on PSTVd RNA remain unclear.

To address this, we developed a new strategy that combines IF and FISH to
simultaneously detect PSTVd RNA and the largest Pol II subunit (RPB1). This approach
is straightforward, does not require extensive cloning or transgenic plants (if a specific
primary antibody is available), and reliably detects RNAs and proteins in the nucleus.
Using this method, we observed the nuclear distribution patterns of Pol II (represented by
RPB1) and PSTVd sense-strand RNA. This technique will be valuable for studying
various nuclear-localized noncoding RNAs and their associated proteins, especially those
involved in liquid-liquid phase separation across diverse biological processes.

Results

An alternative immunofluorescence (IF) approach

To understand viroid replication in cells, we aimed to observe the subcellular localization of Pol II and potato spindle tuber viroid (PSTVd). However, our initial attempts were unsuccessful due to the technical challenges of combining immunofluorescence with RNA in situ hybridization. Inspired by a recent study on RNase L-induced bodies that directly incubate antibodies with culture cells (Watkins & Burke, 2024), we hypothesized that incubating antibodies directly with protoplasts could be an effective alternative IF method.

We tested this approach by observing GFP protein localization in the *Nicotiana benthamiana* 16C line, which expresses a GFP5 variant with an ER localization signal (Philips et al., 2017). Figure 1 shows the GFP fluorescence signal in live protoplasts, as well as in cells incubated with antibodies, with and without chemical fixation. As previously reported, polyclonal antibody binding reduced fluorescence of GFP to almost undetectable (Kubala, Kovtun, Alexandrov, & Collins, 2010; Schneider, Sych, Eggeling, & Sezgin, 2021). Nevertheless, signals from the Alexa Fluor594-conjugated secondary antibody accurately highlighted GFP localization, regardless of fixation, demonstrating that directly incubating antibodies with protoplasts can serve as an alternative IF technique.

Optimizing RNA FISH protocol for detecting RNA in the nucleus

Next, we sought to detect PSTVd RNA in fixed cells. Due to PSTVd's short length (359 nt), designing dozens of oligo probes, as required in some single-molecule RNA FISH protocols, was challenging. Instead, we used traditional *in vitro* transcription method to generate RNA oligos.

The key factor was optimizing probe size. We designed probes around 100 nt to facilitate nuclear entry. Each probe contained approximately 25-30 AlexaFluor488-labeled UTPs, and we used two probes, achieving 54 labeled UTPs per PSTVd RNA to enhance the signal-to-background ratio. We tested two methods reported in previous RNA FISH experiments that observed nuclear PSTVd accumulation. Interestingly, combining the penetration steps from both protocols yielded better, more consistent

125 results (Figure 2). PSTVd displayed a unique distribution pattern, with dominant signals
126 near the nucleolar region, as indicated by the hollow DAPI staining (Figure 2). This PSTVd
127 RNA condensate pattern is consistent with previous reports (Qi & Ding, 2002, 2003).
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A new strategy combining IF and FISH to observe RNA-protein simultaneously

Building on the success of our alternative IF and RNA FISH methods, we developed
a combined IF-FISH protocol to observe proteins and RNA simultaneously in cells (Figure
3). This strategy involves generating protoplasts from leaves, followed by incubating cells
overnight at 4°C with primary antibodies against target proteins. After brief washes, cells
are incubated with fluorescence-labeled secondary antibodies. The IF process is followed
by cell fixation, permeabilization, blocking, hybridization, and finally, observation. The
entire procedure can be completed in four days.
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The new IF-FISH method helps direct observation of the cellular sites of Pol II
transcription on PSTVd sense-strand RNA

Using this system, we aimed to understand the subcellular distribution of Pol II and
PSTVd RNA. Although PSTVd replication depends on Pol II activity, the exact nuclear
distribution pattern involved in PSTVd RNA-templated transcription remain unclear. We
used the well-known 8WG16 monoclonal antibody to detect Pol II localization via its
largest subunit (RPB1). Our previous studies confirmed that 8WG16 specifically
recognizes RPB1 in immunoblots using total protein extracts from *N. benthamiana* leaves
(Wang et al., 2016). As shown in Figure 4A, there is no fluorescence signal from Alexa
Fluor594-conjugated secondary antibody in samples which we did not add primary
antibody, demonstrating the specificity in detecting target protein. Similarly, PSTVd
specific riboprobe did not give any signal in non-infected cells, again support the specific
detection in FISH experiment.
In a selected image from a Z-stack series (Figure 4B), we found that some of the
RPB1 and PSTVd colocalized loci are surrounding bot not overlapping with the highly
enriched PSTVd RNA condensate. There are more colocalized loci spreading in
nucleoplasm. This pattern demonstrates that there is no major locus for Pol II to transcribe
the template of PSTVd sense-strand RNA. Rather, the transcription occurs in multiple loci

mainly in the nucleoplasm.

Discussion

By combining IF and RNA-FISH, we successfully achieved the simultaneous

observation of RNA and protein in the nucleus of plant cells. This approach eliminates the

need for extensive cloning, as required in the MS2–MCP system, or the generation of

transgenic plants when a specific primary antibody is available. Notably, our protocol is

particularly effective for detecting RNAs in the nucleus, which has proven challenging

based on both literature and our experience. Additionally, this method allows the direct

visualization of proteins and RNAs in their native state without ectopic expression, making

it a robust and straightforward approach for plant cell biology studies.

Compared to smFISH, our probe design strategy offers an advantage in detecting

relatively short RNAs that are insufficient in length for designing multiple oligos. While we

used a long probe (~100 nt) to detect PSTVd sense-strand RNA, our method could be

adapted in combination with smFISH to detect endogenous mRNAs. Moreover, multiple

proteins and/or RNAs can be observed within the same cells by utilizing various

AlexaFluor dyes, allowing different targets to be marked with distinct colors. This flexibility

enables researchers to adapt the method to address a range of biological questions.

Recent studies have increasingly highlighted the importance of dynamic RNA

organization and their associated factors within the cellular environment, particularly in

the context of phase separation across diverse biological processes (Miao et al., 2024).

However, most knowledge has been derived either from methods lacking cellular context

(e.g., RIP-Seq) or indirectly by observing either protein or RNA subcellular localization

alone. Our method provides a means to directly investigate the dynamic interactions

between RNA and protein in cells, offering a valuable tool for future research.

By using our method, we now understand that Pol II transcribing sense-strand of

PSTVd in multiple loci in the nucleoplasm. Since Pol II transcription loci do not overlap

with the major PSTVd RNA condensate, this result excludes the PSTVd RNA condensate

as the transcription site. Rather, the PSTVd RNA condensate is possibly the organized

place for processing (e.g., cleavage, ligation, etc) after transcription. We believe this

method is suitable to study the colocalization of RNA and protein, particularly for those

that occurred in the nucleus.

Materials and methods

Plant Growth and Protoplast Preparation

Nicotiana benthamiana (wild type and line 16C) were grown in a growth shelf at 25 °C
with a 16-hour light and 8-hour dark cycle. PSTVd-infected plants were verified by RNA
gel blots as described previously (Takeda, Zirbel, Leontis, Wang, & Ding, 2018).
Protoplasts were isolated from the 4th to 6th leaves of the plants by following a published
protocol with slight modifications (Jiang, Ma, Liu, & Wang, 2019). Briefly, leaves were
digested with 3% cellulose (Onozuka Yakult Pharmaceutical IND., Tokyo, Japan) and 0.8%
macerase (MilliporeSigma, Burlington, MA, USA) in protoplast digestion buffer (0.4 M
mannitol, 20 mM KCl, 20 mM MES, 10 mM $CaCl_2$, 0.1% BSA, 5 mM β-mercaptoethanol,
pH 5.7). The lower epidermis layer of the leaves was removed by tapes before digestion.
After 1 hr of digestion, the protoplasts were pelleted by centrifugation at 150× *g* for 1 min.
The pelleted protoplasts were then washed sequentially with W5 buffer (5 mM MES, 154
mM NaCl, 125 mM $CaCl_2$, 5 mM KCl, pH 5.7) at room temperature. Finally, the protoplasts
were incubated in IF buffer (0.5 M mannitol, 20 mM MES, pH 5.7, 20 mM KCl, 1% BSA,
0.1% Tween-20) before adding primary antibodies.

Immunofluorescence (IF)

The IF method was adapted from a study on *in vivo* antibody uptake (Watkins & Burke,
2024). Freshly prepared protoplasts were incubated overnight at 4°C with primary
antibodies diluted 1:500 in IF buffer (protoplast digestion buffer with 1% BSA and 0.1%
Tween 20). After primary antibody incubation, protoplasts were washed three times with
IF buffer with a 10 min interval. Secondary antibodies were added in IF buffer with a 1:50
dilution and incubated at room temperature for 3 hr. The protoplasts were washed three
times with IF buffer (10 min each) to remove the secondary antibody. Sample fixation was
done by using 3.7% paraformaldehyde and 0.2% picric acid in KE buffer (50 mM KH2PO4,
5 mM EGTA, pH 5.0) at room temperature for 1 hr. Cross-linking was stopped by using
1X KE buffer containing 0.3M Glycine, followed by two times washing with 1X KE buffer
for 1h each. Primary antibodies are mouse monoclonal 8WG16 (ThermoFisherSci,

Waltham, MA) for Pol II RPB1 and anti-GFP polyclonal antibody raised in rabbit

(Genscript, Piscataway, NJ). AlexaFluor594 conjugated anti-mouse or anti-rabbit (both

from ThermoFisherSci) was used as secondary antibody.

RNA Fluorescence in Situ Hybridization (FISH)

Following IF treatment and fixation, the protoplasts were stored in 70% ethanol at 4°C

overnight before FISH steps. The samples were baked onto Superfrost® microscope

slides (ThermoFisherSci) at -20°C for 30 minutes, followed by baking at 70°C for 2 hours.

Next, the samples were washed with 1X PBS containing 2% bovine serum albumin (BSA),

0.1% cellulase, 0.05% macerozyme, 0.3% Triton X-100, and 0.5% Nonidet P-40 at room

temperature for 30 min. Then, samples were washed three times with 100 mM Tris (pH

6.8) containing 1% Nonidet P-40 and 0.5% Triton X-100 at 37°C for 10 minutes each.

Pre-chilled methanol with 2% hydrogen peroxide was added to the samples, which were

incubated at -20°C for 30 min. The slides were subjected to three rounds of liquid nitrogen

treatment, each lasting 5 seconds. The samples were then treated with 0.5% (v/v) Acetic

anhydride in 0.1 M triethanolamine (TEA) buffer (pH 8.0) at room temperature for 20 min.

Samples were then blocked with PerfectHyb™ Plus hybridization buffer

(ThermoFisherSci) at 55°C for 30 min. Probes (corresponding to the 98-188 and 270-13

positions in PSTVd genome but in the complementary orientation) were synthesized

using T3 Maxiscript kit (ThermoFisherSci)(J. Ma et al., 2022). Probes (2.5-5 µg/ml) were

denatured by heating at 100°C for 1 minutes, followed by colling on ice. The denatured

probes, along with 5 nM ribonucleoside vanadyl complex (Sigma-Aldrich, St. Louis, MO,

USA), were added to PerfectHyb™ Plus Hybridization Buffer and applied to samples on

slides, followed by incubation at 55°C overnight.

The samples were then rinsed with 2X SSC, washed with 2X SSC containing 50%

formamide at 37°C for 30 min, and subsequently washed with 2X SSC and 1X SSC at

room temperature for 30 minutes each. 4',6-diamidino-2-phenylindole (DAPI) was added

directly to the samples stain (1 µg/ml) for 5 minutes and then rinsed with distilled water.

Anti-fade reagent (ThermoFisherSci) was applied to each sample, and the slides were

sealed with nail polish.

Microscopy Imaging

Fluorescence signals were obtained by using a Discover Echo Revolve microscope with DAPI, FITC, and TRITC cubes and Leica Stellaris 5 confocal microscope.

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Figure Legends

Figure 1. An alternative immunofluorescence protocol. Protoplasts from Nicotiana

benthamiana 16C were used for testing. GFP5-ER in protoplasts was detected by α-GFP

polyclonal primary antibody and Alexa Fluor594-labeled α-Rabbit secondary antibody. α-

Rabbit secondary antibody was added to all IF samples. Scale bar, 5 μm.

Figure 2. An optimized RNA FISH protocol for observing potato spindle tuber viroid.

Nucleolar-enriched PSTVd detected by Alexa Fluor488-labeled riboprobe. Scale bar, 8

μm.

Figure 3. Schematic workflow of combined IF and FISH.

Figure 4. Combining immunofluorescence (IF) and RNA fluorescent in situ hybridization

(FISH) to colocalize PSTVd and RPB1. A) RPB1 is detected by α-RPB1 polyclonal

antibody and Alexa Fluor594-labeled α-Rabbit secondary antibody (magenta color).

Secondary antibody was applied to all treatments. PSTVd was detected by Alexa
Fluor488-labeled specific riboprobe (green). Probes were added to all treatments. (B) For
the image at the bottom right in (A), single channels and RPB1/PSTVd overlay are shown.
This image is selected from a Z-stack series. White arrow heads point to some colocalized
loci. Scale bar, 5 μm.

Figure 1

Figure 2

Figure 3

Figure 4