UMEPPPI: An ultrasensitive detection method for protein–protein interaction

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Abstract

Figure 1: An ultrasensitive detection method for protein–protein interaction. (A) A schematic representation of the UMEPPPI method. Shot47 is a ribonucleic acid (RNA) aptamer that strongly associates with a histidine tag. The shot47 complex and protein-of-interest is called the Hishot complex. The interaction can be detected by performing reverse transcription polymerase chain reaction (RT-PCR) or quantitative RT-PCR (qRT-PCR) of purified mRNA of the Hishot complex. (B) The stability of mRNA in the Hishot complex. The Hishot complex was extracted from the expression of the host E. coli with a presence or absence of RNase I or RNase inhibitor. The mRNA concentration of the Hishot complex is shown as the relative amount compared with the nontreatment. (C) Semi-qRT-PCR of GL1. The size of the specifically amplified product from GL1 CDS is approximately 270 bp. PC indicates a specific GL1 fragment amplified from the pSpET-GL1 vector. RNA was extracted from precipitates with GST, GST-GL3, or GST-PAP1. (D) The qRT-PCR results. The amount of the GL1 transcript was shown as a relative amount to the input fraction. The amount of the GL1 transcript from the Hishot complex co-precipitated with GST-PAP1 and is higher than that with GST-GL3. NC shows a signal from no template fraction. Error bars represent standard deviations.

Description

The quantification of protein and detection of protein–protein interaction (PPI) largely requires antibody-mediated techniques such as Western blotting and immunoprecipitation. These detection methods for PPI have relatively low sensitivity compared with those for nucleic acids. Because the polymerase chain reaction (PCR) has a powerful amplification of signals derived from nucleic acids, this method for detecting nucleic acids has a higher sensitivity than general PPI detection methods. In this study, we developed a novel method for detecting PPI by converting protein signals to those of nucleic acids, which is called the ultrasensitive detection method for PPI (UMEPPI). UMEPPPI uses an RNA aptamer that tightly associates with a histidine tag. The RNA aptamer is genetically fused to a gene encoding a histidine-tagged protein-of-interest (POI). Because the affinity between the RNA aptamer and the histidine peptide tag is pico mol/l (10⁻¹² M) order as a dissociation constant (K_D) (Tsuji et al., 2009), the RNA aptamer-tagged protein complex is stable through protein purification steps, and the mRNA of POI can be detected by reverse transcription PCR (RT-PCR). The goal of this study was to prove the concept of UMEPPPI. The scheme of UMEPPPI is shown in Figure 1A. UMEPPPI uses an
Expression and purification of the Hishot complex fragments were ligated using a DNA ligation kit <Mighty mix> (TAKARA Bio, Shiga, Japan) at 16°C for 30 min. with XbaI restriction enzyme at 37°C for 1 h. After ethanol precipitation, the digested pET21 and shot47 dsDNA and 1 mM EDTA pH8.0. Then, the oligo fragments were heated at 95°C using a thermal cycler. After 5 min, the thermal CTAGAGGCACTGACATTCCACGAAGGCGCCAATATACCT-3′), were mixed in 10 µL of TE (10 mM Tric-HCl pH8.0). A total of 50 µM of oligo DNA fragments, UM_5′Xba1_shot47 (5′-CTAGAGGTATATTGGCGCCTTCGTGGAATGTCAGTGCCT-3′) and UM_3′Xba1_shot47 (5′-CTAGAGGTATATTGGCGCCTTCGTGGAATGTCAGTGCCT-3′), were mixed in 10 µL of TE (10 mM Tric-HCl pH8.0 and 1 mM EDTA pH8.0). Then, the oligo fragments were heated at 95°C using a thermal cycler. After 5 min, the thermal cycler was turned off, and the fragments were left overnight to reach room temperature. The pET21 vector was treated with XbaI restriction enzyme at 37°C for 1 h. After ethanol precipitation, the digested pET21 and shot47 dsDNA fragments were ligated using a DNA ligation kit <Mighty mix> (TAKARA Bio, Shiga, Japan) at 16°C for 30 min.

For the evaluation of UMEPPI, we used a known combination of PPI that we previously reported (Umeyama and Morohashi, 2020). GLABROUS1 (GL1; At3g27920), PRODUCTION OF ANTHOCYANIN PIGMENT 1 (PAP1; At1g56650), and GLABRA3 (GL3; At5g41315) are transcription factors involved in organ development and metabolite biosynthesis in seed plant, Arabidopsis thaliana. Studies previously determined the $K_D$ of GL1 vs. PAP1 and GL1 vs. GL3 are 4.87 × 10$^{-8}$ M and 9.53 × 10$^{-6}$ M, respectively. Because the affinities of GL1 vs. PAP1 and GL1 vs. GL3 show a difference of approximately 190 times, this is a reasonable evaluation system for UMEPPI. Even though any tagged system can be used, we used the glutathione S-transferase (GST) protein system to handle purification and precipitation. GST proteins were fused to the N-termini of PAP1 and GL3 proteins. The GST-PAP1 and GST-GL3 proteins were expressed in bacteria and purified. To create the Hishot complex, we constructed the pSpET vector, in which the coding sequence of GL1 was inserted downstream of the histidine tag and shot47. The crude soluble fraction of the GL1 Hishot complex was incubated with purified GST, GST-GL3, or GST-PAP1 and followed by precipitation using glutathione sepharose beads. We validated whether the GL1 Hishot complex was co-precipitated with GST fusion proteins using RT-PCR. RT-PCR was performed using primer sets designed from part of a coding region of GL1. As shown in figure 1C, the extract from the GST-GL3 and GST-PAP1 precipitated fraction clearly shows a signal of GL1 transcripts, whereas no signal was detected for the GST protein, which suggests that the GL1 Hishot complex is stably precipitated with the GST-GL3 or GST-PAP1 protein. Semi-qRT-PCR suggests that GST-PAP1 would show a higher affinity with the GL1 Hishot complex. We also performed qRT-PCR. Similarly, figure 1D shows that the amounts of co-precipitated mRNA with GST-PAP1 were more than those with GST-GL3. Considering the $K_D$ between 1,450 monoclonal antibody and antigen values in the 1 × 10$^{-9}$ to 2 × 10$^{-8}$ M range (Landry et al., 2014), the affinity between shot47 and the histidine peptide tag is significantly high ($K_D = 3.78 \times 10^{-12}$ M) (Tsuij et al., 2009), indicating that UMEPPI shows a higher sensitivity than general antibody–antigen approaches. Moreover, UMEPPI successfully detected the difference in these affinities (Figure. 1C and D).

There are various detection methods of PPI that do not require antibodies (e.g., surface plasmon resonance, quartz crystal microbalance, mass spectrometry, the phage display system, and the yeast two hybrid system) (Braun and Gingras, 2012; Rao et al., 2014); however, these approaches are costly and/or labor intensive. Therefore, the antibody-mediated methods are largely used in the field of molecular biology. Nevertheless, antibody-mediated methods have shortcomings. The specificity of the antibody is often variable or unclear. UMEPPI overcomes the problem by using a specific sequence of POI, and the design of the primer sets is straightforward and cost-effective; thus, UMEPPI is a potential and versatile substitute for canonical immunoprecipitation followed by Western analysis. UMEPPI uses PCR as a detection approach and it easily amplifies even very low amounts of protein interactions quantitatively. Ultimately, UMEPPI could become a protein-to-nucleic-acid converter for any type of protein.

**Methods**

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**Construction of the pSpET vector**

A total of 50 µM of oligo DNA fragments, UM_5′Xba1_shot47 (5′-CTAGAGGTATATTGGCGCCTTCGTGGAATGTCAGTGCCT-3′) and UM_3′Xba1_shot47 (5′-CTAGAGGTATATTGGCGCCTTCGTGGAATGTCAGTGCCT-3′), were mixed in 10 µL of TE (10 mM Tric-HCl pH8.0 and 1 mM EDTA pH8.0). Then, the oligo fragments were heated at 95°C using a thermal cycler. After 5 min, the thermal cycler was turned off, and the fragments were left overnight to reach room temperature. The pET21 vector was treated with XbaI restriction enzyme at 37°C for 1 h. After ethanol precipitation, the digested pET21 and shot47 dsDNA fragments were ligated using a DNA ligation kit <Mighty mix> (TAKARA Bio, Shiga, Japan) at 16°C for 30 min.

**Expression and purification of the Hishot complex**
The coding sequence (CDS) of GL1 (At3g27920) was amplified with MU_pET_GL1_F (5′-AATGGGTCGCGGATCCGAAATGAGAATAAGGAGAAGAGATG-3′) and MU_pET_GL1_R (5′-TGTCGACGGAGCTCGAATTAAGGCAGTACTCAACATCACC-3′). The amplified GL1 CDS fragment was inserted into pSpET using HiFi DNA Assembly Master Mix (NEB, Ipswich, MA). The pSpET-GL1 was transformed into *Escherichia coli* Rosetta2 (DE3).

**Expression and purification of host proteins**

The DNA fragments of PAP1 (At1g56650) and GL3 (At5g41315) were cleaved by EcoRI and cloned into a shrimp alkaline phosphatase-treated pGEX6P-1 vector using HiFi DNA Assembly Master Mix (NEB, Ipswich, MA) to construct GST-PAP1 and GST-GL3, respectively. Then, each construct was transformed into *E. coli* Rosetta2 (DE3). The recombinant proteins were expressed and purified as previously described (Umeyama and Morohashi, 2020). Then, GST-fuzed proteins were purified using glutathione sepharose beads based on the manufacturer’s protocol. Finally, the protein concentration was measured with a Pierce BCA Protein Assay Kit (Thermo Fisher Scientific, Waltham, MA), and 100 µL of the 36.6 µM concentration of proteins was used for further analysis.

**Preparation of Hisshot protein**

The induced culture was collected in a 500-mL bottle followed by centrifugation at 3,500 rpm for 15 min at 4°C. After discarding the supernatant, 30 mL of phosphate-buffered saline (PBS) (1,370 mM NaCl, 27 mM KCl, 81 mM Na₂HPO₄·12H₂O, and 14.7 mM KH₂PO₄) was added, resuspended, and centrifuged at 3,500 rpm for 15 min at 4°C.

**Association of the Hisshot complex with the host protein**

Lysozyme was added in 10 mL of the bacteria-expressed GL1-Hisshot protein to achieve 1 mg/mL as a final concentration. In the case of the RNase or RNase inhibitor treatment, RNase I was added to achieve 0.8 U/µL as a final concentration, respectively. Then, the reaction solution was incubated for 30 min at 37°C followed by sonication on ice until the stickiness was gone. The sonicated solution was centrifuged at 9,000 rpm for 15 min at 4°C. Then, 500 µL of the supernatant was transferred into a tube that contained 100 µL of the host protein. Next, 300 µL of a 30% slurry of glutathione sepharose 4B was added in the tube and incubated at 4°C with rotation overnight.

**RNA extraction from the Hisshot complex and reverse transcription**

The reaction extract containing GL1-Hisshot proteins and GST proteins was centrifuged at 500 rpm for 10 min at 4°C, and the supernatant was removed. Then, the beads were washed three times with 500 µL of PBS. Next, 350 µL of TRI Reagent (Cosmo Bio, Tokyo, Japan) was added into the beads. The upper layer was transferred into a new tube, and RNase-free DNase I (Sigma-Aldrich, St. Louis, MO) was added to achieve 0.1 U/µL as a final concentration. Then, the RNA was purified by phenol–chloroform extraction followed by ethanol precipitation. The purified RNA was subject to reverse transcription using a ReverTra Ace qPCR RT kit (Toyobo, New York, NY) in a 20-µL reaction volume according to the manufacturer’s protocol.

**RT-PCR and qRT-PCR**

For semi-qRT-PCR, MU_GL1_seq (5′-GGTTCATCAGTGGCCGACAC-3′) and T7 terminator primer (5′-GCTAGTTATGGTCGAGCG-3′) primer sets were used. After, 25, 30, and 35 cycles of PCR, the reaction was subjected to electrophoresis with 2% agarose gels. For qRT-PCR, the primer sets of YT_GL1_qrt_F (5′-CCGCAACACCCTTCTTCTGATC-3′) and YT_GL1_qrt_R (5′-ATACGACGCGTAAGCTCTTGG-3′) were used.

**Acknowledgments:** We thank Nobutaka Mitusda (National Institute of Advanced Indsutrial Science and Technology) for kindly sharing pDONR vectors.

**References**


**Funding:** This work was supported by Grant-in-Aid for Scientific Research on Innovative Areas “Frontier Research on Chemical Communications” Grant Number 18H04631.

**Author Contributions:** Mikiya Umeyama: Data curation, Investigation, Methodology, Formal analysis. Jun Hirose: Data curation, Investigation. Kengo Morohashi: Writing - original draft, Writing - review and editing, Supervision, Funding acquisition, Conceptualization.

**Reviewed By:** Anonymous

**History:** Received September 1, 2020  Revision received September 10, 2020  Accepted September 14, 2020  Published September 14, 2020

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