Direct isolation of specific RNA-interacting proteins using a novel affinity medium

Ding-Gan Liu* and Li Sun

State Key Laboratory of Molecular Biology, Institute of Biochemistry and Cell Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, 320 Yueyang Road, Shanghai 200031, China

Received; Revised and Accepted

ABSTRACT
Isolation of proteins that specifically interact with a given RNA or RNA regulation element is essential for studies on the molecular mechanisms of gene expression. Here, a novel method for direct isolation of such interacting proteins is described. It uses an affinity medium that consists of an interacting RNA with an artificially added ‘tail’, which is annealed to one end of a DNA ‘arm’, the other end of which is fixed covalently on the surface of aminosilanized glass powder. Thus the RNA itself is fully suspending, facilitating its interactions with proteins in its natural conformation. The proteins bound on the interacting RNA are eluted and subjected to SDS–PAGE, and the Coomassie-stained protein bands are cut and subjected to mass spectrometry (MS) analysis. Using this method, three proteins specifically interacting with the C/EBPβ 3′-untranslated region (3′-UTR) RNA were isolated and identified. This method is simple and convenient, and the DNA-glass powder medium can be used repeatedly.

INTRODUCTION
RNA–protein interactions underlie the most important intracellular biological processes, such as all the steps of gene expression and its regulation (1) and cellular resistance to viral infection (2). Therefore, studies on RNA–protein interactions are essential for understanding the mechanisms of various life activities within the cell. For this purpose, isolation and characterization of the proteins specifically interacting with various RNAs are the first step of most of these studies. The methods for isolation of RNA-interacting proteins and/or their genes or cDNAs are well documented. Screening of a cDNA expression library with a labeled RNA probe is a common and effective method (3). Besides, many others specific for certain protein factors that interact with RNA in their functions are available (4–8). A very valuable in vivo method is the yeast three-hybrid system (9). It is unique in that it has created an intracellular mechanism for the interaction of specific proteins with their target RNAs, leading to expression of a reporter gene, which changes the phenotype of the yeast cell that harbors the cDNA of the protein. These methods are all useful and meet specific requirements and conditions of various studies.

The achievements of the Human Genome Project, and the advent of the protein mass spectrometry (MS) analysis and microsequencing (10) have provided new strong tools for research workers to find specific RNA-interacting proteins. As little as nanomole, or even less, amounts of protein samples can be analyzed using MS; therefore, the specific RNA-interacting proteins can be identified successfully, provided that they can be obtained in these amounts.

Here, a simple and effective method is described for the direct isolation of proteins that specifically interact with RNA. The principle of this method is to isolate RNA-interacting proteins by using an affinity medium, i.e. a protein-interacting RNA with its additional ‘tail’ annealed to an end of a DNA ‘arm’, which is immobilized through its other end on a glass base, and then to separate the bound proteins by SDS–PAGE. The protein bands in stained gels are subjected to MS analysis. The 3′-untranslated region (3′-UTR) of the mRNA of C/EBPβ, a transcription factor currently under our studies, is used as an example.

MATERIALS AND METHODS
Cell line and extraction of cellular proteins
The SMMC7721 human hepatocarcinoma cell line (11) was provided by the Cell Bank of the Chinese Academy of Sciences (Shanghai) and kept in RPMI1640 medium with 10% newborn calf serum (top grade, Si Ji Qing Biotechnological Materials Co. Hangzhou, China, or an equivalent from Invitrogen) and antibiotics supplemented. The cytoplasmic proteins (C-fraction, or mixed C- and E-fractions) were extracted according to literature (12).

*To whom correspondence should be addressed. Tel: +86 21 54921135; Fax: +86 21 54921011; Email: dgliu@sibs.ac.cn

© The Author 2005. Published by Oxford University Press. All rights reserved.

The online version of this article has been published under an open access model. Users are entitled to use, reproduce, disseminate, or display the open access version of this article for non-commercial purposes provided that: the original authorship is properly and fully attributed; the Journal and Oxford University Press are attributed as the original place of publication with the correct citation details given; if an article is subsequently reproduced or disseminated not in its entirety but only in part or as a derivative work this must be clearly indicated. For commercial re-use, please contact journals.permissions@oupjournals.org
In vitro transcription of RNA

The recombinant plasmid pSP64/0.28, which harbors the cDNA of the C/EBPβ 3′-UTR mRNA (0.28 kb fragment, with the poly A sequence deleted), was constructed by our group (13). It was digested with PvuII before in vitro transcription with the RiboMax large scale RNA production kit (Promega) according to the manufacturer’s instructions.

Affinity medium preparation

Preparation of aminosilanized glass powder. Common glass powder (50–100 mesh, made in Shanghai, China) was cleaned thoroughly, dried, and allowed to react with a 1:1 (v/v) solution of 3-aminopropyltriethoxysilane (Sigma) in acetone at room temperature for 30 min. Then the glass powder was washed thoroughly with acetone and dried at 50°C.

Activation of DNA ‘arms’. Plasmid pSP65 (Promega) was cut to its linear form with EcoRI. The linear plasmid (1 mg), dissolved in 100 μl of 0.1 M MES (pH 6) and 0.5 M NaCl, was added to a tube containing 0.4 mg of 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide (EDC) (Sigma) and 1 mg of N-hydroxysuccinimide (Shanghai, China). The mixture was incubated at 70°C for 30 min. The reaction was stopped by the addition of 2 μl of 2-mercaptoethanol, and then washed thoroughly with TE buffer at room temperature. The washed DNA-glass powder can be re-used for annealing with newly prepared RNA, at least for two additional uses.

Binding and UV-crosslinking of specific interacting proteins with C/EBPβ 3′-UTR RNA

The reaction mixtures contained 10 μl of cytoplasmic extract, 4 μl of 5× binding buffer, 5 μl of H2O and 1 μl of 32P-labeled C/EBPβ 3′-UTR RNA probe. The mixtures were incubated at room temperature (20–26°C) for 10 min, followed by UV irradiation with two 15 W UV tubes at 0°C for 30 min. The horizontal distance between UV tubes was 5 cm. The sample tubes (0.5 ml Eppendorf tubes), laid on a sheet of Saran Wrap covered over an ice-cold water surface, were mounted just beneath the UV tubes at a distance of about 10 cm. After UV treatment, each sample was digested with 1 μl of 10 mg/ml RNase A (Promega) at 37°C for 20 min, and then separated by SDS–PAGE as before. The gels were fixed, dried and autoradiographed.

For target removal experiments, 10 μl of cytoplasmic extract were incubated with 1 μl of appropriate antibodies (kindly provided by Rong Zeng and Kan Liao; Santa Cruz) at 4°C for 2 h, and then incubated with 2 μl of protein A-Sepharose (kindly provided by Xue-Jun Zhang and Mu-Jun Zhao) for 2 h. The mixtures were centrifuged and the supernatants were used for binding and UV-crosslinking experiments as above. The mouse anti-IgG antibody was used as a control.

RESULTS

Principle of the method

The principle of this method is illustrated in Figure 1. The interacting RNA is transcribed in vitro from the coding strand (+) of the recombinant pSP64 plasmid, which has been cut to linear form by the restriction enzyme PvuII; thus transcript contains a segment of RNA that is complementary to the vector sequence between the polycloning site and PvuII site, i.e. a ‘tail’, at the 3′ end of the RNA. On the other hand, the plasmid pSP65, which shares the plasmid sequence with pSP64 except for the polycloning sites in reverse orientation, is cut with EcoRI. The linear pSP65 has phosphorylated 5′-termini, which can be activated by the water-soluble carbodiimide (EDC) and then linked covalently to an amino group on the aminosilanized glass. After HindIII treatment and heating, the strand of pSP65 identical to the (+) strand with speed regulator (Pynus Micromotor Factory, Shanghai), and rotated at 1 r.p.m. at 0–4°C for 4 h or overnight. Subsequently, the RNA–DNA-glass powder was washed at 0–4°C with 1× binding buffer 5 times, 1 ml each time, and then with annealing buffer thrice, 1 ml each time. Finally, the RNA–DNA-glass powder was mixed with 1× protein loading buffer, heated at 80°C for 5 min, and the eluted proteins were electrophoresed on an 8% SDS–polyacrylamide gel. The Coomassie- stained protein bands were cut and analysed by MS.
of the pSP64/0.28 was removed. So, only the strand with the sequence complementary to the ‘tail’ of the interacting RNA remains linked to the glass, with the complementary sequence at the end that suspends in the microenvironment. Therefore, the interacting RNA is easy to anneal to that end. This annealing does not affect to the RNA itself, which at least theoretically should keep its natural conformation and bind its specific interacting proteins normally.

The amount of pSP65 DNA linked covalently on the amino glass was estimated to be 2 mg/g glass powder or more, and the C/EBPβ 3'-UTR RNA which can be bound on the DNA-glass powder was about 50–100 μg/g glass powder.

### Direct isolation and identification of C/EBPβ 3'-UTR RNA-specific interacting proteins by using the RNA–DNA-glass medium

Previously, we found that the C/EBPβ 3'-UTR RNA specifically interacts with several cytoplasmic proteins (Figure 2). The method described above was used to isolate and identify them. Accordingly, a C/EBPβ 3'-UTR RNA affinity medium was used for binding the specific cellular interacting proteins, with the DNA-medium without RNA as control. By using Coomassie blue BB250 staining, three apparent protein bands were detected reproducibly, whereas no band was found in corresponding positions in the lane to eluate from the control medium (Figure 3). These three bands were cut and sent to the National University of Singapore for MALDI-TOF-MS analysis. Results indicated that these proteins were vimentin, cytokeratin 8 and cytokeratin 18, respectively.

To confirm these results we performed a gel shift assay. However, when the antibodies to vimentin, cytokeratins 8 and 18 were allowed to interact with the cytoplasmic extract, and the binding was performed, almost all the radioactivity...
remained in the sample wells and could not enter the gel. Considering that these proteins might be interacting with each other (14), efforts were made to do the immune reactions under denaturing conditions, but still failed (data not shown). Therefore, a ‘target removal’ strategy was used in the identification, i.e. to remove the proteins to be checked from the cellular extract before binding with radiolabeled RNA. Should this strategy work, some bands on the autoradiograph, representing the protein bound by a certain antibody, would become weaker. The result is shown in Figure 4. Although, this is not clear-cut, it is discernible that several bands are weaker compared with the control as well as with other bands, showing the likely positions of the three proteins. Therefore, these three proteins existed in the pool crosslinked to C/EBPβ 3′-UTR RNA. The observation that one antibody often caused weakening of more than one band, was perhaps due to the interactions between those proteins.

**DISCUSSION**

This method was designed to meet our needs, that is, to investigate the proteins specifically interacting with C/EBPβ 3′-UTR RNA. Our group has found that this 3′-UTR suppressed the malignant phenotype of the SMMC7721 human hepatocarcinoma cells (15), indicating that the interactions between this 3′-UTR and *trans*-acting proteins should play some role in the cellular phenotypic reversion. Efforts made to isolate those proteins led to develop this direct affinity method.

By using this method, three proteins interacting with C/EBPβ 3′-UTR RNA were identified. The bands of the proteins captured by the RNA–DNA-glass powder were very reproducible, and their amounts were enough for MS analysis. Moreover, the glass powder sediments very quickly, the washing could be performed without centrifugation.

The key point for success of this method is that the capturing should be done at low temperature (0–4°C). At such temperatures, the amounts of bound proteins were not significantly different with incubations of 4 h or overnight, a sign that the RNA was not degraded markedly, even in the absence of added RNase inhibitor. At higher temperatures (e.g. 25°C), RNase inhibitors (e.g. RNasin) must be added to protect RNA integrity. The ProtectRNA™ RNase inhibitor (Sigma), however, should be used with care, because it may prevent the binding of proteins to RNA.

The main disadvantage of this method is that less abundant or weakly interacting proteins may be more difficult to be captured. Furthermore, for different proteins and RNAs, the composition of the binding buffer may need modification.

In our work, three cytoskeleton proteins were found to interact with the C/EBPβ 3′-UTR RNA. Despite the cytoskeletal proteins being components of the cellular architecture, recent data indicate that the cytoskeleton proteins, especially the intermediate filament components such as cytokeratins, are dynamic and motile within the cell (16). Therefore, we are inclined to think that they may also play the role of *trans*-acting factors, and interact with their target RNAs to perform some functions yet to be determined.

**ACKNOWLEDGEMENTS**

The authors thank Rong Zeng, Xue-Jun Zhang, Mu-Jun Zhao and Kan Liao for the antibodies, and Shashikant Joshi, Mok Lim Sum and Xianhui Wang, Protein and Proteomics Centre, National University of Singapore, for their excellent work in protein MS analysis. This work was supported by the grant 39970172 from State Natural Science Foundation of China and by a grant from Creation Foundation from Shanghai Institutes for Biological Sciences. No conflict of interest.

Funding to pay the Open Access publication charges for this article was provided by The Creation Foundation, Shanghai Institutes for Biological Sciences.

*Conflict of interest statement.* None declared.
REFERENCES