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Research paper

# Laser capture microdissection and single-cell RT-PCR without RNA purification

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## Abstract

Chronic infectious diseases of the central nervous system (CNS) are characterized by intrathecal synthesis of increased amounts of immunoglobulin G (IgG) directed against the agent that causes disease. In other inflammatory CNS diseases such as multiple sclerosis and CNS sarcoid, the targets of the humoral immune response are uncertain. To identify the IgGs expressed by individual CD38+ plasma cells seen in human brain sections, we merged the techniques of laser capture microdissection (LCM) and single-cell RT-PCR. Frozen brain sections from a patient who died of subacute sclerosing panencephalitis (SSPE), were rapidly immunostained and examined by LCM to dissect individual CD38+ cells. After cell lysis, we developed two techniques for reverse-transcription (RT) of unpurified total RNA in the cell lysates. The first method performed repeated and rapid freeze–thawing, followed by centrifugation of the cell lysate into tubes for subsequent RT. The second, more successful method performed RT in situ on detergent-solubilized cells directly on the cap surface; subsequent nested PCR identified heavy and light chain sequences expressed by two-thirds of individually isolated plasma cells. These techniques will streamline the identification of gene expression products in single cells from complex tissues and have the potential to identify IgGs expressed in the CNS of inflammatory diseases of unknown etiology.

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**Keywords:** Laser capture microdissection; Single cell RT-PCR; Plasma cells; Subacute sclerosing panencephalitis; IgG

**Abbreviations:** CNS, central nervous system; IgG, immunoglobulin G; LCM, laser capture microdissection; RT, reverse transcription; SSPE, subacute sclerosing panencephalitis; PCR, polymerase chain reaction; DEPC, diethylpyrocarbonate; PBS, phosphate-buffered saline; HRP, horseradish peroxidase; DAB, diaminobenzidine; cDNA, complementary DNA.

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## 1. Introduction

The development of LCM has enabled genetic analysis of groups of similar cells in cancers (Emmert-Buck et al., 1996; Bonner et al., 1997; Glasow et al., 1998; Specht et al., 2002) and has allowed microarray comparisons in multiple tissues (Luo et al.,

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1999; Fuller et al., 2003; Upson et al., 2004; Player et al., 2004). Additional techniques have extended the potential of LCM. For example, immunohistochemical staining before LCM identified targeted cell types when morphological criteria failed (Fend et al., 1999; Ball et al., 2002; Vincent et al., 2002). The study of smaller numbers of cells often required preamplification of RNA from LCM-captured cells (Goldsworthy et al., 1999; Bonaventure et al., 2002; Mikulowska-Mennis et al., 2002; Ginsberg and Che, 2004) and rapid staining to preserve nucleic acid integrity in order to generate accurate gene expression profiles (Fend et al., 1999; Mojsilovic-Petrovic et al., 2004).

Extension of LCM from small populations of cells to individual cells has relied on PCR amplification of cell DNA (Suarez-Quian et al., 1999; Obiakor et al., 2002; Orba et al., 2003) or the perceived need to purify the very small amount of RNA, approximately 20 pg from a single captured cell for RT and PCR (Jin et al., 2001; Parlato et al., 2002; Michel et al., 2003; Kamme et al., 2004; Lu et al., 2004; Fassunke et al., 2004). Hydraulic microdissection has also been coupled with nested-PCR amplification of genomic DNA to identify sequences in single B cells (Obiakor et al., 2002). To analyze the IgG expressed by individual plasma cells resident in the brains of patients with inflammatory CNS disease, without any delay that might degrade RNA, we optimized rapid protocols to immunostain and microdissect individual CD38+ plasma cells in sections of archived frozen brain from a patient who died of SSPE, a progressive fatal encephalitis caused by measles virus. Herein, we describe two methods to use RT-PCR on lysates of individual plasma cells that enables PCR amplification and analysis of expressed heavy and light chain IgG sequences.

## 2. Materials and methods

### 2.1. Tissue processing and immunohistochemistry

Archival SSPE brain was frozen 6 h after death and stored at  $-70^{\circ}\text{C}$ . Brain was embedded in OCT (Sakura Finetek U.S.A., Inc., Torrance, CA) on liquid nitrogen and equilibrated to  $-30^{\circ}\text{C}$  overnight. Cryostat blades, tools, surfaces, slides and staining vessels were pretreated with RNase Zap (Ambion, Austin

TX), and all solutions were prepared with DEPC-treated water containing 200 units/ml RNase inhibitor (Fisher Scientific, Pittsburgh, PA). Sections ( $7\ \mu\text{m}$ ) were cut at  $-30^{\circ}\text{C}$  and immediately placed onto uncharged “non-plus” slides (Fisher). After acetone fixation for 5 min at  $-20^{\circ}\text{C}$  and treatment with 0.1% hydrogen peroxide for 30 s, slides were rapidly immunostained for CD38+ cells on a pre-chilled steel block maintained at  $0^{\circ}\text{C}$ . Sections were blocked in 10% goat serum in PBS for 2 min, followed by incubation for 10 min with a 1:50 dilution of mouse anti-human CD38 (Dako Cytomation, Carpinteria, CA) in 5% goat serum in PBS. After rinsing in PBS, sections were incubated for 5 min with a 1:100 dilution of HRP-labeled horse-anti-mouse antibody (Vector Labs, Burlingame, CA) in 5% goat serum in PBS. Sections were rinsed in PBS and incubated for 5 min with DAB substrate (Dako), counterstained with filtered hematoxylin (Sigma, St. Louis, MO) for 40 s, dehydrated in a series of nucleic acid-free graded alcohols (HistoGene Kit, Arcturus) (75% for 30 s, 95% for 30 s, 100% for 3 min), and cleared in two changes of xylenes for 2 min each. To maximize RNA preservation, tissue exposure to aqueous solutions was limited to less than 25 min.

### 2.2. Laser capture microdissection

LCM was performed on a PixCell Iie microscope (Arcturus Engineering, Mountain View, CA) with CapSure HS caps (Arcturus) using a pulse power of 70 mW, a  $7.5\text{-}\mu\text{m}$  laser spot diameter, pulse duration of 5 ms and a target voltage of 170 mV. Tissue heterogeneity/cell targeting was visualized by applying xylene ( $10\ \mu\text{l}$ ) to sections. When the cell of interest was identified and xylene had evaporated, the cell was captured. Frequently, cells adjacent to the laser-targeted cell were co-isolated onto the cap; they were removed by pressing the cap surface onto a sterile adhesive-backed paper (Post-it note, 3M, St. Paul, MN). Extraction reservoirs were placed on the caps, and the assemblies were immediately placed in a tray (Arcturus) at  $-20^{\circ}\text{C}$  until completion of LCM.

### 2.3. RT-PCR

Six conditions using three CD38+ cells per cap were tested to determine optimal protocols for RT. In

five of the conditions, cells were lysed and centrifuged into tubes for RT, whereas in the sixth method, RT was performed on the lysate directly on the cap surface. All of the lysis conditions were performed in 21  $\mu$ l 1 $\times$  SuperScript III first-strand RT buffer (Invitrogen, Carlsbad, CA) containing 1% or 3% NP40, which was added to the extraction reservoirs on all caps. The first five lysis conditions were carried out by three freeze–thaw cycles over 20 min with 1% NP40 on dry ice as described (To et al., 1998), or with 1% NP40 at 80 °C, or with 3% NP40 at 42 °C, or with 1% NP40 at 42 °C, or with 3% NP40 at 80 °C (one cap with three cells, one cap with 10 cells) for 20 min. 500- $\mu$ l GeneAmp tubes (Perkin-Elmer, Wellesley, MA) were fitted onto the reservoirs, and the inverted assembly was microcentrifuged at 6000 rpm to collect the lysis products from all caps. The sixth lysis condition was carried out with 21  $\mu$ l 1 $\times$  SuperScript III first-strand RT buffer containing 1% NP40 at 42 °C for 20 min, after which the RT reaction was performed on the cap surface. Twelve to 14 individual plasma cells were captured in each LCM session. Positive and negative control tubes in each RT experiment used 10 pg of total RNA purified from the IgG-expressing human lymphoblastoid B cell line ARH-77 (ATCC #CRL-1621), with and without RT enzyme, respectively.

RT was performed as described (Owens et al., 2003). Briefly, 2  $\mu$ l 5 $\times$  first strand buffer, 0.5  $\mu$ l random hexamers (Invitrogen), 0.5  $\mu$ l of an anti-sense IgG1 constant domain primer (CH5A), 1  $\mu$ l H<sub>2</sub>O and 0.5  $\mu$ l RNase inhibitor (Fisher) were added to each tube or the cap. The tubes, or the cap, were incubated at 65 °C for 3 min, and then at 25 °C for 3 min. To each reaction, 3  $\mu$ l 0.1 M dTT, 1.5  $\mu$ l dNTPs, 0.5  $\mu$ l RNase inhibitor, and 0.5  $\mu$ l SuperScript III (Invitrogen) were added, followed by incubation at 37 °C for 60 min, and at 70 °C for 10 min. The product of the RT reaction performed on the cap was centrifuged into a tube, and 5- $\mu$ l aliquots from all reactions were subjected to nested PCR amplification of IgG heavy or light chain sequences as described (Owens et al., 2003). We then compared the freeze–thaw method with performance of RT on the cap surface, using six LCM caps per method and one or three cells per cap. PCR products were resolved on 2% agarose gels. Appropriately sized bands were excised and DNA was purified using the MinElute Gel Extraction kit (Qiagen, Valen-

cia, CA). The IgG amplification products were confirmed by sequencing at the University of Colorado Health Sciences Cancer Center DNA Analysis and Sequencing Core (Denver, CO), and analyzed in DNAsis Max (Miraibio Inc, Alameda, CA). After each experiment, all caps were stored at –80 °C. Caps were thawed and RT was repeated directly on the cap surface. Nested PCR amplification of the cDNA was also performed for kappa and lambda light chains as described (Owens et al., 2003).

### 3. Results

All steps were optimized to enhance LCM and RT-PCR of single immunostained cells. Several features of slide preparation before immunostaining were critical. First, frozen SSPE brain sections were prepared under RNase-free conditions. Besides the normal precautions of wearing gloves at all times and using RNase-free (DEPC-treated) H<sub>2</sub>O in all solutions, the cryostat blade, microscope slides and staining vessels were all routinely treated with the RNase inhibitor RNase Zap after two early attempts failed to obtain RT-PCR amplifiable material from sections cut on new slides with a new blade. Second, slides sectioned before fixation were maintained at temperatures below –20 °C to ensure minimal adhesion of the section to the slide for successful LCM; three sessions at the LCM microscope in which sectioned slides were briefly thawed before fixation at –20 °C did not successfully remove cells from the section. Third, the use of non-plus slides was important for microdissection of cells from the section; repeated attempts to microdissect from immunostained brain sections on charged (+) slides resulted in lifting of only 10–20% of targeted cells from the slide.

Freshly cut sections were acetone-fixed at –20 °C, briefly treated with 0.1% hydrogen peroxide and immunostained. Mouse anti-CD38 antibody identified plasma cells, which were well-separated (Fig. 1a). To ensure RNA integrity, exposure to aqueous solutions during staining was limited to 25 min, and RNase inhibitor was added to every buffer. Peroxidase-conjugated horse-anti-mouse IgG antibody and DAB were used to visualize the stained cells. Two early attempts to use alkaline-phosphatase-conjugated anti-mouse IgG and New Fuschin substrate were unsuccess-

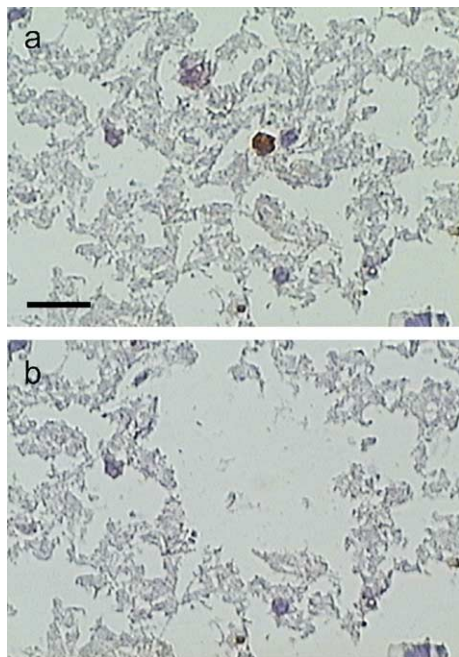


Fig. 1. Laser capture microdissection of CD38+ plasma cells. (a) A single plasma cell identified by DAB staining (brown) for CD38. (b) The stained cell and adjacent unstained cells were successfully removed by microdissection. Bar=20  $\mu$ m.

successful when the New Fuschin disappeared after xylene treatment. Use of DAB provided permanent staining. Pretreatment of the slides with hydrogen peroxide dramatically reduced background staining but was limited to 30 s, since in two earlier experiments, higher concentrations or longer incubations with hydrogen peroxide damaged tissue morphology. After hematoxylin counterstaining, sections were dehydrated with graded alcohols and xylene before LCM. Complete dehydration of the sections was achieved by including molecular sieves in the 100% ethanol used in the final ethanol incubation, for which the HistoGene kit (Arcturus) is ideally designed. Complete dehydration was important to the dissection of cells during LCM and was improved by extending the 100% ethanol stage to 3 min. Slides could be maintained in xylene for several days before successful LCM, but RNA integrity was compromised by the prolonged slide storage (data not shown).

LCM was used to microdissect individual CD38+ plasma cells onto separate caps (Fig. 1). A droplet of xylene was first added to the dehydrated brain section to restore color balance and visualize the stained cells.

However, complete evaporation of the xylene was necessary before positioning the extraction cap over the targeted cell so the laser-pulsed cells could adhere to the cap (Fig. 1b). When surrounding cells were co-dissected with the targeted cell, the cap surface was gently pressed onto an adhesive-backed paper to remove adjacent cells. Extraction reservoirs were added to the caps and the assemblies were stored at  $-20^{\circ}\text{C}$  until 12 cells were individually obtained onto caps. The 7.5  $\mu$ m laser spot size was optimal for lifting the fewest cells from brain sections. In general, a lower pulse duration and higher power setting enabled a more precise capture.

After the targeted cells were transferred to the caps, standard methods for RNA extraction and purification would have been both labor-intensive and costly, involving additional incubation times and treatments of more than 100 caps with extraction buffers before RT. We therefore compared various methods for rapid and efficient RT, with the aims of performing RT-PCR using the unfractionated cell lysate and of testing methods to remove the lysate from caps before RT or to enable RT directly on the cap surface without prior extraction. Six strategies were tested: lysis by three freeze–thaw cycles (To et al., 1998); lysis at  $80^{\circ}\text{C}$ ; 1% or 3% NP40; 3% NP40 and lysis at  $80^{\circ}\text{C}$  (from one cap with three cells, and from one cap with 10 cells); and performing RT on the cap surface after 1% NP40 treatment. Two of these strategies, i.e., lysis by rapid freeze–thaw cycles followed by centrifugation into a reaction tube, and conducting RT on the cap surface after incubation with 1% NP40 at  $42^{\circ}\text{C}$ , yielded products after nested PCR of IgG heavy chain variable regions (Fig. 2). RT controls were always performed in parallel tubes with 10  $\mu$ g of total RNA purified from the IgG-expressing ARH-77 lymphoma cells.

Next, we directly compared the two successful methods: freeze–thawing to remove the cell lysate from the cap before performing RT; and performing RT on the lysate in situ, directly on the cap surface. Each method was tested on four caps containing one immunostained CD38+ cell per cap, and on two caps containing three stained cells per cap. The caps for both methods were collected randomly to ensure that the storage time of each cap did not influence the success of RT performed after all 12 caps had been obtained. Four of six samples processed on the cap

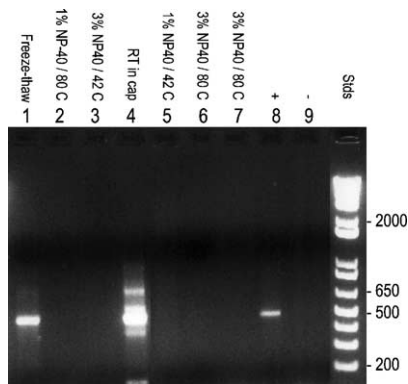


Fig. 2. Nested PCR of heavy chain IgG after preparation of RNA for RT by different methods. Six conditions (see Materials and methods) were used before RT of total RNA from microdissected cells. Only the freeze–thaw method (lane 1) and RT performed on the cap surface (lane 4) yielded positive PCR products. Lane 8 shows an RT-positive control with RNA from an IgG-expressing cell line with enzyme; lane 9 shows an RT-negative control in which enzyme was omitted from the RT reaction. Molecular size standards in bp are shown on the right.

successfully amplified HC products, while one of six samples from the freeze–thaw cycles yielded only barely detectible products; the remaining caps were negative (Fig. 3). Three cells per cap did not increase

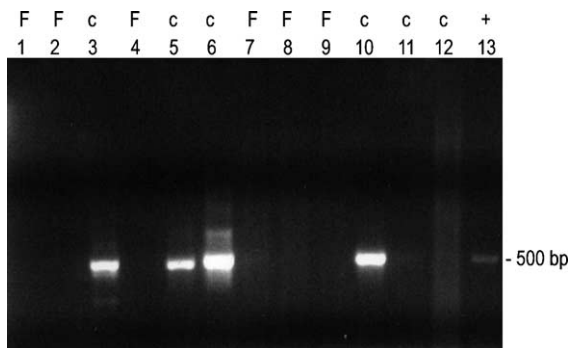


Fig. 3. Nested PCR comparing the freeze–thaw method to performing RT on the cap surface. PCR was performed on reverse-transcribed cDNA after freeze–thawing one cell per cap (lanes 1, 2, 7, and 9) or three cells per cap (lanes 4 and 8), or after performing RT on cap surfaces containing one cell (lanes 3, 6, 10, 11) or three cells (lanes 5 and 12). Performance of RT on the cap surface yielded PCR products in four of six caps, including three caps containing single CD38<sup>+</sup> cells (lanes 3, 5, 6, and 10). Freeze–thawing of cells yielded one faint product (lane 7). F indicates the freeze–thaw method; C indicates that RT was performed on the cap surface; “+” indicates control cDNA reverse-transcribed from the IgG-expressing cell line (lane 13). Approximate size of the amplification product in bp is indicated on the right.

the amount of PCR amplification product over that observed with one cell. Finally, the twelve caps used for this comparative analysis were frozen, and RT was repeated on all cap surfaces the next day (Fig. 4). This produced additional PCR products from caps that were originally positive, including an intense PCR product from the freeze–thaw cap that was originally only weakly positive, and two positive PCR products from caps that were previously negative. In subsequent experiments, repeated RT on refrozen caps routinely revealed several more positives than were originally identified (data not shown).

These tests resulted in a protocol that was repeated on more than 100 caps, in which RT was performed on individual CD38<sup>+</sup> cells on the cap surface, before centrifuging the RT products into a tube. Judged by successful PCR-amplification of IgG heavy chains and light chains, SuperScript III reverse transcriptase routinely synthesized cDNA from two-thirds of approximately 120 cap surfaces containing single CD38<sup>+</sup> plasma cells. A typical experiment from one LCM session showed that after RT was performed on the surface of 13 caps, nested PCR of heavy chain IgG sequences yielded ten positive products (Fig. 5a). Those ten RT products that yielded heavy chain sequences were also subjected to nested PCR for

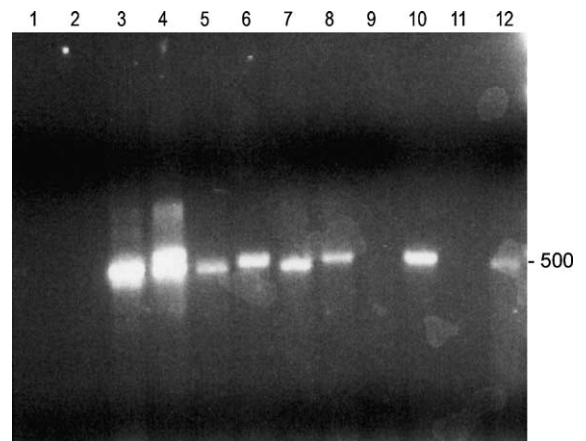


Fig. 4. Nested PCR of additional RT after overnight freeze–thaw of caps. Twelve caps from Fig. 3 were frozen overnight at  $-80^{\circ}\text{C}$ , and RT was repeated on all cap surfaces. Eight of the twelve caps yielded PCR products, including the five that were previously observed (lanes 3, 5, 6, 7, and 10). RT on the caps also revealed additional products in three of five previously negative caps (lanes 4, 8, and 12). Approximate size of the amplification product in bp is indicated on the right.

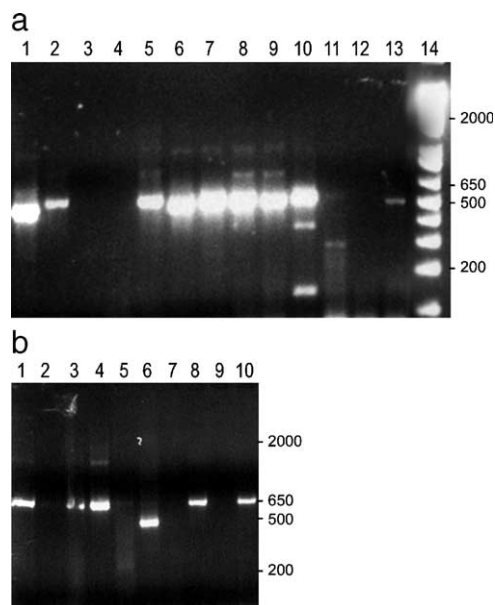


Fig. 5. Nested PCR of individual LCM-captured cells. (a) RT was performed on cap surfaces containing single CD38<sup>+</sup> cells, followed by PCR amplification using IgG heavy chain primers. Ten of the 13 caps yielded heavy chain products (lanes 1, 2, 5–11 and 13). Molecular size markers in bp are indicated on the right (lane 14). (b) cDNA from the ten caps that amplified heavy chain sequences were further subjected to nested PCR amplification of kappa light chains, resulting in the identification of seven kappa light chain products (lanes 1, 3, 4–6, 8 and 10). Molecular size markers in bp are indicated on the right.

kappa light chain sequences, and amplified seven appropriately sized PCR products (Fig. 5b). Early experiments to detect actin PCR products after these protocols did not detect larger numbers of successful amplification products, suggesting that the negatives we encountered were not simply IgG-negative cells. When the SuperScript III enzyme was omitted from caps or from 11 negative control reactions with B lymphoma cell RNA, amplified IgG sequences were never observed by nested PCR (data not shown).

#### 4. Discussion

We have described protocols optimized to: 1) rapidly immunostain archival brain sections and identify individual (CD38<sup>+</sup>) plasma cells; 2) capture individual CD38<sup>+</sup> cells by LCM; and 3) perform single-cell RT-PCR on the expressed Ig transcripts for sequence

analysis. The most successful strategy microdissected single immunostained CD38<sup>+</sup> plasma cells from frozen brain sections by LCM, and after lysis, allowed RT in situ on the cap surface without RNA purification. Using this strategy, more than 100 individual CD38<sup>+</sup> cells were rapidly isolated from sections of an SSPE brain and analyzed for individually expressed IgG antibodies (Burgoon et al., *PNAS*, in press). Immunostaining protocols before LCM must be conducted quickly to preserve RNA (Fend et al., 1999; Burgess and McParland, 2002; Mojsilovic-Petrovic et al., 2004). However, since LCM was first described, few studies have examined RNA expression in individual cells from human post-mortem CNS (Bahn et al., 2001; Lu et al., 2004), likely reflecting the challenge of isolating single cells from a complex tissue and the subsequent purification of 10–20 pg of total RNA from each cell for analysis (Michel et al., 2003; Parlato et al., 2002). One advantage of our study is the need to isolate only small clusters of 5–10 cells to analyze single immunostained cells contained therein, since the plasma cell is the only one that expresses IgG. Several caps contained multiple amplified IgG sequences, which may have resulted from the simultaneous expression of two IgG sequences by a single cell as may occur with receptor editing (Kouskoff and Nemazee, 2001), or from expression of a nearby CD38-negative B cell that was accidentally captured with the CD38<sup>+</sup> plasma cell. Double-staining protocols for CD38<sup>+</sup> plasma cells and CD19<sup>+</sup> B cells might reduce the frequency of capturing multiple IgG-expressing cells.

Previous studies have determined that the duration of the LCM process may adversely affect RNA integrity (Michel et al., 2003; Nawshad et al., 2004), and that mRNA quality is better in frozen sections than paraffin-embedded tissues (Fend and Raffeld, 2000). Our methods described herein streamline the process to analyze RNA contained in archived frozen brain tissue without purification or further risk of degradation. Features of specific tissues, such as low pH or high concentrations of degradative enzymes, may influence RNA stability throughout the staining or LCM procedures (Kingsbury et al., 1995; Harrison et al., 1995; Bahn et al., 2001). Tissue treatment with 30% sucrose has also been suggested to preserve morphology and RNA integrity (Parlato et al., 2002). The agonal status (particularly hypoxia in prolonged ago-

nal states) and storage temperature of tissue are also important (Bahn et al., 2001), and might be further inducement for speed and cold temperatures. Cresyl violet, thionin, hematoxylin and eosin, but not silver stain or acridine orange, have been recommended for use in immunostaining (Ginsberg et al., 2004). Other influences on the success of RT-PCR suggest the desirability of precipitative fixatives such as ethanol and acetone rather than cross-linking fixatives such as formalin (Goldsworthy et al., 1999). We have incorporated many of these earlier findings into studies of the IgG repertoire expressed by single plasma cells in frozen, archived SSPE brain tissue.

Earlier reports have suggested that staining times in aqueous media should be limited to less than 20 min (Fend et al., 1999; Mojsilovic-Petrovic et al., 2004). The staining protocol used here is completed in less than 25 min and the total time required from tissue sectioning until cDNA production is less than 4 h. Careful RNase-free conditions throughout the entire procedure, conducting immunostaining on ice, and the inclusion of RNase inhibitor at every step are logical precautions to preserve RNA. Allowing slides to thaw during sectioning also prevented the dissection of cells, possibly due to the activation of endogenous glycolases, which form a strong bond with glass when hydrated. Sections prepared for LCM were maintained at  $-30^{\circ}\text{C}$  until fixation in  $-20^{\circ}\text{C}$  acetone. Essential to capturing cells from tissue sections was complete dehydration after immunostaining, in agreement with earlier studies (Fend et al., 1999; Ball et al., 2002). The use of non-plus slides was helpful since frozen tissue adhered too strongly to charged slides for effective laser dissection. This application must be carefully balanced against the possibility of picking up additional cells with the targeted cell when tissue adheres loosely to the slide. An effective method to remove extraneous material after LCM was to gently press the cap surface against a sterile, adhesive-backed paper such as a "Post-It note" (3M). Alternatively, prep strips provided by Arcturus may be applied to the cap. Only the cell area directly below the laser pulse remained visibly attached to the thermoplastic coating on the cap surface after application of the paper (data not shown).

LCM was most effective when tissue was sectioned on the same day as cell capture (LCM on sections prepared the previous day lifted cells, but

RT-PCR was unsuccessful) (data not shown). After cell capture by LCM, RNA purification or extraction was not desirable due to: (1) the limited amount of RNA contained on each cap; (2) the number of samples to be individually treated and analyzed; (3) the time required to treat the greater number of single-cell samples; and (4) the cost involved in hundreds of RNA purifications needed for a repertoire of individual cells. Furthermore, extraction and purification protocols, both customized and those outlined in commercial kits, are intended for much larger amounts of RNA. Therefore, we sought to perform RT-PCR directly on cell lysate on the cap surfaces, without prior RNA purification. Although this method was superior to freeze-thawing under the conditions analyzed, repeating RT on refrozen caps may be useful to obtain additional PCR products on caps that were previously negative and may even supplement cDNA recovered from the positive caps. This accelerated method probably prevented RNA degradation or loss that occurs during purification steps. Although RNase-free DNase may be added to the cell lysis step to ensure amplification only from reverse-transcribed cDNA, we did not treat samples in this study because genomic DNA could not contribute to our nested RT-PCR analysis of IgG sequences. The PCR primers that we used would have amplified a different-sized product from the recombined genomic DNA in the plasma cells than from the transcripts (Abbas and Lichtman, 2003). Furthermore, surrounding cells that were co-isolated but were not in the B cell lineage would not contain a recombined IgG variable region in their genomes. Finally, when RT was not added to control caps, PCR products were never observed.

Overall, we have described techniques that allow genetic analysis of single plasma cells in the complex milieu of the brain. Although it remains difficult to isolate a single cell by LCM reliably, such analysis is possible in well-defined circumstances after immunostaining single, well-separated cells surrounded by unstained tissue. The presented features critical to staining, LCM and RT procedures allowed successful identification of IgG expression in a repertoire of plasma cells in an efficient and cost-effective manner. These IgG sequences can then be functionally characterized after cloning into suitable expression vectors to generate recombinant immunoglobulins (Burgoon

et al., PNAS, in press). These techniques will permit the application of LCM to gene expression analysis in single cells without the need for RNA purification.

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