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Gene Therapy

Volume 1 • Number 4 • July 1994

Contents

Editorial

News and comment

Review

223 *Strategies to achieve targeted gene delivery via the receptor-mediated endocytosis pathway*
SI Michael & DT Curiel

Papers

233 *Tumor cell bystander killing in colonic carcinoma utilizing the Escherichia coli DeoD gene to generate toxic purines*
EJ Sorscher, S Peng, Z Bebok, PW Allan, LL Bennett Jr & WB Parker

239 *Lipopolysaccharide is a frequent contaminant of plasmid DNA preparations and can be toxic to primary human cells in the presence of adenovirus*
M Cohen, A Baker, M Saltik, E Wagner & M Buschle

247 *Gene therapy for phenylketonuria: phenotypic correction in a genetically deficient mouse model by adenovirus-mediated hepatic gene transfer*

B Fang, RC Eisensmith, XHC Li, MJ Finegold, A Shedlovsky, W Dove & SLC Woo

255 *Receptor-mediated gene delivery employing lectin-binding specificity*
RK Batra, F Wang-Johanning, E Wagner, RI Garver, Jr & DT Curiel

261 *Expression of the human glucocerebrosidase and arylsulfatase A genes in murine and patient primary fibroblasts transduced by an adenovirus vector*
J-F Wei, F-S Wei, RJ Samulski & JA Barranger

269 *Gene therapy for Lewis lung carcinoma with tumor necrosis factor and interleukin 2 cDNAs co-transfected subline*
T Ohira, Y Ohe, Y Heike, ER Podack, KJ Olsen, K Nishio, M Nishio, Y Miyahara, Y Funayama, H Ogasawara, H Arioka, H Kato & N Sajio

Calendar

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Lipopolysaccharide is a frequent contaminant of plasmid DNA preparations and can be toxic to primary human cells in the presence of adenovirus

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Endotoxin (lipopolysaccharide, LPS) is commonly found as a contaminant in plasmid DNA preparations. We demonstrate here that the quantities of LPS typically contaminating DNA preparations can generate a toxicity to primary cells (primary human skin fibroblasts, primary human melanoma cells) in the presence of entry-competent adenovirus particles. Toxicity

can be observed with as little as 100 ng/ml free LPS or 100 pg/ml LPS when the LPS is assembled into polylysine/adenovirus complexes. Simple and effective methods of removing the contaminating LPS using either a polymyxin B resin or Triton X-114 extraction are described. Treatment of DNA samples to remove LPS eliminates the toxicity to primary cells.

Introduction

Endotoxin (lipopolysaccharide, LPS) is a major component of the Gram-negative bacterial cell wall. The LPS monomer is a diglucosamine diphosphate bearing six lipid moieties, linked to either two or three 2-keto-3-deoxyoctonate (KDO) residues linked to an inner core of carbohydrate residues linked to the outer (O-antigen) carbohydrate residues (see [1, 2] for details). The LPS molecule is an extremely potent stimulator of the mammalian immune system and a number of mechanisms exist to detect LPS and to respond to the presence of either this molecule or Gram-negative bacteria [3–12]. LPS is a common contaminant of plasmid DNA preparations grown in *Escherichia coli*. Up to 40% of the surface LPS of *E. coli* can be released by treating intact bacteria with Tris/EDTA solutions [1, 13], conditions that are normally used in the initial steps of preparing plasmid DNA. The negative charges associated with the lipid A and inner core of LPS cause the LPS molecule to behave like DNA on anion exchange chromatographic resins. The large size of the micellar form of LPS causes the molecule to behave like a large DNA molecule on size exclusion resins. The density of LPS in CsCl is similar to that of plasmid–EtBr complexes (1.37 g/ml versus 1.5 g/ml), so that CsCl-banded DNA can be easily contaminated. We document here a toxicity in primary human skin fibroblasts as well as primary human melanoma cells exposed to LPS-containing DNA or pure LPS in the presence of adenovirus. Toxicity appears at levels of 100 ng/ml free LPS or 100 pg/ml when the LPS is assembled into polylysine/adenovirus complexes. Methods to remove the contaminating LPS and eliminate the toxicity are described.

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Results

Fractionation of CsCl gradient to show position of LPS relative to DNA

The plasmid pCLuc was grown in *E. coli* DH5α in the presence of 100 µg/ml ampicillin and a cleared lysate of the bacteria was prepared and fractionated by CsCl density gradient centrifugation (see Materials and methods). The gradient was subsequently fractionated (2 ml fractions) and fractions from the gradient (2 ml) were assayed for plasmid DNA content (A_{260} and gel electrophoresis) and LPS content (*Limulus* assay). The results are shown in Figure 1. We find that the original cleared lysate contains LPS at more than 500 000 endotoxin units (EU)/ml (>500 µg/ml; results not

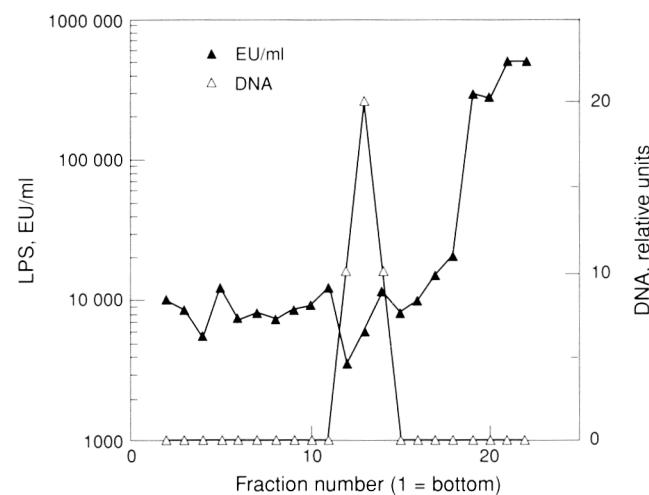


Figure 1 Location of LPS in CsCl density gradient purification of plasmid DNA. A cleared lysate of *E. coli* bearing an ampicillin resistance plasmid was prepared and subjected to CsCl density gradient centrifugation in the presence of ethidium bromide as described in the Materials and methods. After 18 h at 200 000 $\times g$ (Beckman VT150 rotor) the gradient was partitioned into 22 fractions. Fractions were analyzed for plasmid DNA content by agarose gel electrophoresis and for LPS content by *limulus* assay.

shown). This is not surprising as Tris/EDTA treatment of Gram-negative bacteria releases large amounts of LPS [1, 13]. After a single fractionation on a CsCl gradient, we find that the plasmid DNA, as expected, bands near the middle of the gradient (centered around fraction 14) while the bulk of the LPS is present in fractions near the top of the gradient. Substantial amounts of LPS, however, are distributed throughout the interior of the gradient so that the plasmid DNA-bearing fractions still contain as much as 10 µg/ml LPS, accounting for the LPS content of CsCl-purified DNA samples (see Table 1).

Table 1 LPS content of DNA preparations

Method	No. of samples	Mean LPS content (EU/6 µg DNA)	Range (EU/6 µg DNA)
DNA preparation			
CsCl	13	4.3	0.6 – >25
Qiagen	5	10.3	3.8 – >25
Nucleobond	7	20.2	0.5 – >25
Treatment to remove LPS			
CsCl/Triton X-114	7	0.09	0.05 – 0.195
Qiagen/Triton X-114	4	0.08	0.016 – 0.2
Nucleobond/polymyxin	7	0.02	0.001 – 0.075

Note: 1 EU (endotoxin unit) ≈ 1 ng LPS

LPS content of DNA prepared by different methods
 Column chromatographic methods of purifying plasmid DNA fractionate the DNA based largely on its charge density. The LPS molecule possesses a high negative charge density due to the presence of phosphate groups on the lipid A moiety as well as phosphate and carboxyl groups on the octolonic acid sugar groups (reviewed in [1, 2]). Because of the negative charge density of LPS as well as the molecule's ability to assemble into high molecular weight micelles, the LPS has a structure that shares features with the chemistry and size of plasmid DNA. Ion-exchange resins used for purifying plasmid DNA (e.g. Qiagen, Nucleobond) generate plasmid preparations that contain significant quantities of LPS (see Table 1). Like DNA, LPS precipitates from ethanol and isopropanol solutions. Furthermore, because the LPS is not detected by either ethidium bromide staining in agarose electrophoresis or by absorbance at 260 nm, the presence of LPS can be largely undetected in DNA preparations. Table 1 lists the LPS contents of plasmid DNA prepared by a variety of methods.

We have subjected three types of DNA preparations to two methods of LPS removal. A simple and effective method of LPS removal employs the detergent Triton X-114. At temperatures below its cloud point of 20°C, Triton X-114 is miscible with aqueous solutions; at temperatures above 20°C, the detergent partitions into a separate phase [14]. This phase partitioning can be used to extract the lipophilic LPS molecule from aqueous protein solutions [15] as well as DNA preparations [16]. An alternative LPS removal method employs polymyxin B, a cyclic fungal peptide that binds the lipid A/KDO component of LPS with high affinity [9, 17, 18]. Chromatographic resins bearing this peptide can be used to remove LPS from

protein or DNA solutions. We obtain similar LPS removal success with either method (Table 1). Both the Triton extraction method and the polymyxin resin generate DNA preparations with comparable absence of LPS (<0.1 EU/6 µg DNA). We have occasionally encountered difficulty using either method to remove the LPS that contaminates CsCl purified DNA. It is possible that the CsCl purification enriches for a form of LPS that does not avidly bind either the detergent phase or the polymyxin. Sodium dodecylsulfate/polyacrylamide gel electrophoresis (SDS/PAGE) resolution of DNA samples stained with an LPS-specific silver stain [19, 20] demonstrates that the form of LPS most frequently found contaminating DNA preparations is a higher molecular weight, heterogeneous form of LPS consistent with the smooth LPS phenotype of the *E. coli* strains used to propagate the plasmid DNA (results not shown).

Toxicity of LPS to primary cells in the presence of adenovirus

In an initial study to determine if LPS could generate a toxicity to mammalian cells, cultures of primary human melanoma cells were exposed to purified LPS samples (from either *E. coli* 0111:B4 or *Salmonella minnesota*) in the absence or presence of psoralen-inactivated adenovirus dl1014. After 48 h, the cultures were processed to determine surviving cells by washing the cell monolayers, fixing with formaldehyde and staining with crystal violet (Figure 2) or incubating with the viability stain MTT (3-[4,5-dimethylthiazol-2-yl]-2,5-diphenyltetrazolium) (Figure 3).

We find that incubation of primary cells with LPS alone (up to 250 µg/ml) or psoralen-inactivated adenovirus alone (up to 10⁵ virus particles/cell) has no toxic effect (Figure 2a). However, combined treatment of these cells with mature adenovirus (10⁵ virus particles/cell) plus LPS (down to 50 ng/ml) kills these cultures, as measured by crystal violet staining (Figure 2a).

Purified preparations of immature adenovirus particles (with a density of 1.31 g/cm³) possess the full complement of outer capsid proteins yet are defective at cellular entry and cytoplasmic release of co-endocytosed material [21, 22] (M.C. and M.S., unpublished results). These immature adenovirus particles are an assembly intermediate, are deficient for viral DNA (hence their lighter density) and are inactive in the pH-dependent membrane disruption reaction that is required for adenovirus entry into host cells (M.C. and M.S., unpublished results). Exposure to LPS in the presence of immature adenovirus particles does not result in cellular toxicity (Figure 2b), demonstrating that cytoplasmic entry of the adenovirus (and possibly co-entry of LPS) is required for toxicity.

When the viability stain MTT is used to measure toxicity in the presence of mature virus particles and LPS, similar results are obtained (Figure 3). No toxicity is apparent with LPS alone, a slight decline in viability is observed with adenovirus alone (10 000 or 100 000 virus particles per cell) but a severe decline in viability is observed with the higher virus input in the presence of LPS (Figure 3).

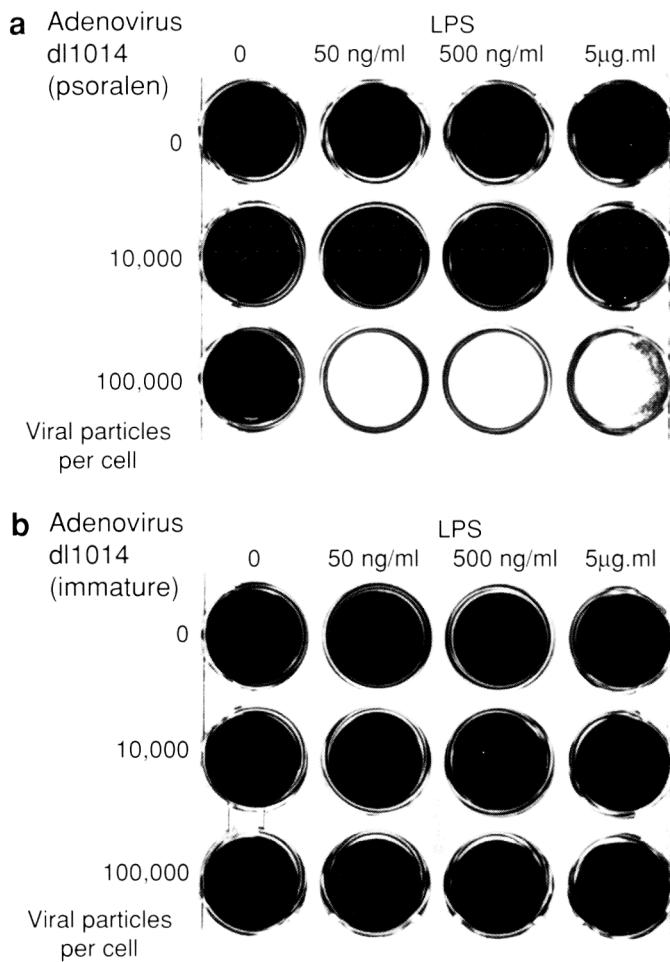


Figure 2 LPS is toxic to primary human melanoma cells in the presence of mature but not immature adenovirus particles. Primary human melanoma cells (isolate H 226) were plated at 40 000 cells per well of a 24-well dish. The cells were exposed to the indicated quantities of LPS (*S. minnesota* wild type) and adenovirus [(a) dl1014, psoralen-inactivated; (b) dl1014, light, 1.31 g/cm² particles] in 1 ml of DMEM/2% horse serum for 2 h at 37°C, after which 1 ml of RPMI/10% FCS were added. After 48 h, the cell samples were washed once with HBS, fixed in formaldehyde and stained with crystal violet (see Materials and methods).

Similar toxicities are observed with *E. coli* 0111:B4 LPS (smooth), *S. minnesota* wild type LPS (smooth) and *S. minnesota* Re 595 LPS (rough E; results not shown). The virus and LPS must be exposed to cells simultaneously to generate the toxicity. Exposure to virus or LPS alone for 2 h followed by washing and then exposure to the second component does not result in toxicity (results not shown). The toxicity does not appear to involve adenovirus gene expression. No viral gene expression can be detected with psoralen-inactivated adenovirus dl1014 (results not shown) and similar levels of LPS toxicity are observed with either psoralen-inactivated adenovirus dl1014 or non-inactivated dl1014. Although we have not yet performed an exhaustive survey, the toxic response appears to be a function of primary cell cultures and the toxic response does not occur with established cell lines (e.g. HeLa, Vero, 3T3 or K562). In addition, there appear to be species differences in the response to LPS/adenovirus toxicity. We have found that primary mouse muscle fibroblasts are

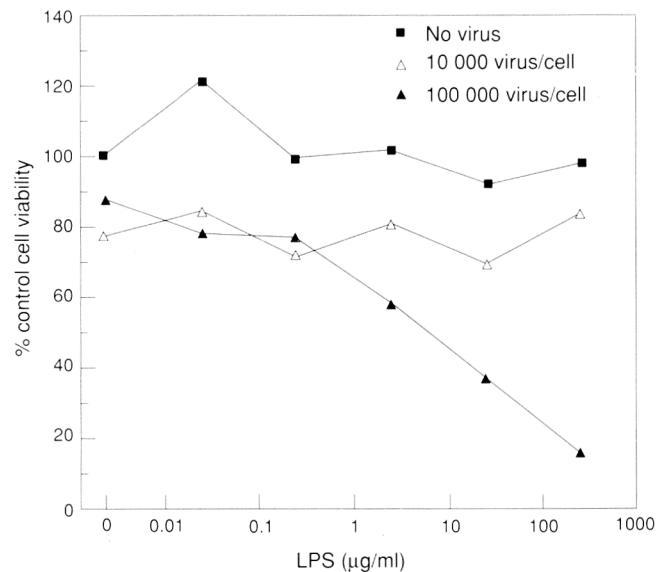


Figure 3 Toxicity to primary human melanoma cells in the presence of free LPS and adenovirus. Primary human melanoma cells (isolate H 225) were plated at 4000 cells per well of a 96-well dish. Triplicate samples (in 100 μl of DMEM, 2% HS) were incubated with the indicated quantity of LPS (*S. minnesota* wild type) in either the absence of virus, or the presence of 10 000 or 100 000 particles/cell of adenovirus dl1014 (psoralen inactivated). After 2 h, 100 μl of RPMI 1640/10% FCS was added to each well; 48 h later the medium was replaced with 100 μl of RPMI 1640/10% FCS plus 15 μl of MTT reagent (Promega), processed according to the manufacturer's directions and the absorbance at 540 nm (subtracting a background at 620 nm) was measured with an ELISA plate reader. Each point in the graph represents the average of three independent samples.

sensitive to the toxicity but primary chicken embryo fibroblasts and primary dog muscle fibroblasts are not sensitive.

Purification of DNA eliminates toxicity

Several preparations of pGS-hIL-2, a plasmid bearing the human interleukin 2 (IL-2) gene driven by the CMV promoter, were purified with a modified Nucleobond protocol (see Materials and methods) and the LPS content was found to range from 0.5 to >25 EU/6 μg DNA (Figure 4). Each plasmid preparation was subjected to polymyxin B chromatography or Triton X-114 extraction to remove LPS. After treatment, all samples contained less than 0.1 EU/6 μg DNA. The original and the purified DNA preparations were then assembled into adenovirus streptavidin-polylysine-(StrpL)-transferrin-polylysine (TfpL) complexes and transfected into primary human melanoma cells. The culture supernatants at 24–48 h post-transfection were harvested and the IL-2 content was measured by enzyme-linked immunosorbent assay (ELISA). In all cases we find that LPS removal leads to increased gene expression (from 3–26-fold; Figure 4). From the morphology of the transfected cultures at 48 h post-transfection, cellular toxicity could easily account for the poor IL-2 expression from the LPS-bearing DNA samples.

LPS assembled into polylysine complexes is more toxic than free LPS

The observation of toxicity that initiated this investigation was due to LPS contamination of DNA

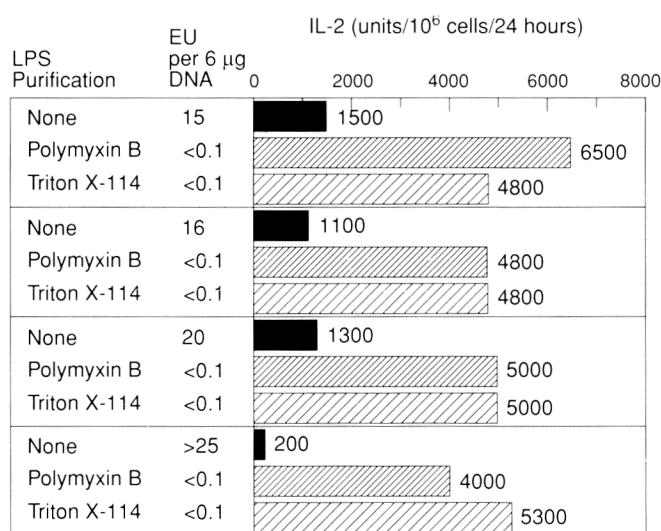


Figure 4 Primary human melanoma cells (isolate H 225, 2×10^5 cells/6 cm dish) were transfected with 6 µg of various preparations of the human IL-2 construct pGS-hIL-2tet assembled into biotinylated-adenovirus-StrpL-TfpL-DNA complexes as described in Materials and methods. The endotoxin levels of the plasmids before purification are indicated. After passage through polymyxin resin or extraction with Triton X-114 all preparations contained less than 0.1 EU/6 µg DNA. The secreted IL-2 levels from culture supernatants 24–48 h post-transfection were measured by ELISA and are expressed as units/10⁶ cells/24 h.

which was seldom more than 5–10 EU/6 µg DNA (comparable to 5–10 ng of LPS, used in 2–5 ml of culture medium = 1–5 ng/ml). However, the toxicity demonstrated with the addition of pure LPS to cell cultures requires the presence of >50 ng/ml of pure LPS for toxicity measured by crystal violet staining (Figure 2) or >5 µg/ml LPS for toxicity by MTT reduction (Figure 3). Simple charge considerations suggest that the negatively charged LPS molecule could interact with the positively charged polylysine of our transfection complexes. We considered the possibility that polylysine-LPS complexes, bound to adenovirus might be present in transfection complexes prepared with LPS-contaminated DNA preparations and the loading of LPS onto polylysine-adenovirus complexes might enhance the cellular interactions of the LPS molecule and increase the toxicity of the LPS molecule. We tested this idea directly in the following experiment.

Standard biotinylated-adenovirus-StrpL-TfpL-DNA complexes were prepared. However, the DNA used (Triton X-114 extracted to remove LPS) was premixed with known quantities of pure LPS prior to the assembly of the polylysine complexes. The complexes were then supplied to primary fibroblasts and primary melanoma cells and the resulting toxicity was quantitated by MTT assay (Figure 5). We begin to observe toxicity at concentrations of LPS of 5 ng/ml, obtained with adenovirus/polylysine/DNA complexes containing as little as 10 ng of LPS/6 µg DNA (Figure 5). These are concentrations comparable to those that produce toxicity with contaminated DNA and are toxicities at 10–1000 times lower concentrations than the conditions that generate toxicity with free LPS and adenovirus mixtures.

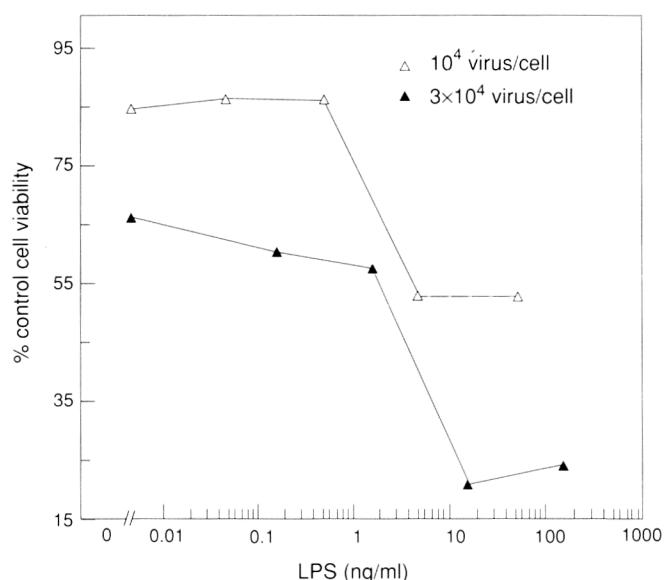


Figure 5 Toxicity generated by premixing LPS and DNA before assembly into polylysine-adenovirus complexes. Primary human skin fibroblasts (passage 8) were plated at 2000 cells per well of a 96-well dish. Samples (in 100 µl of DMEM, 2% HS) were incubated with the indicated quantity of LPS (*S. minnesota* wild type) in the presence of 10 000 or 30 000 particles/cell of adenovirus dl1014 (psoralen inactivated)/DNA complexes. LPS samples were premixed with LPS-free plasmid DNA and assembled into adenovirus-StrpL-DNA-TfpL complexes as described in Materials and methods. After 2 h incubation with the LPS-virus-DNA complexes, an additional 150 µl of DMEM/10% FCS was added to each well; 48 h later the medium was replaced with 100 µl of DMEM/10% FCS plus 15 µl of MTT reagent (Promega) and processed for MTT reduction as described in the legend to Figure 3. Each point in the graph represents the average of three independent samples.

Including purified LPS in DNA assembled into adenovirus transfection complexes results in loss of gene expression

We have shown that removing the LPS from contaminated IL-2 DNA results in an improvement of gene expression, most likely due to an elimination of toxicity (Figure 4). Furthermore, addition of LPS at typical contamination levels generates toxicity when the LPS is premixed with DNA before assembly into polylysine-adenovirus complexes (Figure 5). To establish that addition of pure LPS can result in a decline in gene expression, an LPS-free preparation of the luciferase-encoding plasmid pCLuc was premixed with known quantities of *E. coli* LPS and assembled into adenovirus-polylysine complexes. Aliquots of the complexes were then supplied to primary fibroblasts and 48 h later extracts were prepared and luciferase gene expression was measured (Figure 6).

We find that the inclusion of as little as 10 ng of LPS/6 µg DNA results in a substantial loss in recovered luciferase activity (compare Figure 6, lane 1, no LPS, with lane 2, 10 ng LPS). This quantity of LPS in the DNA samples results in a final concentration of LPS of 240 pg/ml. Further decline in luciferase gene expression occurs with increasing LPS concentration (Figure 6, lanes 3 and 4). Substantial toxicity was apparent in the sample 2, 3 and 4 cultures and this could largely account for the decline in gene activity. The toxicity is apparent in Figure 6 at 240 pg/ml LPS, whereas toxicity by MTT assay was

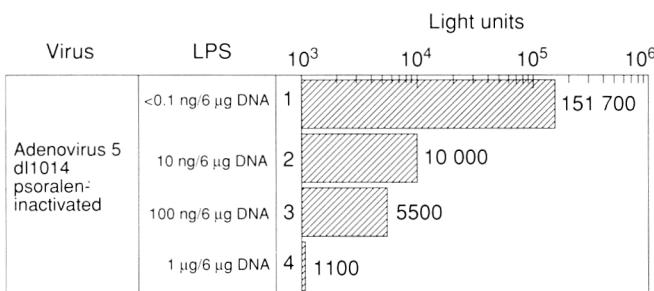


Figure 6 Decline in luciferase activity as a function of LPS content of pCLuc DNA. Primary human skin fibroblasts (passage 9) were plated at 20 000 cells per well of a 24-well dish in DMEM/2% horse serum. Transfection complexes containing biotinylated, psoralen-inactivated dl1014 adenovirus-StrpL-pCLuc DNA-TfpL and the indicated quantity of *E. coli* 0111:B4 LPS were prepared as described in Materials and methods. Complexes representing 0.6 μg of DNA and 1×10^9 virus particles were supplied to the cells in 500 μl of DMEM/2% FCS for 2 h at 37°C. A sample of 1.5 ml of DMEM/10% FCS was then added to each sample and 48 h later the samples were processed for luciferase activity measurement. Each value represents the average of two independent transfections.

not observed below LPS concentrations of 5–50 ng/ml. This difference in concentration probably reflects the mode of assay. With the luciferase assay we are measuring the fate of the cells that actually endocytose the DNA–virus–LPS complex whereas with the MTT assay we are measuring the fate of the entire culture.

The toxicity does not require the high virus:cell ratios used in these experiments. When the delivery of a luciferase marker gene is used to follow the fate of the cells that ingest the DNA–LPS complex, the toxicity at 10^3 virus per cell is comparable to that at 10^5 virus per cell. Therefore, the toxicity due to LPS contamination appears under the same conditions employed for efficient DNA delivery.

Discussion

Previous work has demonstrated the utility of adenovirus particles for enhancing the delivery of DNA to eukaryotic cells [23–28]. Most evidence suggests that the primary function of the adenovirus particle in these applications is to increase the cytoplasmic entry of endocytosed material, a function that was initially characterized in detail by the Pastan and Carrasco groups [29, 30]. This enhanced intracellular delivery of material applies to toxins as well as to the DNA molecules that we seek to deliver. Endotoxin (LPS) is a common contaminant of *E. coli*-grown plasmid DNA preparations. These LPS contaminations are simple to overlook because the molecule is not visualized either by ethidium bromide staining or by absorbance at 260 nm, the two methods commonly used to analyze and quantify DNA preparations. We have demonstrated here that the levels of endotoxin contaminating DNA preparations can be toxic to primary cells in the presence of entry-active adenovirus particles. We have demonstrated that DNA purified with techniques for removing contaminating LPS molecules enhances gene expression in primary cells and eliminates the toxicity.

It is not yet clear if the toxicity is due to physical damage to the cell by the LPS, if the cytoplasmic

delivery of LPS is a signal or if the combined interaction of adenovirus particles and LPS molecules activates a toxic signalling pathway. Experiments to clarify the mechanism generating this toxicity are in progress.

The use of adenovirus particles to enhance receptor-mediated gene delivery is a powerful technique, generating high levels of transient gene expression in a variety of cell types. However, the use of this system *in vivo* for long-term expression has been hampered by the rapid decay in gene expression [31]. Our observation that the LPS commonly contaminating DNA preparations is responsible for a toxicity, and the demonstration here of a simple remedy for this problem, should increase the utility of this transfection method for primary cells.

Materials and methods

DNA preparation

All DNA plasmids carried either the β-lactamase ampicillin resistance gene or the tetracycline resistance gene and were propagated in the bacterial strains HB101 or DH5α in the presence of 100 μg/ml ampicillin or 5 μg/ml tetracycline in either LB or Terrific medium [32]. Saturated overnight cultures of the plasmid-transformed bacterial strains were prepared, collected by centrifugation and processed for plasmid DNA purification in the following manner.

CsCl. This procedure is described in detail [33]. Briefly, the bacterial pellet from a 1-liter culture was suspended in 10 ml of 20% (w/v) sucrose, 10 mM EDTA, 50 mM Tris pH 7.5 (solution 1) incubated on ice for 10 min, 2.2 ml lysozyme (10 mg/ml in solution 1) was added for an additional 10 min on ice, 5 ml 0.2 M EDTA pH 7 was added and the sample was incubated for 10 min on ice and finally, 10 ml 2% (v/v) Triton X-114, 60 mM EDTA and 40 mM Tris pH 7.5 were added followed by incubation for 15 min on ice. This lysate was then centrifuged for 30 min (Sorvall SS34, 17K) and 28.5 g CsCl and 400 μl ethidium bromide (10 mg/ml) were added to the supernatant (26 ml initial volume). The material was centrifuged for >18 h in a Beckman VTi50 rotor at 200 000 × g at 20°C. The lower of the two ethidium-rich bands was collected and centrifuged again, in a Beckman VTi65 rotor for >4 h at 350 000 × g at 20°C. The ethidium-rich band was again harvested, extracted with CsCl-saturated isopropanol until the pink ethidium color was gone, dialyzed extensively against TE (10 mM Tris, 0.1 mM EDTA pH 7.4), mixed with 1/10 vol. 3 M sodium acetate pH 5.0 and precipitated with 3 vol. of ethanol at -20°C. The collected DNA precipitate was further processed with RNase A, proteinase K, phenol/chloroform and chloroform, reprecipitated and the final DNA pellet was suspended in TE and quantified by optical absorbance, assuming that 0.05 mg/ml DNA has an absorbance at 260 nm of 1.

Qiagen and Nucleobond. Qiagen (Diagen GmbH, Hilden, Germany) and Nucleobond (Macherey-Nagel, Düren, Germany) plasmid DNA resins were used following the directions supplied by the manufacturers, with the

exception that Nucleobond columns were rinsed four times with high stringency wash buffer (rather than twice) following binding of the DNA to the resin.

Triton X-114 extraction. Triton X-114 (Sigma) was passed through three 0°C/30°C temperature cycles (as described by Bordier [14]) to isolate a homogeneous preparation of the detergent. Extraction of LPS from DNA samples was performed as follows, a modification of previously published methods [15, 16]. DNA samples at 0.5–1.5 mg/ml in TE were adjusted to 0.3 M sodium acetate pH 7.5. Triton X-114 (3 µl per 100 µl DNA solution) was added and the samples were vortexed thoroughly and incubated on ice for 10 min. The samples were then transferred to 30°C for 5 min to allow the two phases to separate, centrifuged in a prewarmed Eppendorf centrifuge (ca. 30°C) for 2 min at 2000 and the aqueous phase was transferred to a fresh Eppendorf tube. This extraction was repeated two additional times and the DNA in the final aqueous phase was precipitated with 0.6 vol. of isopropanol at room temperature. The precipitate was collected by centrifugation, washed twice with 80% ethanol (–20°C), air-dried, resuspended in TE and quantified.

Polymyxin B chromatography

A volume of polymyxin B resin slurry (Affi-Prep polymyxin, BioRad) equal to the DNA sample volume was briefly exposed to 3 vol. 0.1 N NaOH, followed by three washes of five resin volumes with TE (10 mM Tris, 0.1 mM EDTA pH 7.4). The pelleted resin was resuspended with the DNA samples (in TE at 0.8–1.2 mg/ml) and the mixture was agitated by rotation overnight at 4°C. The sample was then transferred to a disposable column (BioRad, Poly-Prep) that had been pretreated with 0.1 N NaOH and washed with TE. The eluate was collected, the resin was washed with an additional bed volume of TE and the eluate plus wash were pooled. The DNA in this pooled sample was precipitated with 1/10 vol. 3 M sodium acetate pH 5 and 2 vol. of ethanol. The precipitate was collected, washed with 80% ethanol, dried, dissolved in TE and quantified as described above.

LPS preparations

As specified in the figure legends, the pure LPS preparations used in these studies were either a smooth LPS from *S. minnesota*, extracted by the phenol/water method and further purified by gel filtration, a similar preparation of LPS from *E. coli* 0111:B4 or LPS from the *S. minnesota* rough mutant Re 595 (all from Sigma). All three LPS types yielded similar results. LPS preparations were suspended in LPS-free water by sonication for 5 min in a Transsonix 570/H (360 W) sonicating bath. Serial dilutions were prepared in LPS-free water with 30 s of vortexing between dilutions. The final dilutions were sonicated for 5 min before use.

Virus procurement, biotinylation and psoralen inactivation

The E4-defective adenovirus 5, dl1014 [34] was grown on the complementing cell line W162 [35]. Pellets of

infected cells were suspended in 20 mM hydroxyethylpiperazine sulfonate (HEPES) pH 7.4, 1 mM phenylmethylsulfonyl fluoride (PMSF) at 2 ml per 3×10^7 cells and subjected to three freeze/thaw cycles (liquid nitrogen, 37°C). The suspension was then mixed with an equal volume of Freon and vortexed for 3 \times 30-s bursts and centrifuged 10 min at 1700 \times g (Heraeus Sepatech, 2705 rotor). The aqueous phase (upper) was saved and the Freon phase was vortexed with 1/5 vol. 20 mM Hepes pH 7.4 and centrifuged as before. The aqueous phases were pooled, transferred to a Beckman VTi50 centrifuge tube (15 ml/tube) and underlaid with 15 ml of 1.2 g/cm³ CsCl, 20 mM Hepes pH 7.4 and then with 7 ml of 1.45 g/cm³ CsCl, 20 mM Hepes pH 7.4. The samples were centrifuged at 200 000 \times g in a Beckman VT150 rotor for 40 min at 20°C. The lower opalescent band of mature virus particles at 1.34–1.35 g/cm³ (as measured by refractive index) and the upper band (immature particles at 1.31–1.32 g/cm³) were collected separately and centrifuged to equilibrium (>4 h) at 350 000 \times g in a VTi65 rotor. The opalescent virus bands (either 1.31 g/cm³ for immature or 1.34 g/cm³ for mature) were harvested and either processed directly for biotinylation and psoralen inactivation or diluted with an equal volume of 86% glycerol (Fluka) and stored at –80°C.

Virus biotinylation with *N*-hydroxysuccinimide-biotin (Pierce), inactivation with 8-methoxypsoralen/360 nm UV light and purification by gel filtration using a Pharmacia PD10 column equilibrated with HEPES-buffered saline (HBS, 150 mM NaCl, 20 mM HEPES pH 7.4)/40% glycerol were performed as described previously [21, 22]. Virus samples were quantified by protein concentration (BioRad Bradford assay with bovine serum albumin, BSA, as a standard) using the relationship of 1 mg/ml protein = 3.4×10^{12} adenovirus particles/ml [36].

Cell culture

Primary human melanoma cultures were isolated and grown in RPMI-1640 medium (GIBCO/BRL) supplemented with 100 IU/ml penicillin, 100 µg/ml streptomycin, 2 mM L-glutamine, 1% sodium pyruvate and 10% heat-inactivated (30 min, 56°C) fetal calf serum (RPMI/10% FCS). Primary human skin fibroblasts were isolated from skin biopsies and propagated in Dulbecco's modified Eagle's medium (DMEM) plus 2 mM glutamine, 50 µg/ml gentamicin and 10% heat-inactivated fetal calf serum (DMEM/10% FCS). The primary fibroblast cultures were used at passage 5–10; primary melanoma cultures were used at passage 16–25 for these experiments.

Preparation of adenovirus–DNA complexes

StrpL and TfpL were prepared as previously described [23, 37]. Samples of biotinylated, psoralen-inactivated adenovirus dl1014 (8 µl, 1×10^{12} particles/ml) were diluted into 150 µl HBS and mixed with 1 µg StrpL in 150 µl HBS for 30 min at room temperature. Aliquots of 6 µg plasmid DNA were diluted in 100 µl containing the indicated quantities of LPS (see figure legends). The DNA

(LPS) solutions were then mixed with the adenovirus-StrpL solution for 30 min at room temperature. Finally, a 100- μ l aliquot of HBS containing 5 μ g Tfpl was added to each sample, followed by incubation for 30 min at room temperature. Aliquots of these transfection complexes were then supplied to cells as described in the figure legends (generally 5–50 μ l per 20 000–50 000 cells).

Cell viability assays

Crystal violet staining was performed 48–72 h after exposure of cell samples to test agents. The culture medium was removed, the cell layer was washed once with HBS, fixed for 5 min with 4% formaldehyde/150 mM NaCl and then stained for 10 min with 0.1% crystal violet in 2% ethanol. The staining solution was then removed and the well washed once with phosphate-buffered saline (PBS) and once with distilled water. An alternative determination of cell viability was performed using the MTT reduction assay [38] as modified by Promega.

Endotoxin (LPS) assays

LPS was measured with the BioWhittaker QCL-1000 chromogenic *Limulus* assay, based on the *Limulus* amoebocyte clotting reaction (reviewed in [39]). All solutions used for DNA and virus preparations as well as Tfpl, StrpL and adenovirus preparations were demonstrated to be LPS free (<0.1 endotoxin units/50 μ l solution) before use.

Miscellaneous

Luciferase gene expression was measured as described previously [33]. Human IL-2 in cell culture supernatants was determined between 24 and 48 h after transfection by ELISA (T Cell Diagnostics Inc., Cambridge, MA, USA). Supernatants were collected, centrifuged at about 3000 \times g in an Eppendorf Microfuge to remove debris and stored at –20°C until assayed. Values reported are in BRMP (Biological Response Modifier Program) units per 10⁶ cells per 24 h.

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