Polyamidoamine Dendrimer Nanoparticle Cytotoxicity, Oxidative Stress, Caspase Activation and Inflammatory Response: Experimental Observation and Numerical Simulation

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**Abstract**

Mechanisms underlying the in vitro cytotoxicity of Polyamidoamine nano-dendrimers in human keratinocytes are explored. Previous studies demonstrated a systematic, dendrimer-generation-dependent cytotoxicity, oxidative stress, and genotoxicity. The emerging picture is of dendrimer endocytosis, endosomal rupture and subsequent mitochondrial attack and cell death. To understand the underlying mechanisms, the evolution of reactive oxygen species, intracellular glutathione, caspase activation, mitochondrial membrane potential decay, and inflammatory responses have been examined. Early-stage responses are associated with endosomal encapsulation, later-stage with mitochondrial attack. In all cases, the magnitude and evolution of responses depend on dendrimer generation and dose. The early-stage response is modelled using a rate equation approach, qualitatively reproducing the time, dose and generation dependences, using only two variable parameters. The dependence of the response on the nanoparticle physicochemical properties can thus be separated from internal cellular parameters, and responses can be quantified in terms of rate constants rather than commonly employed effective concentrations.

**Key words:** Polyamidoamine Dendrimer; Molecular mechanism of cytotoxicity; Rate equation model; Numerical simulation

The rapid advance of nanotechnology has rendered it imperative that possible hazardous effects of nanomaterials on humans and the environment are elucidated. Nanoparticles (NPs) with different chemical composition and size have been shown to induce different levels of injury to cells and organisms, and thus a fundamental understanding of the mechanisms of their interaction is critical. In vitro studies have demonstrated that the generation of intracellular reactive oxygen species (ROS) by NPs is a key to their toxicity by triggering different cell-death pathways, including cytokine expression and caspase-activation and mitochondrial-DNA damage. To elucidate the mechanisms underlying toxic responses and establish structure-activity-relationships, NPs of well-defined physicochemical properties that are systematically variable and elicit systematically variable cellular responses can play a key role. PAMAM dendrimers are widely explored, commercially available NPs of well-defined structure. They have a 2-carbon ethylenediamine core with terminal amidoamines attached, yielding a highly branched radial structure having tertiary amine branches and primary surface amino-groups. The diameter and number of surface amino-groups increases systematically with increasing generation.

PAMAM dendrimers have been proposed for a range of biomedical applications, from MRI contrast agents, to targeted delivery of drugs, DNA, and siRNA. However, they have been reported to be toxic to mammalian cell lines and aquatic species. The polar surface amino groups impart an effective cationic charge, and endocytosis leads to oxidative-stress, mitochondrial and DNA damage, and ultimately apoptosis.

PAMAM dendrimers have also been reported to activate expression of different cytokines, such as tumor necrosis factor (TNF-\(\alpha\)), interleukin-6 (IL-6), and macrophage inflammatory protein-2 (MIP-2), in a mouse macrophage cell line. Previous studies have demonstrated the cytotoxicological responses to these species to vary systematically with increasing dendrimer generation and therefore number of surface amino groups. A similar systematic response was observed for the generation of ROS, onset of apoptosis, and levels of DNA damage. The mechanism of the toxic response has been at least partially elucidated, based on standard cytotoxicity assays including MTT, AB, and NR and microscopic co-localization studies.

No conflict of interest was reported by the authors of this article.

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**Competing interests**

No conflict of interest was reported by the authors of this article.

**Supplementary materials**

The online version of this article (available at http://dx.doi.org/10.1016/j.nano.2012.05.002) contains two figures and three tables shown here in the main text.

**References**

The mechanistic model which has emerged is one of endocytosis, oxidative stress, endosomal rupture through the proton-sponge effect, followed by mitochondrial damage and the onset of apoptosis. The use of amine groups to induce endosomolytic behavior is a well-established strategy in drug delivery, and the endosomolytic activity observed for PAMAM dendrimers is consistent with this. The cellular toxicity thus has primarily two phases; an early-stage, in which oxidative stress is primarily due to the presence of particles in endosomes, and a later stage, in which the particles migrate to the mitochondria, generating further oxidative-stress. However, the toxicity of a specific NP to different cell lines can differ, due to the differences in intracellular constituent levels. Understanding the metabolic pathways in the target cell, and their dose and time dependencies, is therefore critical to understanding the toxic responses in vitro, and ultimately in vivo.

In this study, the mechanism of PAMAM toxicity to the human keratinocyte, HaCaT, cell line is further explored. ROS production upon exposure to different PAMAM generations and doses is monitored as a function of time. Intracellular levels of the antioxidant glutathione (GSH), representative of the natural cellular antioxidant defense mechanisms, are also monitored. Changes in caspase-8 and caspase-3 activity, mitochondrial membrane potential (MMP) and TNF-α, IL-8 expression, over an exposure period of 24 hours are also explored. Based on the observations, potential underlying pathways for the early- and late-stage cellular responses are proposed.

The early-stage responses are visualized with the aid of a phenomenological rate-equation model, which qualitatively reproduces the generation and dose dependence of the sequence of events. It is highlighted that, although simplistic, such a rate-equation approach is a valuable tool in visualizing and elucidating cellular responses. It identifies response rates as critical parameters in determining toxicity and potentially a more reliable route towards quantitative structure-activity relationships than commonly employed cytotoxicological endpoints.

Methods

Commercially available PAMAM dendrimers of generation 4 (G4), 5 (G5) and 6 (G6) were used in this study. The nominal diameters of the PAMAM G4, G5, and G6 dendrimers are 4.5, 5.4, and 6.7 nm respectively. Full physicochemical characterization has been reported. All studies were performed using HaCaT cells. Assays were performed to evaluate ROS generation, GSH depletion, caspase-8 and 3 activation, mitochondrial membrane potential decay (MMPD), and TNF-α and IL-8 expression upon PAMAM exposure at different doses and time points. A detailed description of the materials used and experimental methods is given in the Supplementary Material available online at http://www.nanomedjournal.com.

Experimental results

The generation of ROS shows a complex behavior as a function of time and dose for all PAMAM dendrimer generations, although the response is somewhat systematic as a function of generation. As a function of exposure time, a biphasic response is observed over a 24-hour time period at lower concentrations of PAMAM, as shown in Figure S1. At a fixed time point, the increase in ROS levels has been shown to increase monotonically with generation (Figure S1, C), and when expressed in terms of molar concentration of surface NH2 groups, the dose dependences of ROS for the different generations are overlaid.

For PAMAM G6, an initial or early-stage maximum in ROS levels is observed after ~1 hour, for doses of 0.5 μM to 1.16 μM, whereas for higher doses (1.3 μM and 2.23 μM), the maximum is observed at ~0.5-hour exposure (Figure 1, A). At ~4 hours, exposure at all concentrations results in a reduction of the ROS levels below those of the control, whereas a later increase in the ROS levels is observed at ~24 hours for doses of 0.5 μM and 1 μM.

A similar behavior is observed for exposure to PAMAM G5, although the early-stage maximum for the lower doses has shifted toward the longer time of ~2 hours (Figure S1, A). This trend is continued for G4, all but the highest exposure concentration exhibiting a maximum response after ~3 hours (Figure S1, B). After ~24 hours, only the lowest dose exposure results in ROS levels above the control, all others being significantly quenched in comparison with the control levels.

At a concentration of 1 μM, the maximum amount of ROS was produced after ~24-hour exposure, the levels increasing with increasing generation of PAMAM (G4<G5<G6). Notably, this concentration is close to the EC50 of G5 and G6, as previously determined in HaCaT cells using MTT assay (Table S1), and at this concentration, increased lysosomal activity in comparison with control after ~24-hour exposure was also observed. It was found that, at this concentration, in early stages after exposure (e.g., 1 hour), ROS levels increased linearly with 169 number of surface amino groups per generation, as shown in Figure S1, C. With increasing doses, for all generations, after 151 initial increase in ROS levels, the levels are seen to be reduced 152 significantly below those of negative controls and do not recover over a 4-hour period.

ROS localization by CFM

Confocal fluorescence microscopy (CFM) demonstrates that early-increased (~1 – 2 hour) levels of ROS localized in sacs/vesicles in cytosol (Figure S2, A), consistent with previous observations of early-stage trafficking of endocytosed PAMAM dendrimers in endosomes. However, in the later stages (~24 hours), ROS are co-localized in the mitochondria (Figure S2, B), potentially indicating that they are generated through different mechanisms.

GSH measurement

In control cells, intracellular GSH level increases approximately linearly as a function of time over 24 hours, as shown in Figure 1, B. Such a linear increase is commonly observed when studying in vitro cell cultures. Upon exposure to PAMAM dendrimer solutions at a 1-μM concentration, initial linear increase in GSH levels follows the trend observed for control, but an abrupt deviation from the levels of controls is observed.
within 1 – 5 hours. For G4, the deviation is observed after 4 hours, for G5 3 hours, and for G6 1 hour. Following these timepoints, the degree of reduction of the GSH levels is also seen to be systematic in dendrimer generation (G4 < G5 < G6).

Caspase-8 and -3 activity

The activity of caspase-8 and 3 was studied at different time points for 1-μM doses of PAMAM G4, G5, and G6. For both the caspases, a biphasic activity was observed (Figure 2). For PAMAM G4 and G5, an initial or early-stage maximum of caspase-8 levels was observed after ~4 hours’ exposure, whereupon a minimum was observed before subsequent increase after 24 hours’ exposure (Figure S3, A, S3, B). For G6, the early-stage maximum was found after ~2 hours’ exposure (Figure S3C). Comparing the percentage increase of caspase-8 with control upon exposure to 1 μM for the different PAMAM generations after 24 hours, a systematic increase is observed (G4 < G5 < G6).

A similar behavior is observed for the time evolution of caspase-3 levels. For PAMAM G4 and G5, early-stage maximum were observed at ~4 hours’ exposure and after an intermediate decrease, a late increase of caspase-3 activity was observed at 24 hours (Figure-S3, A, S3, B). For G6, early-stage increase of caspase-3 activity was observed at ~2 hours’ exposure (Figure S3, C). Again, a systematic generation dependence of the percentage increase of caspase-3 levels in
comparison with control upon 1-μM exposure after 24 hours is observed (G4<G5≤G6). Thus, although, in a similar way to the behaviour of ROS levels, the temporal evolution is complex, a clear systematic variation in the response with dendrimer generation is also evident.

Mitochondrial membrane potential decay

Upon exposure to 1-μM solutions of the respective PAMAM dendrimer generations over a 24-hour period, the percentage of mitochondrial membrane potential decay (MMPD), in comparison with controls, also shows a biphasic response, as shown in Figure 1, C. For all generations, the degree of MMPD increases initially within early stages of exposure. It then decreases to a minimum after ~6–7 hours of exposure, after which a further increase is observed up to 24 hours of exposure. The early-stage MMPD was observed after ~4–5 hours for G4 and ~2–3 hours for G5 and G6. At all time points, percentage of MMPD in comparison with control was seen to vary systematically with dendrimer generation (G4≤G5<G6).

TNF-α and IL8 expression

An upregulation of TNF-α expression that is time, dose, and generation dependent was observed. For G4, the maximum amount of TNF-α was expressed at a concentration of 3.21 μM after ~6-hour exposure, as shown in Figure S4, A. For G5, the maximum amount of TNF-α expression was observed for 1 μM after ~4-hour exposure (Figure S4, B). For G6, the maximum amount of TNF-α is expressed at 1 μM after ~4-hour exposure (Figure S4, C). For a 1-μM dose, maximum percentage of TNF-α expression in comparison with the controls increases with increasing PAMAM generation (G4<G5≤G6), although the maxima occur at different exposure times (Figure 3, A).

Over a 24-hour period, IL-8 expression shows a monotonic increase for all doses, for all dendrimer generations, and the maximum response was observed after a 24-hour exposure. For G4, the maximum amount of IL-8 was expressed at 3.21 μM (Figure S5, A), for G5, at 1 μM (Figure S5, B) and for G6 at 1 μM (Figure S5, C). The percentage of IL-8 expression in comparison with controls increases with increasing generation of PAMAM (G4<G5≤G6), as shown for 1-μM dose in Figure 3, B.

Discussion and numerical simulation

The cellular responses upon exposure to PAMAM dendrimers are a complex function of generation, dose, and time. Figure 4 summarizes the time evolution of the cellular responses for the case of 1-μM exposure to the G6 dendrimer. The plot indicates a defined sequence of events, and the relative temporal evolutions of the different responses indicate some degree of interdependence of the responses.

Previous studies have demonstrated a two-phase response of cells to exposure to PAMAM dendrimers; early-stage localization in endosomes, followed by a later-stage localization in mitochondria. These two phases are well visualized in Figure S2, A and S2, B, whereby, at early stages, the ROS are primarily localized in smaller vesicles assumed to be endosomes, whereas after 24 hours, the ROS are mostly localized in the mitochondria. This two-stage process is further manifest in the time-dependent profile of the ROS levels at low doses, for all generations, as shown in Figure 1, A.

Key to the onset of the toxic response is the increase in ROS levels upon PAMAM exposure and the concomitant changes in intrinsic cellular antioxidant levels. As shown in Figure 1, B, a linear increase in cellular GSH levels is observed in control cells. Upon exposure to PAMAM dendrimers, a generation-dependent reduction in the rate of increase of GSH levels is observed. The degree and rate of reduction is generation dependent, associating the phenomenon with early-stage increase of ROS levels as a result of exposure. It should be noted, upon careful inspection, that there is an apparent time lag between the onset of ROS and the deviation of the GSH levels from linearity. This lag is understandable in terms of differing experimental protocols used to monitor the respective responses. To monitor ROS levels, carboxy-H₂DCFDA dye was uploaded in the cells before particle exposure, whereupon ROS levels were measured after different exposure times. For the measurement of TNF-α, IL-8, and caspases, the cells were lysed immediately after exposure and so the exposure time was equal to the measurement time. To monitor GSH levels, however, cells were stained with ThioiTracker™ Violet for a period of ~30 minutes post exposure.
exposure. Thus, including sample washing and preparation, there is a gap of 30 – 60 minutes from exposure time.

Although the results indicate systematic dependences of responses on dose and dendrimer generation, the four-dimensional response/dose/time/generation system is not easily visualized. To better visualize and elucidate the mechanisms of response, the system can be modeled using a simple phenomenological rate-equation model, similar to those commonly employed for modeling molecular photodynamics.\textsuperscript{21} The particle dose and levels of ROS, GSH, etc., are described by populations, and changes in populations are governed by rate constants. The rate equations can be numerically integrated using an iterative Euler approach,\textsuperscript{22} to yield the temporal evolutions of the populations. Salvati et al have demonstrated that the cellular uptake of polystyrene NPs occurs by endocytosis at a constant rate over a time period of 24 hours and that the rate is dose dependent.\textsuperscript{23} In the case of PAMAM dendrimers, endocytotic process is assumed to be generation dependent, and thus the number of particles in the cells, $N$, increases as:

$$\frac{dN}{dt} = GK_{\text{endo}}D$$ \hspace{1cm} \text{Equation 1}

where $K_{\text{endo}}$ is an endocytosis rate constant, $G$ is a generation-dependent scaling factor, and $D$ represents the dose. Once endocytosed, particles continuously generate ROS, build-up of ROS is counteracted by increased levels of GSH, and the interaction quenches both the levels of ROS and GSH. Thus:

$$\frac{dN_{\text{ROS}}}{dt} = NGK_{\text{ROS}} - K_{q}N_{\text{ROS}}N_{\text{GSH}}$$ \hspace{1cm} \text{Equation 2}

$$\frac{dN_{\text{GSH}}}{dt} = K_{\text{GSH}} - K_{q}N_{\text{ROS}}N_{\text{GSH}}$$ \hspace{1cm} \text{Equation 3}

The first term in Equation 2 is a generation- ($G$) and dose- ($D$) dependent term describing continuous ROS generation at a rate $K_{\text{ROS}}$. This rate is independent of dendrimer generation, $G$, but $D_{\text{ROS}}G$ scales linearly with the number of surface amino groups per generation and dose. The second term describes the quenching of the ROS at a rate $K_{q}$ which depends on both ROS levels, $N_{\text{ROS}}$, and GSH levels, $N_{\text{GSH}}$. In Equation 3, the linear increase of the control levels of GSH, at a rate of $K_{\text{GSH}}$, is described by the first term, and the second term describes the quenching of the GSH levels. Thus, as a $G$ function of generation, for the same molar concentration, simply changing the parameter $G$ for successive generations should reproduce the generation-dependent behaviors observed in Figures 1, A and 1, B, and, for a given dendrimer generation, changing $D$ should similarly mimic the dose dependences of Figure 1, A.

Using a constant generation rate, however, the model predicts a monotonic increase in ROS levels over the exposure time, in contrast to early increase and decrease observed experimentally.\textsuperscript{21} If, however, the ROS population is constrained to saturate, a generation- and dose-dependent rise and fall is reproduced. To simulate such saturation, the rate of generation is proposed to be dependent on the number of ROS generated and thus time such that:

$$\frac{dK_{\text{ROS}}}{dt} = -K_{\text{ROS}}N_{\text{ROS}}$$ \hspace{1cm} \text{Equation 4}

Figure 5, A shows the predicted time and generation dependence of the rate of generation of ROS. Based on such a saturable ROS generation rate, Figure 5, B and 5, C show the...
Caspase-8 activation acts as an abrupt behavior observed in Figure 1, B. The time delay between experimental ROS and GSH generation observed by comparing Figures 1, A and 1, B is further manifest here, as the modeled GSH follows the modeled increase in ROS levels. Because of the complexity of multiple processes leading to ROS generation and saturation, the simulation cannot therefore be considered to be a fit to the experimental data. Nevertheless, the simplistic approach qualitatively reproduces generation-dependent departure from linearity of the GSH levels in both extent and rate.

The simulations similarly faithfully predict an approximately linear dependence of the relative amounts of ROS on generation number, and therefore on number of surface amino groups for a fixed time and dose, as shown in Figure S6, A for the case of 1 hour of exposure of G6. At the 6-hour time point, however, a notably different behavior is observed, highlighting the importance of experimentally monitoring the full-time evolution of the response. Moreover, as the maxima shift in time as a function of dose and generation, at specific time points, complex dose dependences similar to those in Figure 1, A, can be reproduced, as shown in Figure S6, B for the cases of 1 hour, 1.5 hours and 2 hours of G6 exposure.

It should be noted that biphasic ROS generation is observed only at low doses in a generation-dependent fashion. At elevated doses, the levels of GSH are depleted such that the ROS levels are not quenched and no intermediate time-scale minimum in their levels is observed. In Figure 5, C, the generation dependence of this process is apparent in the prolonged timescales of GSH depletion, which further increase with increasing dose.

The activities of both caspase-8 and 3 upon 1 μM PAMAM exposure were also found to be biphasic over 24 hours for all generations (Figures 2, S3). The maximum percentages of early caspase-8 were activated after ~4 hours’ exposure of G4 and G5, whereas those for G6 occurred after ~2 hours’ exposure (Figure 2, A). The activity then decreased to, or below, the level of the control after ~12 hours for G4 and G5 and after ~6 hours for G6, before subsequently increasing to a maximum after 24 hours’ exposure (Figure 2, A). Variations in activity of caspase-3 follow a trend similar to that of caspase-8 (Figure 2, B). In both cases, the activity profile and the percentage activity in comparison with control are dependent on generation.

In an attempt to understand the possible underlying response pathways, it is noted that apoptosis can be mediated through two major pathways, the death-receptor pathway (extrinsic) and the mitochondrial pathway (intrinsic). Notably, caspase-8 and 3 activations are seen to occur almost instantaneously after ROS generation, both in early and late stages. The observation of the early-stage maximum activation of caspase-8 before the maximum early-stage MMPD and activation of TNF-α indicates that caspase-8 activation in the current study is via the Fas/FasL mediated FADD pathway, independent of the TNF-α mediated FADD or mitochondrial pathway (Figure 4). Previously it was also shown that intracellular ROS mediates Fas-ligation that leads to caspase-8 and 3 activation. It is therefore proposed that activation of early caspase-8 and 3 is mediated via extrinsic FasL mediated Fas-signaling pathway. Caspase-8 activation acts as an

Figure 5. The simulated behaviors for all dendrimer generations of (A) the rate of ROS generation, $K_{\text{ROS}}$, (B) the levels of intracellular ROS, and (C) the levels of intracellular GSH as a function of time. In (C), the solid line depicts the linear increase of GSH levels in negative controls.

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<th>Figure 5</th>
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upstream process for caspase-3 activation by activating pro-
caspase-3. FADD pathway can be naturally inactivated by
caspase-8-like inhibitory protein (cFLIP) or can be inhibited
by the inhibitors of apoptosis proteins (IAPs), for example X-
linked inhibitor of apoptosis protein (XIAP). Such mecha-
nisms can potentially decrease the activity of caspase-8 and 3
after its early activation (Figures 2, S3).

The activation of caspase-8 by intrinsic mitochondrial
pathway, which is independent of the classical FADD pathway,
is also well known. Through this pathway, caspase-8 can be
activated either via mitochondrial p38-MAPK or mitogen- and
stress-response kinase 1 (MSK1), which are sequentially
activated upon mitochondrial oxidative-stress (Michichi et al,
2007). The second-phase of caspase-activation follows the
second-phase of ROS, generated in the mitochondria, thereby
causing mitochondrial oxidative-stress. Therefore, its activation
could potentially occur through the mitochondrial p38-MAPK or
MSK1 pathway.

The expression of TNF-α, a pro-inflammatory cytokine, can
also be activated by p38-MAPK and other MAPKs upon
oxidative stress. NPs have been shown to upregulate TNF-α
and CXCL8 via ROS and MAPK activation. TNF-α activation
in turn activates the expression of the chemokine IL8. It has
also been reported that TNF-α downregulates FasL expression in
the vascular endothelial cells. Therefore, sequential TNF-α
and IL8 expressions following early-stage maximum in ROS
generation caspase activation, and MMPD is consistent with its
activation by a MAPK pathway. TNF-α activation before the
second-phase of caspase activation possibly activates Smac/
Diablo, which inhibit IAPs, resulting in the second stage of
caspase activity with prolonged exposure time.

The mitochondrial membrane potential study reveals that the
decay rapidly follows the caspase activation, in both early and
later stages, with a delay of ~45 minutes to 1 hour (Figures 2 and
1, C). This delay comes in part from the staining of the cells with
rhodamine-123 for measuring mitochondrial membrane potential
after the exposure time point, whereas in caspase study the cells
were lysed immediately after exposure. Therefore, caspase
activation, which is an instantaneous effect of ROS generation,
probably via Fas pathway, results in rapid decay of MMP. The
extent of MMPD and the time evolution is generation dependent
(Figure 1, C). The biphasic response is consistent with the model
of early-stage ROS generation by particles in subcellular
vesicles, most likely endosomes, which cause oxidative stress
to the mitochondria, followed by endosomal release and
localization of the dendrimer particles in the mitochondria,
leading to cell death via the mitochondrial injury pathway,
generating further ROS as a result. The decrease in MMPD
after the early-stage increase could be due to the effects of
mitochondrial chaperones, e.g., prohibitin, which elevate the
synthesis of ATP and stabilize MMP, delaying the onset of
apoptosis.

The inflammatory study indicates a subsequent sequential
activation of TNF-α and IL-8. The maximum TNF-α
expression was observed after ~6 hours’ exposure at 3.21 μM
for G4 and after ~4 hours’ exposure at 1 μM for G5 and G6
(Figure 3, A). Having reached the maximum, the expression is
seen to decrease with exposure time to levels less than control.
The expression of IL-8 increases monotonically with exposure
time to a maximum at 24 hours’ exposure at 3.21 μM for G4,
and 1 μM for G5 and G6 (Figure 3, B). Above and below these
concentrations, the expression of TNF-α and IL-8 decreases.
Notably, these concentrations are also the EC50 values obtained
from the dose response from MTT assay in HaCaT cells (Table S1).
The maximum percentage of increase of TNF-α and IL-8
expression was also seen to increase with increasing
generation of PAMAM dendrimer, and therefore number of
surface amino groups.

It is notable that TNF-α activation is only observed in the
early stages and does not follow the biphasic evolution of ROS
and caspase activation and MMPD. In the early stages, the NPs
are located in vesicles, proposed to be endosomes, and thus
oxidative stress is generated external to the mitochondria. At the
later stages, dendrimer NPs and generation of ROS have been
located in the mitochondria. Although derived from the
mitochondria, it has been demonstrated that acute, internal stress
can suppress the expression of pro-inflammatory cytokines, such
as TNF-α, without affecting IL-8 expression. Similarly, G4
PAMAM generates acute stress when incorporated into
mitochondria (24 hours) and the second phase of TNF-α
expression is not observed in our study.

In the first phase of evolution, the rate-equation model can be
simply extended to include the ROS-dependent activation of
caspases, and subsequent MMPD and generation of TNF-α and
IL-8, and thus visualize the generation and dose dependences,
as described in the Supplementary Material. Figure 6, A–C
illustrates the time evolution of the process as well as generation-
dependent behavior predicted by the model, simply by changing
the parameter G in Equations (1) and (2). All rates are kept
constant and the differing rates of evolution of subsequent stages
are the result of the early-stage generation- (or dose-) dependent
increase in ROS levels. For example, maximum TNF-α
expression is predicted for G4 at 5.1 hours, for G5 at 4.4 hours
and for G6 at 4 hours. Although the experimental time intervals
do not differentiate the maxima for G5 and G6, the model
predicts a sequence of activation of G6→G5→G4. Furthermore,
although the magnitudes of responses are normalized to the
maximum for graphical representation, at each step in the
cascade, the generation dependence of G6→G5→G4 is also
reproduced faithfully, as shown by the approximately linear
dependence of the maximum levels of TNF-α, as a function
of number of surface amino-groups per dendrimer generation
Figure 7.

In all cases, only the early stage of the cellular responses has
been modeled. This stage is proposed to originate from initial
endocytosis of the particles and encapsulation in endosomes.
ROS is most likely generated via the proton-pump mechanism,
resulting in depletion of GSH and other antioxidants and the
onset of caspase activation, MMPD, and inflammatory re-
sponses via TNF-α activation. The second phase appears to be
spatially distinct, in that it is associated with localization of
dendrimer NPs and ROS generation in the mitochondria.
Although the second phase is not modeled here, a similar
rate-equation approach could be employed to simulate the
responses, their time evolution and dependences on dose and
dendrimer generation. A more complete understanding of
generation and dose dependence of the process of endosomal rupture, particle migration to and uptake by the mitochondria, and recovery of intracellular antioxidant levels would be required. Between the two phases, such phenomena as the quenching of ROS levels to below those of controls, the recovery of antioxidant levels, and migration of antioxidants to localised subcellular sites should be considered. Nevertheless, the phenomenological model is readily adaptable to include more complex phenomena, simply by adding additional terms to the rate equations (Equation S1–S5).

The overall mechanism that can be postulated from the cellular responses is diagrammatically represented in Figure S8. PAMAM dendrimers enter the cells by endosomal uptake or by rupture of the plasma membrane. Initial oxidative stress results from early-stage ROS generation whereas the dendrimers are encapsulated in early-stage subcellular vesicles, most likely endosomes. Generation rate and yield point to the reactive NH₃ surface groups as the origin of oxidative stress. Intracellular antioxidants result in a quenching of early-stage ROS and are themselves quenched by the action. The study of GSH levels and their time evolution, as an example of intracellular antioxidants, highlights the importance of intracellular defense mechanisms, and potentially points to a source of differentiation of different cellular responses to NP exposure. The ROS probably play a pivotal role in the possible FasL/Fas mediated activation of caspase-8 which further activates caspase-3, leading to the initial MMPD. Maximum TNF-α expression after early-stage maximum ROS, caspase-8 and 3 activities and MMPD suggests TNF-α activation by mitochondrial pathway. TNF-α subsequently induces IL-8 expression and therefore its expression gradually increases with exposure time. After recovery of early-stage ROS, it is proposed that the action of different caspase inhibitor proteins results in reduction of caspase-8 and 3 activities and MMPD similarly recovers, possibly through the action of mitochondrial chaperones. In the second phase, PAMAM dendrimers rupture the endosomes by so-called "proton-sponge effect" and are released into the cytosol and interact directly with other cellular organelles. After ~16 hours they have been located in the mitochondria, whereupon the oxidative stress is increased, resulting in further MMPD. No further TNF-α expression is observed, but a second phase of activation of caspases is observed, which is possibly through the mitochondrial pathway. The sequential and potentially independent pathways of caspase activations that are associated with the early and late stage of ROS generation can be understood by further studies of activation of Fas and mitochondrial p38MAPK or MSK1. The potential role of IAPs and cFLIP in the inhibition of caspase-8 and 3 after their early-stage activation and the contribution of Smac/Diablo activation profile should also be studied for further elucidation of the biphasic caspase 6 activation. Following the activation of these different cell death pathways and the activation of caspases, the cell enters apoptosis, its nuclear DNA undergoes fragmentation, and finally it dies.

Although simplistic at this stage, the numerical modeling approach enables a visualization of the complex generation, dose and time dependences of the cellular responses. A fundamental understanding of in vitro cytological responses is becoming increasingly important, given the implications of EU Directive 2010/63/EU on reduction, replacement, and refinement of animal models for scientific experimentation. Consideration of the responses in terms of rate equations elucidates their sequence, interdependencies, and relative magnitudes. It is a potential route towards quantifying nanotoxicological responses in terms of response rates that are determined by NP properties and cellular and even cell-line-dependent parameters, independently. The overall cytotoxicological response, as frequently monitored by classic cytotoxicological assays and expressed, for example, as an EC₅₀, is a convolution of a cascade of events, which can potentially be better expressed as response rates that can be defined per NP and cellular system.

A nonlinear response and saturation are required to reproduce the experimental observations, but the origin and mathematical form of this nonlinearity and saturation requires clarification. In cytotoxicity, dose dependences are commonly empirically represented by the Hill function, but this is not...
easily represented in a form that indicates the rates of contributing processes.\textsuperscript{48} In pharmacokinetics, it is simply acknowledged that to account for a nonlinear response to a linear dose, at least one of the intermediate stages must be nonlinear.\textsuperscript{49}

The endocytotic process is assumed to be linearly dependent on dose, but a low-dose exposure of many cells to few NPs is most likely significantly different from one in which there are many particles per cell, and ultimately the capacity of a single cell to endocytose NPs must be limited. In the simplistic treatment presented here, no changes to cell population due to cell proliferation or death have been included. The doubling time for HaCaT cells is 23 hours.\textsuperscript{50} The Alamar Blue assay shows that, upon exposure to 1μM PAMAM G6 for 24 hours, the percentage cytotoxicity in comparison with control was 28% (data not shown). Therefore, it is predictable that after 6 hours’ exposure the effect of 1μM G6 on HaCaT cell proliferation and viablility was not significant.

Notably, the dose dependence of ROS generation is nonlinear and potentially originates in its time evolution. However, although the model demonstrates how a complex dose dependence can arise, the results are by no means a fit with the experimental data, and further work utilizing model NP systems is required to accurately predict the dose dependence. Ultimately, however, such a rate-equation model may provide the basis for quantification of NP toxicity and cellular susceptibility, and thus quantitative structure-activity relationships.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at http://dx.doi.org/10.1016/j.nano.2012.05.002.

References


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Polyamidoamine dendrimer nanoparticle cytotoxicity, oxidative stress, caspase activation and inflammatory response: experimental observation and numerical simulation

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Structural dependence of cytotoxic responses to PAMAM dendrimers derive from ROS generation and resultant cascades can be visualized and simulated mathematically.
Supplementary Material