The Activation of DNA Damage Detection and Repair Responses in Cleavage-Stage Rat Embryos by a Damaged Paternal Genome

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Male germ cell DNA damage, after exposure to radiation, exogenous chemicals, or chemotherapeutic agents, is a major cause of male infertility. DNA-damaged spermatozoa can fertilize oocytes; this is of concern because there is limited information on the capacity of early embryos to repair a damaged male genome or on the fate of these embryos if repair is inadequate. We hypothesized that the early activation of DNA damage response in the early embryo is a critical determinant of its fate. The objective of this study was to assess the DNA damage response and mitochondrial function as a measure of the energy supply for DNA repair and general health in cleavage-stage embryos sired by males chronically exposed to an anticancer alkylating agent, cyclophosphamide. Male rats were treated with saline or cyclophosphamide (6 mg/kg/day) for 4 weeks and mated to naturally cycling females. Pronuclear two- and eight-cell embryos were collected for immunofluorescence analysis of mitochondrial function and biomarkers of the DNA damage response: γH2AX foci, 53BP1 reactivity, and poly(ADP-ribose) polymer formation. Mitochondrial activities did not differ between embryos sired by control- and cyclophosphamide-exposed males. At the two-cell stage, there was no treatment-related increase in DNA double-strand breaks; by the eight-cell stage, a significant increase was noted, as indicated by increased medium and large γH2AX foci. This was accompanied by a dampened DNA repair response, detected as a decrease in the nuclear intensity of poly(ADP-ribose) polymers. The micronuclei formed in cyclophosphamide-sired embryos contained large γH2AX foci and enhanced poly(ADP-ribose) polymer and 53BP1 reactivity compared with their nuclear counterparts. Thus, paternal cyclophosphamide exposure activated a DNA damage response in cleavage-stage embryos. Furthermore, this damage response may be useful in assessing embryo quality and developmental competence.

Key Words: cyclophosphamide; γH2AX; 53BP1; poly(ADP-ribose) polymers; spermatozoa; embryo; epigenetic marks.

Millions of men of reproductive age now survive cancer as a consequence of improvements in cancer treatment regimens consisting of chemotherapeutic agents and/or radiation (Green et al., 2010). However, fertility is of concern to many of these men because these treatment regimens usually lead to an initial drop in sperm production that may be sustained for months to years, causing infertility in a large proportion of subjects (Green et al., 2010). Even men who recover spermatogenesis may still be infertile and may be faced with the possibility of transmitting heritable genetic diseases to their offspring. Cyclophosphamide, a nitrogen mustard compound, is commonly used as a cancer therapeutic and immunosuppressant agent. This drug is a bifunctional alkylating agent, forming DNA adducts, DNA cross-links, and single and double-strand DNA breaks in dividing cells. The exposure of male rats to cyclophosphamide induces DNA damage in spermatozoa that ranges from DNA double-strand breaks (DSBs) and single-strand breaks to chromosomal aberrations (Barton et al., 2003; Codrington et al., 2004). Furthermore, this paternal cyclophosphamide treatment results in dose-dependent and time-specific effects on progeny outcome, including pre- and postimplantation loss, malformations, and deficits in learning behavior; some of these outcomes are observed in subsequent generations (Auroux et al., 1990; Hales et al., 1992; Trasler et al., 1986). Our labs, and others, have used cyclophosphamide to elucidate the mechanisms underlying male-mediated developmental toxicity (Barton et al., 2007; Grenier et al., 2011).

The male genome is tightly packaged for delivery to the oocyte (Ward, 2010); paternal drug exposures may disturb the packaging of male germ cell chromatin. Indeed, paternal cyclophosphamide treatment alters the sperm basic proteome, and specifically, some components of the nuclear matrix that may be involved in events during spermigenesis and fertilization (Codrington et al., 2007a,b). The timing of spermatzoal decondensation and the deposition of modified histones are accelerated in zygotes fertilized by spermatozoa from cyclophosphamide-treated males (Grenier et al., 2010). In pronuclear-stage embryos sired by drug-treated males, the epigenetic programming of both parental genomes is disrupted, as manifested by changes in the regulation of histone H4 acetylation at lysine 5 and in DNA methylation (Barton et al., 2005). The incidence of micronuclei is dramatically elevated in two-cell embryos fertilized by spermatozoa from cyclophosphamide-treated fathers; moreover, the presence of these
micronuclei is associated with developmental delay (Grenier et al., 2011) and is reflected by the proportion of peri-implantation embryonic loss observed in previous studies (Trasler et al., 1986). Together, these findings demonstrate that paternal exposure to cyclophosphamide damages the male genome and disrupts postfertilization events in the early embryo.

Functional mitochondria are crucial for fertilization and determine the developmental potential of early embryos. Stage-specific changes in the functional compartmentalization of mitochondria are required to meet the energy needs of embryos throughout preimplantation development (van Blerkom, 2011). Furthermore, the activation and maintenance of DNA damage responses require the energy produced by mitochondria.

There are multiple DNA damage and repair pathways in cells. DNA damage, in the form of DSBs, is detected by the rapid phosphorylation of histone H2AX at serine 139 (Rogakou et al., 1998). Small γH2AX foci are associated with cell-cycle regulation and mitosis, medium foci (0.30–9.99 μm²) act as repair platforms, recruiting DNA repair proteins to sites of damage, and large foci are indicative of DNA damage accumulation and DNA DSB aggregates (McManus and Hendzel, 2005; Paull et al., 2000). γH2AX foci are induced in the male pronuclei of zygotes sired by cyclophosphamide-treated male rats (Barton et al., 2007; Grenier et al., 2010).

Large γH2AX foci colocalize with DNA DSB repair proteins (McManus and Hendzel, 2005), including p53-binding protein 1 (53BP1) and poly(ADP-ribose) polymerase-1 (PARP-1) (Paull et al., 2000). 53BP1, a component of the nonhomologous end joining repair pathway, is involved in DNA damage-induced cell cycle arrest and participates in DNA repair (Wang et al., 2002; Ward et al., 2003). In somatic cells, 53BP1 displays both cytoplasmic and nuclear localizations (Iwabuchi et al., 1998). Inhibition of the nuclear importation of 53BP1 decreases ionizing radiation-induced 53BP1 focus formation, delays DNA repair, and impairs cell survival (Moudry et al., 2011). In the early mouse zygote, 53BP1 is present only in the cytoplasm, whereas by the late pronuclear stage, some staining is found in the pronuclei (Ziegler-Birling et al., 2009). In the two- and eight-cell stages, staining is enriched in the nuclei, but no particular association is observed with any nuclear structure.

Poly(ADP-ribose) (PAR) polymerase-1 (PARP-1) is activated by DNA single-strand breaks and at stalled replication forks to facilitate DNA repair. In response to DNA damage, PARP-1 catalyzes the formation of poly(ADP-ribose) (PAR) polymers, with nicotinamide adenine dinucleotide (NADH) as an energy cofactor, covalently modifying acceptor structural chromatin proteins (Schreiber et al., 2006) and decondensing the chromatin to allow access of other repair factors to sites of DNA damage (Zhou et al., 2010). The removal of PAR polymers is primarily catalyzed by PAR glycohydrolase (PARG) (Brochu et al., 1994). The metabolism of PAR is important during chromatin dynamics, DNA replication, and repair (D’Amours et al., 1999; Kim et al., 2004). The proper regulation of PARP-1 is critical for the maintenance of genomic stability (Schreiber et al., 2006) because PARP-1 functions as a DNA repair protein in response to single-strand breaks, in the base excision repair pathway (Dantzer et al., 1999), and in the induction of cell death in response to genotoxic stress (Yu et al., 2002). Interestingly, in pronuclear-stage zygotes sired by cyclophosphamide-treated males, PARP-1 immunoreactivity is substantially elevated, not only in the damaged paternal genome but also in the maternal genome (Barton et al., 2007).

The genetic disruption of maternal DNA DSB repair in mice significantly increased the frequency of zygotes with chromosomal structural aberrations after paternal exposure to ionizing radiation (Marchetti et al., 2007). Thus, DNA damage detection and repair responses play an important role in determining progeny outcome. The first goal of these studies was to elucidate the impact of a damaged male genome on mitochondrial bioenergetics and DNA damage detection and repair responses in the cleavage-stage embryo. The second goal was to determine the impact of the formation of micronuclei and of developmental delay in the cleavage-stage embryos on their capacity to mount appropriate DNA damage responses.

MATERIALS AND METHODS

Animals, drug treatment, and embryo collection. This study was done in accordance with the guidelines of the Canadian Council on Animal Care for the ethical use and care of animals in science. The animal treatment protocol (Protocol Number: 2144) was approved by the Animal Care Committee of McGill University.

Adult male (350–400 g) and virgin female (225–250 g) Sprague Dawley rats were purchased from Charles River Canada (St Constant, Quebec, Canada) and housed at the Animal Resources Centre, McIntyre Medical Building, McGill University (Montreal, Canada). Animals received food and water ad libitum and were maintained on a 0700 h–1900 h light/dark cycle. The drug treatment and zygote protocols previously described (Grenier et al., 2011; Trasler et al., 1986) were followed with minor modifications. After 1 week of acclimatization, male rats were randomly assigned to one of two treatment groups and gavaged with saline (SAL, vehicle control) or cyclophosphamide (CAS 6055-19-2; Sigma Chemical Co., St Louis, Missouri), 6 mg/kg/day, six times per week for 4 weeks.

On the fifth week of treatment, control virgin females in proestrus (as assessed by a vaginal wash in mid-afternoon) were caged overnight in groups of two with either a control- or cyclophosphamide-treated male. Pregnancies were confirmed with sperm-positive vaginal smears the following morning, designated as gestation day 0. Sperm-positive females were euthanized on day 0 at 1300 h, on day 1 at 1000 h, and day 3 at 1000 h to collect pronuclear zygotes, 2-cell and 16-cell embryos, respectively. Oviducts and whole uteri were isolated and cleaned in prewarmed (37°C) M2 culture medium (Sigma Chemical Co.); pronuclear zygotes were collected from the ampullae in warm M2 medium, and early cell cleavage embryos were flushed with a 30 gauge needle from the infundibulum of the oviduct with 0.2 ml of warm M2 medium.

Detection of mitochondrial activity in cleavage-stage embryos. Functional mitochondria were visualized in cleavage-stage embryos using MitoTracker Green FM (catalog number M7514; Invitrogen, Burlington, Ontario, Canada) and MitoSox Red mitochondrial superoxide indicator (catalog number M36008; Invitrogen) probes. Embryos were incubated in vitro in...
modified rat 1-cell embryo culture medium (mR1ECM) milieu (Oh et al., 1998). Final concentrations of 100nM for MitoTracker Green FM and of 2μM for MitoSox Red were prepared in mR1ECM plus bovine serum albumin (BSA, 4.0 mg/ml; pH equilibrated to 7.4 with 12N HCl). This yzotic development milieu was covered with light mineral oil to prevent evaporation and pre-equilibrated for 3 h before incubation at 37°C and 5% CO2. All solutions and dilutions were prepared fresh the day of the experiment.

Sperm-positive females were euthanized at 1000 h on days 1 and 3 to collect two- and eight-cell embryos in prewarmed (37°C) M2 culture medium (Sigma Chemical Co.). Embryos were flushed with prewarmed (37°C) M2 medium, washed three times in prewarmed (37°C) mR1ECM plus BSA, and incubated in pre-equilibrated (37°C and 5% CO2) mR1ECM plus BSA with either 100nM MitoTracker Green FM or 2μM MitoSox Red. The time from embryo collection to the in vitro incubation was completed in less than 7 min to preserve embryo quality. Live in vitro embryos were incubated with MitoTracker probes for 20 min to allow the accumulation of the probes in active respiring mitochondria. For the immunodetection of MitoTracker mitochondrion-selective probes, the same immunofluorescence protocols were used as previously described for the Invitrogen molecular probes under the experimental protocol requiring fixation and permeabilization after staining with minor changes. Fixed and permeabilized embryos were incubated for 1 h in goat blocking solution (10% goat serum, 3% BSA, and 0.1% Tween 20 in PBS), and DNA was then stained with 4',6-diamidino-2-phenylindole, dihydrochloride (DAPI), 10 μg/ml, diluted in goat blocking solution, for 20 min. Embryos were then washed in 0.05% Tween 20 in PBS for 10 min and mounted in 3 μl of VectaShield mounting medium (Vector Laboratories) on a premarked pap pen slide and covered with a cover slip. Slides were then stored at 4°C and visualized with confocal microscopy within 2 days.

Confocal microscopy. A Zeiss LSM 510 Axiovort 100M confocal microscope with a Plan-Apochromat ×63/1.4 oil differential interference contrast objective was used to visualize the fluorescence of early cleavage-stage embryos. The best settings for laser scanning fluorescence imaging were determined experimentally for all primary antibodies and maintained for all cell cleavage-stage embryos. All embryos were scanned at a speed of 5–7 with an optical slice of 0.6 μm, zoom factor equal to 1, and a pinhole setting of 96 μm. Two scans of each optical section were compiled and averaged by the Zeiss LSM 510 computer software to give a final image that was 1024 x 1024 pixels in size. The embryonic cell cleavage stage was determined by counting the number of nuclei stained with propidium iodide or DAPI and confirmed with phase-contrast images. The presence of micronuclei as nuclear entities detached from the main nucleus in an embryo was determined with the nuclear propidium iodide stain or DAPI. In addition, the nuclei of blastomeres containing micronuclei were identified using the phase-contrast images. The γH2AX, 53BP1, PAR, and MitoSox embryo immunofluorescence images from Z-stacks were further analyzed and quantified using the ImageJ analysis program version 7.2.3 (Bitplane, Inc., South Windsor, CT).

Quantitative Analysis. The unit of measure (N) was the number of males; the number of embryos that are indicated below was the average number per male. Quantification of mitochondrial activity was done using the MitoSox probe because the quality of the images with this probe was superior to those obtained with MitoTracker Green; at the two- and eight-cell stages, N = 5 control males, with 28 and 41 embryos, and N = 6 cyclophosphamide-treated males, with 32 and 39 embryos, respectively, were analyzed. We analyzed all mitochondria above a set minimum threshold intensity; the mitochondrial MitoSox intensity means and counts of all mitochondria were compared in control- and cyclophosphamide-sired embryos from each cleavage stage.

Immunofluorescence z-stack images were used to quantify γH2AX foci per nucleus in two- and eight-cell embryos sired by control- and cyclophosphamide-treated males and in the micronuclei found in embryos sired by cyclophosphamide-treated males. For the control group, N = 7 males with 64 embryos and N = 10 males with 99 embryos were analyzed at the two- and eight-cell stage, respectively, and in the cyclophosphamide-sired embryo group, N = 5 males with 56 embryos and N = 7 males with 112 embryos were analyzed at the two- and eight-cell stage, respectively. For the analysis of 53BP1 reactivity, at the pronuclear, two- and eight-cell stages in the control group, the sample size was N = 6 males with 58 embryos, N = 8 males with 57 embryos, and N = 7 males with 63 embryos, respectively; in the cyclophosphamide-treated group, there were N = 5 males with 39 embryos, N = 4 males with 32 embryos, and N = 7 males with 68 embryos analyzed. PAR polymers were quantified in pronuclear zygotcs, two- and eight-cell embryos: in controls, sample sizes of N = 6 males with 51 embryos, N = 7 males with 58 embryos, and N = 8 males with 72 embryos, respectively, were studied; in the cyclophosphamide-treated group, a sample size of N = 4 males with 45 embryos, N = 5 males with 34 embryos, and N = 6 males with 52 embryos was analyzed at each cleavage stage, respectively. The chromatin structure in nuclei was compared at the two- and eight-cell stages to that in micronuclei in cyclophosphamide-sired embryos, using N = 5 and 7 males with 41 and 112 embryos for γH2AX analysis, N = 4 and 6 males with 24 and 45 embryos for 53BP1, and N = 5 and 6 males with 23 and 37 embryos for PAR detection, respectively.

Measurements relevant to our hypothesis and specific for each DNA damage response marker were analyzed using Imaris (Bitplane Inc.). In our analysis of DNA damage with γH2AX as a marker, a nuclear surface was created from propidium iodide staining for each embryo to measure the average nuclear and micronuclear volume; within that surface, the total number of nuclear and micronuclear γH2AX foci were quantified based on their volume: small foci, 0–0.29 μm3; medium foci, 0.30–9.99 μm3; or large foci, 10 μm3 and above. The data were graphed as the average number of γH2AX foci per nucleus on each embryo collection day. To compare the DNA damage in nuclei to that in micronuclei, the nuclear value was set to 1, and the fold difference between the micronuclei and nuclei was examined; all values were corrected for nuclear and micronuclear volume.

The 53BP1 and PAR average nuclear and micronuclear intensity means were assessed relative to the DNA intensity assessed based on the nuclear surface created from propidium iodide staining for each embryo. A second surface was created inversely from propidium iodide staining to capture all the cytoplasmic staining to measure the average intensity mean of 53BP1 and PAR immunofluorescence in the cytoplasm. To characterize the micronuclear chromatin content of these DNA repair indicators, data were graphed as the 53BP1 and PAR fold difference from nuclear average intensity, comparing the micronuclear to nuclear ratios; the 53BP1 and PAR intensity ratio are relative to the micronuclear to nuclear DNA intensity ratio, set at 1 to correct for the difference in DNA intensity.
Statistical analyses. All statistical analyses were done using Systat (program version 10.2, Chicago, IL). Kruskal-Wallis analysis was done to analyze for the drug effect between control- and cyclophosphamide-sired embryos with respect to 53BP1 and PAR nuclear and cytoplasmic staining and nuclear to cytoplasmic intensity mean ratios at each cleavage stage. Kruskal-Wallis analysis, with Bonferroni’s correction when needed, was done to determine a time effect between cleavage stages within a treatment group on the 53BP1 and PAR nuclear, cytoplasmic, and the nuclear to cytoplasmic intensity mean ratios.

Mann-Whitney U-test was used to assess any differences in the number of γH2AX foci between treatment groups at a specific cleavage stage and between cleavage stages within a treatment group. We also used the Mann-Whitney U-test to assess the difference in the micronuclear and nuclear chromatin structure for γH2AX, 53BP1, and PAR immunoreactivity, as well as the average numbers of small, medium, and large γH2AX foci per micronucleus (corrected for volume) between cleavage stages. Values are reported either as an average number of foci or intensity mean per embryo per replicate ± SEM or fold difference from the nuclear number of foci or micronuclear to nuclear DNA intensity means, set to 1 ± SEM.

RESULTS

Mitochondrial Function

Because mitochondrial activity is a useful measure of embryo quality, we monitored their localization, numbers, and activity within each blastomere of live cleavage-stage embryos using MitoTracker green and MitoSox red probes (Fig. 1). These fluorescent mitochondrial probes are selective indicators of mitochondrial function and energy production. In addition, MitoSox red provides a measure of oxidative stress because it indicates the presence of superoxide generated as a byproduct of oxidative phosphorylation by a leaky mitochondrial electron transport chain during adenosine triphosphate (ATP) production. We obtained similar mitochondrial staining patterns with both MitoTracker probes, but for stability, reproducibility, and image quality reasons, the data analysis was focused on the MitoSox red probe. As anticipated, the mitochondrial staining pattern was excluded from the nucleus in all cleavage-stage embryos. In two- to four-cell embryos, we detected the presence of numerous bean shape mitochondria distributed throughout each individual blastomere (Fig. 1a). Furthermore, at the two-cell stage, following the first zygotic division, there was an even distribution of mitochondria between blastomeres. Due to the differences in staining patterns observed with the mitochondrial probes in embryos collected on day 3, we analyzed the 6- to 12-cell embryos separately from the 13- to 16-cell embryos. In 6- to 12-cell embryos, a clear compartmental distribution of mitochondria between the nucleus and the exterior membrane of the embryo in each blastomere was observed. In 16-cell embryos, there was a very limited number of mitochondria in the central blastomeres; many more mitochondria, with a specific compartmental distribution, were found in the external blastomeres. In addition, in 16-cell embryos, the staining intensity of mitochondria in the central blastomeres was extremely low compared with the high staining intensity in mitochondria located in the external blastomeres. The pattern of distribution of mitochondria was influenced by cell cycle phase in all cleavage-stage embryos; mitochondria in mitotic blastomeres lost their bean shape, were diffusely distributed in the whole cell, and stained less intensely than those in interphasic blastomeres (Fig. 1b). The specific localization of mitochondria in the blastomeres of cleavage-stage embryos may dictate the plan of cellular division with a concentration of

FIG. 1. Distribution of MitoTracker probes in cleavage-stage embryos. Immunodetection of active mitochondria by MitoSox red, indicated in red, and MitoTracker green, depicted in green, in 2-, 8-, and 16-cell embryos. (A) Even distribution of mitochondria in blastomeres of two-cell embryos compared with the stage-specific functional compartmentalization in eight-cell embryos. A faint low count of mitochondria was observed in central blastomeres compared with the specialized darker distribution of mitochondria in the external blastomeres of 16-cell embryos. (B) Cell cycle–dependent mitochondrial pattern of staining, mitotic blastomeres, circled in white, had a fainter diffuse pattern of staining, as opposed to the darker, specific distribution, in interphasic blastomeres.
all the energy producing organelles where they are most needed, thus playing a role in the cell fate decision.

Although quantification revealed a trend toward an increase in the mitochondrial mean intensity and a decrease in mitochondrial count per embryo from the two- to the eight-cell stage, these parameters were not significantly different between cleavage stages and treatment groups (Supplementary fig. 1a), nor did the presence of micronuclei within a cell influence our results with MitoTracker probes at any of the cell cleavage stages (Supplementary fig. 1b).

The Characterization of γH2AX Foci in Control- and Cyclophosphamide-Sired Cleavage-Stage Embryos

To evaluate the level of DNA damage as a consequence of paternal exposure to cyclophosphamide in cleavage-stage embryos, we assessed the distribution pattern of γH2AX signals (Fig. 2). In both control- and cyclophosphamide-sired two-cell embryos, γH2AX foci were uniformly distributed, suggesting that these foci may be indicative of replication stress (Fig. 2, top two rows). The staining pattern with γH2AX in embryos collected on day 3 did not differ in 8- and 16-cell embryos; therefore, we pooled these data and show only the eight-cell embryos. In the eight-cell embryos, γH2AX foci appeared to be increased in size and be more irregularly distributed in embryos sired by cyclophosphamide-treated males compared with controls (Fig. 2, bottom two rows).

To further characterize the population of γH2AX foci, we subdivided them into three subgroups, based on their volumes, and calculated the average number of each type of focus per nucleus (Fig. 3). Control- and cyclophosphamide-sired two-cell embryos had nearly four times as many foci as eight-cell stage embryos; paternal exposure to cyclophosphamide had no impact on the number of small foci at the two-cell and eight-cell stages (Fig. 3a, left panel). Although a similar decreasing trend, by just over 50%, in the number of medium-sized γH2AX foci was observed between two- and eight-cell embryos in the control group, embryos sired by cyclophosphamide-treated males showed a steeper decline, and the numbers were more elevated than for control at the eight-cell stage (p ≤ 0.05) (Fig. 3a, middle panel). In contrast to the decrease observed in small and medium-sized foci between two- and eight-cell embryos, a significant increase was observed in the number of large γH2AX foci in both treatment groups (p ≤ 0.05) (Fig. 3a, right panel). Few large γH2AX foci were observed in control- and cyclophosphamide-sired two-cell embryos. A dramatic increase in the number of large γH2AX foci was observed in eight-cell embryos sired by cyclophosphamide-treated males compared with same stage control embryos (p ≤ 0.01). The decrease in small and medium γH2AX foci per nucleus between the two- and eight-cell embryos may reflect important events in preimplantation embryo development, such as the major and minor waves of transcription and active DNA replication in two- and four-cell embryos; the significant increase in the number of large γH2AX foci in eight-cell embryos sired by males treated with cyclophosphamide compared with control eight-cell embryos is likely to reflect an increase in the formation of DNA DSB aggregates.

Because the amount of DNA damage, represented by γH2AX foci, depends on the nuclear volume to compare DNA damage in micronuclei to nuclei, we divided the number of foci by the average nuclear volume for the nucleus and by the average micronuclear volume for the micronucleus and report the fold differences for the relative values in two- and eight-cell embryos (Fig. 3b). The majority of micronuclei were punctuated with numerous γH2AX foci. There were no differences between the nuclei and micronuclei in the numbers of small, medium, and large γH2AX foci in two-cell embryos (Fig. 3b). However, in cyclophosphamide-sired eight-cell embryos, a 1.5-fold increase in the medium γH2AX foci (p ≤ 0.001) and a 45-fold increase in the large γH2AX foci (p ≤ 0.001) were observed in micronuclei compared with nuclei (Fig. 3b). Thus, medium (p ≤ 0.05) and large foci (p ≤ 0.01) accumulate in the micronuclei of cyclophosphamide-sired eight-cell embryos (Fig. 3c). This accumulation of damage marks may represent an increase in the formation of DNA DSBs or in the sites of replication errors or a failure to recruit the appropriate DNA repair proteins.

Because micronuclei represent visible signs of DNA damage in cyclophosphamide-sired embryos, we hypothesized that the DNA damage response would be elevated in embryos with micronuclei compared with those without. To test this hypothesis, we compared the number of γH2AX foci in the nuclei of cyclophosphamide-sired two- and eight-cell embryos with and without micronuclei (Supplementary fig. 2). Strikingly, the number of γH2AX foci within each subgroup, classified by their volume, was not dependent on the presence and/or abundance of micronuclei in the embryos; there was also no correlation between the nuclear DNA damage response in individual blastomeres and the presence or absence of micronuclei within the cell (Supplementary fig. 2a). Embryos fertilized by cyclophosphamide-exposed spermatozoa and collected on day 3 were considered developmentally delayed if they were at the three- and four-cell stage; normally dividing embryos, sired by control- or cyclophosphamide-treated males, were at the 5- to 16-cell stage at this time (Grenier et al., 2011). Developmentally delayed cyclophosphamide-sired embryos, with the highest incidence of micronuclei, had the same DNA damage response profile, as assessed by the numbers of γH2AX foci, as normally dividing embryos (Supplementary fig. 2b). Thus, the presence of micronuclei did not affect the numbers of γH2AX foci in the nuclei of cells within cleavage-stage embryos.

53BP1 in Cleavage-Stage Embryos

Our next objective was to determine whether fertilization with cyclophosphamide-exposed spermatozoa would affect markers of DNA repair in cleavage-stage embryos. The localization of 53BP1 immunoreactivity in pronuclear, two- and eight-cell
embryos is depicted in Figure 4. The 53BP1 signal was distributed throughout the nucleus and cytoplasm. To determine the relative amounts of 53BP1 reactivity in these two compartments, we quantified the average intensities in the nucleus and the cytoplasm as well as the nuclear to cytoplasmic ratio in the female and male pronuclei of the two- and eight-cell embryos (Fig. 4b). Because intensities did not differ between the male and female pronuclei, the average nuclear staining intensity is given as a single value for the pronuclear-stage embryos (Fig. 4b, left graph day 0.5, pronuclear stage embryos, PN). The staining pattern of 53BP1 in 8- to 16-cell embryos collected on day 3 was identical irrespective of the treatment group; therefore, we pooled these data and show only the eight-cell embryos. The nuclear staining tended to increase as the embryos progressed from the pronuclear stage to the 8-cell stage in both the control- and cyclophosphamide-sired groups (Fig. 4b, left graph); this was accompanied by a trend toward a decrease in the cytoplasmic 53BP1 signal (Fig. 4b, middle graph). Together,
these changes resulted in a significant increase in the nuclear to cytoplasmic ratio of the localization of the 53BP1 signal from the pronuclear-stage to the 8-cell embryo in both the control- (0.84–1.74, p < 0.01) and the cyclophosphamide-treated group (0.85–1.45, p < 0.05) (Fig. 4b, right graph).

To characterize DNA repair capacity in the chromatin of micronuclei found in cyclophosphamide-sired embryos, we compared the intensity of 53BP1 reactivity in the micronuclei with that in the nuclei. The 53BP1 intensities in the micronuclei and nuclei were adjusted by the ratios of DNA intensity because micronuclei have less DNA per equivalent volume. In both the two- and eight-cell cyclophosphamide-sired embryos, the micronuclear chromatin contained significantly more 53BP1 repair protein (1.4-fold in two-cell, p < 0.05; 1.2-fold in eight-cell, p < 0.01) compared with the nuclear chromatin (Fig. 4c). Thus, this repair protein is actively recruited to micronuclear chromatin.

Similar to the number of γH2AX foci, 53BP1 nuclear reactivity was not affected by the presence and/or abundance of micronuclei in the embryos; there was also no correlation between the nuclear DNA damage response in individual blastomeres and the presence or absence of micronuclei within
In addition, developmentally delayed cyclophosphamide-sired embryos had the same DNA damage response profile, assessed by the nuclear reactivity with 53BP1, as normally dividing embryos (Supplementary fig. 3b).

Poly(ADP-ribose) Polymers in Cleavage-Stage Embryos

The immunoreactive poly(ADP-ribose) polymers (PAR), representing the product of poly(ADP-ribose) polymerase activities, in pronuclear two- and eight-cell embryos are shown in Figure 5a. The PAR signal was consistently more intense in the nucleus compared with the cytoplasm. As for 53BP1, the PAR immunoreactivity did not differ between the male and female pronuclei of pronuclear-stage embryos. The staining pattern also did not differ between 8- and 16-cell embryos irrespective of the treatment group. Neither developmental stage nor treatment significantly affected the intensity of the PAR signal in the cytoplasm or the nuclear to cytoplasmic ratio (Fig. 5b, middle and right graph). In contrast, embryos sired by cyclophosphamide-treated males displayed a dramatic decrease in PAR nuclear mean intensity at the eight-cell cleavage stage ($p \leq 0.01$) (Fig. 5b, left graph). In both the two- and eight-cell cyclophosphamide-sired embryos, the micronuclear chromatin contained significantly more PAR polymers (1.5-fold in two-cell, $p \leq 0.01$; 1.3-fold in eight-cell, $p \leq 0.01$) compared with the nuclear chromatin (Fig. 5c).
Once again, the nuclear signal of PAR polymers was not affected by the presence and/or abundance of micronuclei in the two- and eight-cell cyclophosphamide-sired embryos (Supplementary fig. 4a) or, in eight-cell cyclophosphamide-sired embryos, by a delay in the rate of development (Supplementary fig. 4b).

**DISCUSSION**

Paternal exposure to cyclophosphamide did not affect mitochondrial functional compartmentalization or bioenergetic activities in cleavage-stage embryos. However, markers of the DNA damage detection and repair responses were affected. In the eight-cell embryo, paternal cyclophosphamide exposure led to the selective formation of medium and large γH2AX foci and a decrease in nuclear PAR polymers in the absence of an effect on 53BP1 reactivity. All three DNA damage response indicators were enriched in micronuclei. However, cells with micronuclei had a similar DNA damage response to those without micronuclei.

The specialized localization of mitochondria during embryonic development is hypothesized to play a critical role in the regulation of energy production and consumption as well as roles in calcium homeostasis, cytoplasmic redox state, and...
signal transduction (van Blerkom, 2011). As observed for human and mouse embryos (van Blerkom, 2011), the staining intensities and distribution patterns of MitoTracker green and MitoSox red in early embryos display embryonic developmental stage and compartmental specificity. In eight-cell embryos, the localization of mitochondria between the nucleus and the plasma membrane on a specific side of the embryo may determine the plane of the next cycle of division by concentrating the energy necessary to allow normal developmental progression. In 16-cell embryos, we observed a very faint diffuse type of staining for mitochondria in central blastomeres, as opposed to a stronger and compartmentalized type of staining in blastomeres surrounding the embryo. These stage- and space-specific mitochondrial distributions closely resemble the differences in mitochondrial structure and number between the two cell types in the future blastocyst; inner cell mass cells are hypopolarized, almost metabolically quiescent, as opposed to the trophectoderm cells that are hyperpolarized at the basal aspect of the plasma membrane and produce almost 80% of the net ATP (Houghton, 2006; van Blerkom et al., 2002). Because the initial pool of mitochondria in the oocyte is not replenished until after blastocyst implantation and development even in the presence of heavy DNA damage. The significant increase in medium $\gamma$H2AX foci in cyclophosphamide-sired eight-cell embryos, compared with controls, suggests that these medium foci may be important in the recognition of DNA damage. The large $\gamma$H2AX foci visualized in eight-cell embryos sired by cyclophosphamide-treated males are likely to represent the accumulation of $\gamma$H2AX at hot spots of DNA damage, perhaps as a consequence of the failure to complete the repair process in early embryos (Barton et al., 2007; Grenier et al., 2010). Earlier studies have reported a similar phenomenon in a murine model; paternal exposure to radiation impaired blastocyst development due to inappropriate repair during the first cell cycle division and led to de novo mutations (Derijck et al., 2008). Interestingly, the presence of micronuclei in early embryos did not influence the quantity or nature of the $\gamma$H2AX foci in the nuclei of these embryos.

DNA damage repair capacity in cleavage-stage embryos was assessed in the pronuclear zygote, two- and eight-cell embryo with two markers of DNA repair, 53BP1 and poly(ADP-ribose) polymers, that are known to be recruited to the sites of DNA DSBs detected by $\gamma$H2AX. It is not likely that the 53BP1 immunoreactivity is strongly colocalized with $\gamma$H2AX in these embryos because a faint diffuse and homogenous pattern of 53BP1 distribution was observed in both the nuclear and cytoplasmic compartments throughout the early cleavage stages studied. In addition, 53BP1 protein expression was unaffected by the presence of a damaged male genome. Similar findings were reported previously in a damage free mouse embryonic model in which 53BP1 protein localization changed upon blastocyst formation. The failure of 53BP1 and $\gamma$H2AX to colocalize in the embryo (Ziegler-Birling et al., 2009) reinforces the notion that the high levels of H2AX phosphorylation may be linked to chromatin remodeling in the early embryo rather than directly to a DNA damage response (Ziegler-Birling et al., 2009). The developmental significance of the nuclear retention of 53BP1 as a partial mediator of p53 activity in regulating cell cycle checkpoints, allowing the progression of cell cycle division of cleavage-stage embryos, has been established previously (Fernandez-Capetillo et al., 2003).

A decrease in nuclear poly(ADP-ribose) polymers was observed in eight-cell embryos sired by cyclophosphamide-exposed spermatozoa. The presence of micronuclei did not influence the amount of poly(ADP-ribose) polymers in the nucleus. In general, a decrease in poly(ADP-ribose) polymers is suggestive of a decrease in the poly(ADP-ribosylation) of histones and/or PARP-1 (Zhou et al., 2010). This may result in...
the recondensation of chromatin, reducing the accessibility of potential DNA damage repair proteins to DNA (Zhou et al., 2010); however, examination of the gross nuclear morphology of cyclophosphamide-sired eight-cell embryos did not reveal any apparent increase in condensed chromatin. Numerous scenarios could lead to a decrease in poly(ADP-ribosylation) in early embryos; these include NADH energy depletion, reducing PARP-1 activity, an increase in PARP-1 activity, leading to auto-poly(ADP-ribosylation) of PARP-1 and its inactivation, or an increase in PARG catalytic activity, removing poly(ADP-ribose) polymers. Previously, we reported that paternal exposure to cyclophosphamide led to an increase in PARP-1 immunoreactivity in both male and female pronuclei (Barton et al., 2007). Our data show that there is no drug treatment effect on the level of poly(ADP-ribosylation) in pronuclear or two-cell embryos, suggesting that the increase in PARP-1 immunoreactivity may be accompanied by an increase in PARG catalytic activity, dampening the repair capacity of cleavage-stage embryos. The reduced PARP-1 activity observed in eight-cell embryos was not associated with a decrease in mitochondrial energy status, as assessed with the MitoTracker probes; therefore, the reduction in PAR polymers does not appear to be due to a decrease in energy stores in the embryo. Energy depletion as a result of PARP-induced NADH depletion may contribute to the delay in cell cycle progression seen at the eight-cell stage (Grenier et al., 2011). Developmental arrest was reported in pronuclear-stage mouse embryos treated with a PARP inhibitor (Osada et al., 2010). It is clear that the proper functioning of the complex poly(ADP-ribosyl)ation system is necessary for the early stages of mouse embryogenesis (Osada et al., 2010).

Micronuclei are a readily identifiable mark of DNA damage in the paternal genome in embryos sired by cyclophosphamide-treated males. In two- and eight-cell embryos, both 53BP1 and poly(ADP-ribose) polymers were enriched in chromatin in the micronuclei compared with the nucleus; this enrichment was observed in the absence of any increase in γH2AX foci, tagging DNA DSBs. These findings suggest that there may be a γH2AX-independent mechanism of recruitment of 53BP1 and poly(ADP-ribose) polymers in micronuclei at the two-cell stage. By the eight-cell stage, a marked accumulation of medium and large γH2AX foci was observed in micronuclei; this occurred in the absence of an increase in the intensity of the staining for 53BP1 or poly(ADP-ribose) polymers in comparison with the two-cell embryos. The accumulation of γH2AX foci in the micronuclei of eight-cell embryos may indicate the failure of DNA repair processes to resolve DNA DSBs (Celeste et al., 2003). Micronuclei may gradually lose functionality as the embryo progresses from two-cells to eight-cells; indeed, we reported previously that the incorporation of EdU (5-ethynyl-2′-deoxyuridine) into DNA was decreased in micronuclei at the eight-cell stage (Grenier et al., 2011).

In summary, we have demonstrated that fertilization by sperm from cyclophosphamide-treated male rats produces a conceptus with a heavily damaged paternal genome. The damaged paternal genome triggers both a γH2AX-dependent and a γH2AX-independent DNA damage response with respect to micronuclear formation, within the same cells. The two-cell embryo is capable of mounting a DNA damage response because there is a recruitment of 53BP1 and an increase in poly(ADP-ribose) polymers in micronuclei. However, the DNA repair response is not adequate to prevent the accumulation of medium and large γH2AX foci in micronuclei by the eight-cell stage. The accumulation of DNA damage and the inability of the embryo to adequately repair the paternal genome are likely to contribute to the elevated pre- and postimplantation death observed as a consequence of paternal cyclophosphamide exposure.

SUPPLEMENTARY DATA

Supplementary data are available online at http://toxsci.oxfordjournals.org/.

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