REVIEW

Cytometric assessment of DNA damage in relation to cell cycle phase and apoptosis

Xuan Huang*, H. Dorota Halicka*, Frank Traganos*,
Toshiki Tanaka*†, Akira Kurose*‡ and Zbigniew Darzynkiewicz*

*Brander Cancer Research Institute, New York Medical College, Valhalla, NY, USA, †First Department of Surgery, Yamaguchi University School of Medicine, Yamaguchi, Japan and ‡Department of Pathology, Iwate Medical University, Iwate, Japan

Received 3 June 2005; revision accepted 17 June 2005

Abstract. Reviewed are the methods aimed to detect DNA damage in individual cells, estimate its extent and relate it to cell cycle phase and induction of apoptosis. They include the assays that reveal DNA fragmentation during apoptosis, as well as DNA damage induced by genotoxic agents. DNA fragmentation that occurs in the course of apoptosis is detected by selective extraction of degraded DNA. DNA in chromatin of apoptotic cells shows also increased propensity to undergo denaturation. The most common assay of DNA fragmentation relies on labelling DNA strand breaks with fluorochrome-tagged deoxy-nucleotides. The induction of double-strand DNA breaks (DSBs) by genotoxic agents provides a signal for histone H2AX phosphorylation on Ser139; the phosphorylated H2AX is named γH2AX. Also, ATM-kinase is activated through its autophosphorylation on Ser1981. Immunocytochemical detection of γH2AX and/or ATM-Ser1981(P) are sensitive probes to reveal induction of DSBs. When used concurrently with analysis of cellular DNA content and caspase-3 activation, they allow one to correlate the extent of DNA damage with the cell cycle phase and with activation of the apoptotic pathway. The presented data reveal cell cycle phase-specific patterns of H2AX phosphorylation and ATM autophosphorylation in response to induction of DSBs by ionizing radiation, topoisomerase I and II inhibitors and carcinogens. Detection of DNA damage in tumour cells during radio- or chemotherapy may provide an early marker predictive of response to treatment.

DNA FRAGMENTATION DURING APOPTOSIS

Involvement of different nucleases in DNA fragmentation
Condensation of chromatin and internucleosomal DNA fragmentation, together with cell shrinkage and shedding of apoptotic bodies (‘blebbing’), are widely recognized hallmarks of apoptosis.

Correspondence: Dr Z. Darzynkiewicz, Brander Cancer Research Institute at NYMC, 19 Bradhurst Avenue, Suite 2400, Hawthorne, NY, 10532, USA. Tel.: 914-347-2801; Fax: 914-347-2804; E-mail: darzynk@nymc.edu

© 2005 Blackwell Publishing Ltd.
Several nucleases have been identified as contributing towards DNA degradation; their activity is modulated by divalent cations. Depending on cation concentration, three distinct steps of DNA fragmentation, likely mediated by different enzymes, can be identified: (i) in the presence of Mg\(^{2+}\) (2 mM, DNA is fragmented to about 0.05–1 megabase (Mb)-size sections (type-I, high molecular weight DNA fragmentation)); (ii) at low (nanomolar) Ca\(^{2+}\) concentration, nuclear DNA is cleaved into intermediate (\(~\sim 300\) kb) fragments (type-II, intermediate DNA fragmentation); (iii) at micromolar levels of Ca\(^{2+}\), internucleosomal (type-III) DNA fragmentation takes place leading to formation of DNA sections of the size of mono and oligonucleosomes, which form a characteristic ‘DNA-ladder’ pattern during electrophoresis (Arends \textit{et al.} 1990).

Among the nucleases associated with DNA fragmentation during apoptosis, the best characterized is CAD (caspase-activated DNase) with its inhibitor ICAD (inhibitor of CAD) in mice, and its human homologue DFF40/DFF45 (DNA fragmentation factor) (Enari \textit{et al.} 1998). CAD and ICAD (or DFF40 and DFF45) remain inactive in a complex with its respective inhibitor until proteolytic cleavage of the inhibitor by activated caspase during apoptosis leads to their activation (Fig. 1). These DNases then translocate to the nucleus where they cleave DNA between nucleosomes. In some human tissues, DNase-X appears to substitute of DFP40 (Los \textit{et al.} 2000). CIDeA and CIDeB (CIDe: cell death-inducing DFF45-like effector) show significant similarity with DFF45 and, when overexpressed, induce apoptosis (Inohara \textit{et al.} 1998). Also involved in DNA fragmentation during apoptosis is DNase-I, initially crystallized by Kunitz (1950). Its activity is modulated by Ca\(^{2+}\) and Mg\(^{2+}\) and inhibited by Zn\(^{2+}\) (Walker \textit{et al.} 1994). DNase-I is localized in the perinuclear space (Peitsch 1993) and its overexpression induces apoptosis (Polzar \textit{et al.} 1993). Other nucleases linked to apoptotic DNA fragmentation...
are human DNAS1L3 (Boulares et al. 2002; Boulares & Ren 2004), NUC18 (Gaido & Cidlowski 1991) and NUC70 (Urbano et al. 1998), all activated by Ca^{2+} and Mg^{2+} and blocked by Zn^{2+}. Acidic endonucleases such as DNase-II (Barry & Eastman 1993) and L-DNase-II (Scovassi & Torriglia 2003) also appear to be involved in DNA degradation during apoptosis. It should also be mentioned that AIF (apoptosis inducing factor), the protein which is released from the intermembrane compartment of mitochondria, is also capable of inducing chromatin condensation and DNA cleavage on megabase-size fragments (Susin et al. 1999).

Detection of cells with fractional DNA content after extraction of low molecular weight DNA

When apoptotic cells are fixed in precipitating fixatives such as ethanol, methanol or acetone, or permeabilized by detergent, the small-size fragments of DNA, the product of internucleosomal DNA cleavage during apoptosis, are often extracted from the cells during their staining in aqueous solutions (Fig. 1). As a consequence of DNA loss, apoptotic cells end up with deficit in their DNA content, and when stained with a DNA-specific fluorochrome they can be recognized as having a fractional DNA content. On DNA content frequency histograms, they often form a characteristic, ‘sub-G_{1}’ or ‘hypodiploid’ peak (Umansky et al. 1981; Nicoletti et al. 1991; Gong et al. 1994). Shedding apoptotic bodies containing fragments of nuclear chromatin additionally contributes to the loss of DNA from apoptotic cells. Identification of a sub-G_{1} cell population is usually carried out to estimate the frequency of apoptotic cells (apoptotic index; AI) (Darzynkiewicz et al. 1992). Commercially available software designed to deconvolute DNA frequency histograms to estimate the proportion of cells in particular phases of the cell cycle often allows one to quantify the percentage of apoptotic cells in the ‘sub-G_{1}’ peak.

It is desirable that the ‘sub-G_{1}’ peak representing apoptotic cells should be separated from the G_{1} peak of the non-apoptotic cell population, with no overlap between them (Fig. 1e). However, the degree of extraction of fragmented DNA varies depending on the extent of DNA degradation (duration of apoptosis), the number of cell washings, pH and salt concentration of the washing and staining buffers. Although extraction of DNA from apoptotic cells can be enhanced by rinsing cells in high molarity buffer prior to staining (Gong et al. 1994), separation of the ‘sub-G_{1}’ peak is not always achievable. Furthermore, when DNA fragmentation during apoptosis terminates at 50–300 kb fragments and does not proceed to internucleosomal sized fragments (Oberhammer et al. 1993), little DNA can be extracted and this approach fails to identify apoptotic cells in such instances. It should also be noted that the extraction of DNA from apoptotic G_{2}, M or S phase may not be adequate to have them at the ‘sub-G_{1}’ peak position as they may end up as ‘sub-G_{2}M’ or ‘sub-S’ peaks, located on DNA content histograms in place of S- and G_{1}-phase peaks, respectively. Figure 2b illustrates such a case when the NF-κB inhibitor parthenolide initially arrested HL-60 cells in G_{1} and G_{2}M, after which both populations underwent apoptosis giving rise to the populations marked Ap1 and Ap2, respectively (Pozarowski et al. 2003). Figure 2(c and d) also demonstrate that bivariate analysis of cellular DNA and RNA content, which allows one to distinguish G_{0} from G_{1} cells based on differences in their RNA content (Darzynkiewicz et al. 1976, 1980), also makes it possible to reveal whether G_{0} or G_{1} cells preferentially undergo apoptosis (Bruno et al. 1992).

Instead of fixation, hypotonic solutions containing detergent are often used to make cells permeable to the dye in DNA staining protocols (Nicoletti et al. 1991). Such treatment causes lysis of the plasma membrane which leads to significant bias in estimation of the apoptotic index. The bias stems from the fact that nuclei of apoptotic cells are often fragmented and therefore several chromatin fragments are released from a single lysed cell. Furthermore, lysis of mitotic cells releases individual chromosomes or chromosome aggregates. In the case of micronucleation (e.g. after cell irradiation or treatment with clastogens) the micronuclei are released.
as well. Each nuclear fragment, chromosome, or micronucleus is recorded by a flow cytometer as an individual object characterized by a ‘sub-G$_1$’ DNA content, and therefore often erroneously classified as an individual apoptotic cell. This bias is particularly evident when a logarithmic scale is used to display DNA content on the histograms, which allows one to record events with as little as 1%, or even 0.1% of the DNA content of a G$_1$ cell. Such events certainly cannot be classified as individual apoptotic nuclei, and their percentage grossly exceeds the actual percentage of apoptotic cells in the sample. It should be noted, however, that cell permeabilization with detergent in isotonic solution, particularly in the presence of serum proteins (e.g. as in the protocols for differential staining of RNA and DNA with acridine orange (AO)) (Darzynkiewicz et al. 1976; Traganos et al. 1977) does not lyse the cells and therefore can be used to quantify apoptotic cells, identifying them as cells with a fractional DNA content (Fig. 1).

Increased propensity of DNA to undergo denaturation
Free DNA in aqueous solutions at physiological pH and ionic strength has a double-stranded structure. Its exposure to heat, acid or alkali causes the two strands to unwind and separate. This is known as DNA denaturation or melting and is the consequence of destruction of the hydrogen bonding between the paired bases of the opposite strands. The sensitivity of free DNA to denaturation depends on its GC/AT ratio, because, as a result of an additional hydrogen bond, the GC pair confers increased stability compared with AT. In nuclear chromatin, DNA is additionally
Cytometry of DNA damage

227

stabilized by interactions with histones and other proteins and the degree of stability depends on chromatin structure (Darzynkiewicz 1990). The cytometric method for assaying the sensitivity of DNA in situ to denaturation utilizes the metachromatic property of AO. Namely, the dye fluoresces green (~530 nm) when it intercalates between the neighboring base pairs of the double-stranded DNA, while its binding to single-stranded DNA sections leads to red fluorescence (> 600 nm) (a). (b, c) Untreated (b) and topotecan-treated (c) HL-60 cells; their RNA was removed by incubation with RNase and DNA was subjected to partial denaturation by HCl-treatment and stained with AO (Darzynkiewicz et al. 1977). The shift from 530 to > 600 nm emission reflects DNA denaturation. In the untreated culture (b) the mitotic (M) and immediately post-mitotic (pM) cells show an increased propensity to denaturation compared with interphase cells. The DNA topoisomerase I inhibitor topotecan induces apoptosis preferentially in S-phase cells (Del Bino et al. 1991). Compared with non-apoptotic cells, the cells undergoing apoptosis (Ap) show markedly decreased 530 nm- and increased > 600 nm fluorescence, indicative of extensive of DNA denaturation (c).
DNA in nuclei of cells subjected to ionizing radiation, similar to that in apoptotic cells, is also highly susceptible to denaturation and AO-cytometry has been used to the estimate extent of the damage vis-à-vis radiation dose (Rydberg 1984).

It should be noted that, as an alternative to the AO-methodology, the presence of denatured DNA in chromatin can be detected immunocytochemically using antibodies reactive with ssDNA; this approach has been used to identify apoptotic cells by flow cytometry as well (Frankfurt 1999). However, whether using AO or immunocytochemical detection of DNA single strandedness as a marker of DNA damage during apoptosis, caution should be exercised to distinguish live cells with highly condensed chromatin such as mitotic or G0 cells from cells that undergo apoptosis. The distinction is particularly difficult, for instance, when cells that initially were arrested in mitosis, e.g. by microtubule poisons such as taxol or vinca alkaloids, subsequently die by apoptosis. The morphology of these cells has to be then assessed by microscopy to distinguish live from apoptotic mitotic cells. Chromosomes of the latter lose their structural framework and resemble spherical droplets of structureless chromatin which often coalesce with each other (Darzynkiewicz et al. 1992, 1997).

Detection of DNA strand breaks (TUNEL assay)

Fragmentation of DNA during apoptosis generates a large number of DNA nicks (single-strand breaks) and double-strand breaks (DSBs) in the nucleus (Arends et al. 1990; Oberhammer et al. 1993). The nicks may be labelled by attaching fluorochrome-tagged triphosphodeoxynucleotides in a reaction catalysed by exogenous DNA polymerase I (in situ nick translation, ISNT; Darzynkiewicz et al. 1992; Gold et al. 1994). The 3′-OH termini in DSBs, in turn, can be labelled in a reaction employing terminal deoxynucleotidyltransferase (TdT; Gorczyca et al. 1992, 1993a; Li & Darzynkiewicz 1995; Li et al. 1995, 1996). The assay is often called ‘TUNEL' from ‘TDT-mediated dUTP-biotin nick-end labelling' (Gavrieli et al. 1992). This acronym is a misnomer as DSBs rather than DNA nicks are labelled in this reaction. Several variants of this assay, as shown in Fig. 4, have been developed (Li et al. 1995). Of all the variants, the one based on incorporation of BrdU (Fig. 5) appears to be the most advantageous, in terms of high sensitivity, low cost and simplicity (Li & Darzynkiewicz 1995). In this variant, BrdU attached to DSBs (as poly BrdU) is detected with an FITC-conjugated anti-BrdU antibody. In fact, the very same antibody is used as the one that serves to detect BrdU incorporated during DNA replication (Dolbeare et al. 1983). However, poly BrdU at the site of DSBs is accessible to the antibody without the need for DNA denaturation, which otherwise is required to detect the precursor incorporated during DNA replication.

The detection of DSBs by this assay requires prefixation of cells with a crosslinking agent such as formaldehyde. Unlike precipitating fixatives, formaldehyde prevents the extraction of small DNA fragments. Labelling DSBs in this procedure, which is accomplished with fluorescein-conjugated anti-BrdU antibody (Fig. 5), can be combined with the staining of DNA with another colour fluorochrome (e.g. PI, red fluorescence). Multiparameter cytometry of cells that are differentially stained for DNA strand breaks and for DNA allows one to distinguish apoptotic from non-apoptotic cell subpopulations and to reveal the cell cycle distribution in these subpopulations, respectively (Gorczyca et al. 1992, 1993a). As is evident in Fig. 4, for example, camptothecin preferentially induces apoptosis of S-phase cells. It should be noted, however, that, as a result of prior shedding of apoptotic bodies (which may contain nuclear fragments), or as a result of extensive DNA fragmentation such that even after fixation with formaldehyde, minute DNA fragments cannot be retained and therefore cells at later stages of apoptosis may have diminished DNA content. Such late apoptotic cells may have a sub-G1 DNA content and be highly positive in the TUNEL assay. A variety of kits which represent all the variants of the assay.
Figure 4. Detection of DNA fragmentation during apoptosis using different variants of the assay of detection of DNA strand breaks by fluorochrome-labelling-3’OH termini in the reaction catalysed by exogenous terminal deoxyribonucleotidyl transferase (TdT). Bivariate distributions (contour maps) of DNA content versus DNA strand-break labelling showing HL-60 cells treated with 0.15 µM of the DNA topoisomerase I inhibitor camptothecin, which preferentially induces apoptosis of S-phase cells (Del Bino et al. 1991). The three panels to the left illustrate indirect labelling, utilizing either BrdU (see Figure 5), digoxygenin-conjugated dUTP (d-dUTP), or biotinylated dUTP (b-dUTP). The two right panels show cell distributions after a single-step labelling with either BODIPY or FITC-conjugated dUTP. The numbers show an n-fold separation (note exponential scale) of the G1 versus apoptotic peak values of fluorescence intensity, in respective variants of the assay (Li & Darzynkiewicz 1995).

Figure 5. Schematic illustration of DNA strand-break labelling by TdT-mediated Br-dUTP attachment to 3’OH ends and polymerization, followed by immunocytochemical (FITC) detection of BrdU.
as illustrated in Fig. 4, are commercially available. The TUNEL assay has been found particularly useful in clinical studies, to reveal the extent of apoptosis in relation to cell cycle phase during treatment of leukaemias (Gorczyca et al. 1993a; Halicka et al. 1997).

DETECTION OF DNA DAMAGE INDUCED BY GENOTOXIC AGENTS

The comet assay

Compared with the severity of DNA damage during apoptosis which generates an overabundance of DNA strand breaks, the DNA damage induced by genotoxic agents, including pharmacological doses of radiation and anti-tumour drugs, is less extensive and therefore more difficult to be directly assayed by cytometry. Unless DNA damage is very extensive, the TUNEL assay is not sensitive enough to detect it. As mentioned earlier in this review, the detection of DNA propensity to undergo denaturation as measured by AO metachromasia, has been shown to detect DNA damage induced by ionizing radiation (Rydberg 1984), but this methodology has not been accepted in wider practice. During the past two decades, analysis of DNA damage in individual cells was essentially limited to a single-cell-DNA gel electrophoresis technique, the so-called ‘comet’ assay. Individual cells with damaged DNA embedded in agarose gels, when subjected to an electric field, generate a characteristic pattern of DNA distribution which, after staining with a fluorochrome, results in an image that resembles a comet. The extent and length of the comet’s tail correlates with the severity of DNA damage (Ostling & Johanson 1984). By using different electrophoresis buffers and lysing conditions, several variants of this methodology have been developed, including assays designed to detect DSBs and single-strand breaks (SSBs) (Singh & Stephens 1998; Olive 2002). To obtain quantitative estimates of DNA damage, the extent and length of the comet tail can be evaluated by fluorescence image analysis, or by laser scanning cytometry (Bacso & Eliason 2001; Petersen et al. 2000; Chandna 2004). While in principle it is possible to measure fluorescence intensity integrated over the comet to obtain information about total DNA content of the measured cell and thereby identify the cell’s position in the cell cycle, this approach has not been used in practice to correlate DNA damage with the cell cycle phase.

Immunocytochemical detection of DNA adducts

Antibodies have been successfully developed to detect a variety of DNA adducts induced by different genotoxic agents. Thus, for example, DNA adducts were visualized in mouse tissues and human blood cells following treatment with ben[α]pyrene or its diol epoxide (Van Schooten et al. 1991). Also, the methylated bases O6-methylguanine and 7-methylguanine were immunocytochemically identified in rodent tissues after exposure to the tobacco-specific nitrosamine-4(methylnitrosamino)-1-(3-pyridyl)-1-butane (Van Benthem et al. 1994). The list of different DNA adducts which can be detected immunocytochemically is extensive (den Engelse et al. 1990; Meijer et al. 1997; Mistry et al. 2003), but it is not in the scope of this review to cover this topic. Potentially, all these adducts that can be immunocytochemically identified can be studied by multiparameter cytometry with respect to cell cycle phase specificity and induction of apoptosis. As yet, however, such studies have been isolated (Shinozaki et al. 1998).

Histone H2AX phosphorylation as a marker of DNA double-strand breaks (DSBs)

DNA damage that involves formation of DSBs induces phosphorylation of Ser139 at the carboxy terminus of histone H2AX (Rogakou et al. 1998; Sedelnikova et al. 2002), one of several variants
of the nucleosome core histone H2A (West & Bonner 1980; Thatcher & Gorovsky 1994; Pehrson & Fuji 1998), the gene for which it codes being located on chromosome 11 (11q23.2–23.3; Ivanova et al. 1994). Phosphorylation takes place on H2AX molecules in megabase chromatin domains flanking the DSBs (Fig. 7), and is mediated by the PI-3-like protein kinases, ATM- (Rogakou et al. 1998; Anderson et al. 2001; Burma et al. 2001; Sedelnikova et al. 2002), ATR- (Furuta et al. 2003), and/or DNA-dependent protein kinase (DNA-PK) (Park et al. 2003; Wang et al. 2005). The Ser139 phosphorylated H2AX has been named γH2AX (Rogakou et al. 1999). Development of an antibody specific to γH2AX made it possible to detect H2AX

phosphorylation and thus to assay immunocytochemically DNA damage and repair in situ, in chromatin of individual cells (Banath & Olive 2003). Compared with the alternative method of DNA damage assessment which is based on analysis of electrophoretic mobility of DNA released from individual cells, the comet assay, the immunocytochemical approach is less cumbersome and offers much greater sensitivity (Huang et al. 2004). Shortly after induction of DSBs, e.g. by ionizing radiation or other genotoxic agents, the presence of γH2AX in chromatin can be detected with this antibody in the form of discrete nuclear foci (Fig. 7) (Rogakou et al. 1999; Sedelnikova et al. 2002; Sedelnikova et al. 2003). Because each focus represents a single DSB (Sedelnikova et al. 2002) their frequency is considered to report the incidence of DSBs. Several checkpoint and DNA repair proteins such as Rad50, Rad51 and Brc1 co-localize with γH2AX (Paull et al. 2000). It was recently proposed that phosphorylated H2AX may function as an anchor holding broken DNA ends in close proximity in chromatin, facilitating their repair (Bassing & Alt 2004). γH2AX also mediates translocation of the p53 binding protein 1 (53BP1) to the radiation-induced foci (Anderson et al. 2001).

The loss of H2AX in mice leads to genomic instability; H2AX(−/−) mice are radiation sensitive, growth retarded, and immunodeficient (Celeste et al. 2002). Even H2AX haploinsufficiency compromises genetic integrity, enhancing susceptibility to cancer when p53 remains non-functional (Celeste et al. 2003a). Thus, H2AX appears to be a guardian of genomic integrity and both its alleles are required for optimal protection against carcinogenesis (Bassing et al. 2003). It should be noted, however, that, while the translocation of repair and signalling proteins to DSBs is not abrogated in H2AX(−/−) cells, these proteins do not assemble in chromatin to form the characteristic irradiation-induced nuclear foci (Celeste et al. 2003b).

Western blotting and detection of γH2AX immunofluorescence (IF) provide two major approaches to analyse H2AX phosphorylation. Measurement of γH2AX IF by multiparameter flow or laser-scanning cytometry (Anderson et al. 2001; Banath & Olive 2003; Huang et al. 2003; MacPhail et al. 2003a,b; Bassing & Alt 2004; Huang et al. 2004; Olive 2004) is particularly advantageous. The major benefit of the cytometric approach stems from the fact that H2AX phosphorylation in situ, in chromatin of individual cells, can be measured with high sensitivity and accuracy and the expression of γH2AX can be directly correlated, within the same cells, with their DNA content, induction of apoptosis or any other cell attribute of interest. Large cell numbers, thus, may be rapidly analysed and the data provide information on the extent of H2AX phosphorylation with respect to their cell cycle phase, commitment to die in response to DNA damage and their surface immunophenotype, amongst others. Cytometry also allows one to analyse intercellular variability in H2AX phosphorylation within cell populations and to identify rare cell subpopulations, otherwise undetectable by western blotting. The review which follows is focused on applications of multiparameter cytometry in analysis of H2AX phosphorylation as a reporter of the presence of DSBs.

**Intrinsic (‘programmed’) H2AX phosphorylation**

Histone H2AX is phosphorylated on Ser139, not only in response to DNA damage caused by environmental genotoxic factors, but also in healthy, untreated cells. This has been called ‘intrinsic’, ‘programmed’ or ‘scheduled’ H2AX phosphorylation (Banath & Olive 2003; Huang et al. 2004). One instance of such phosphorylation occurs in response to transient formation of DSBs in the course of V(D)J and class-switch recombination in immune system development (Downs et al. 2000; Jackson 2001; Modesti & Kanaar 2001; Fernandez-Capetillo et al. 2002). H2AX is also phosphorylated, in the absence of externally induced damage to DNA, during cell cycle progression, particularly during DNA replication (Fig. 6; MacPhail et al. 2003b). As is evident in Fig. 6, the extent of H2AX phosphorylation during the cell cycle varies significantly depending
on cell line (MacPhail et al. 2003a,b). In some cell types, such as A549 and NHBE, significant expression of γH2AX is observed, not only in S-phase cells, but also cells in G2/M. The nuclear γH2AX IF foci reflecting the intrinsic H2AX phosphorylation are generally smaller in size and less distinct compared with foci that are formed upon induction of DNA damage by extrinsic factors (Fig. 8; Huang et al. 2004). The multitude of DSBs generated in the course of DNA fragmentation during apoptosis (Huang et al. 2004) also induces extensive H2AX phosphorylation (MacPhail et al. 2003b).

To assess H2AX phosphorylation induced by external genotoxic factors, one has therefore to account for the extent of the ‘intrinsic’ expression of γH2AX in the untreated cells. This is often done by subtracting the mean values of γH2AX IF of the G1, S and G2/M subpopulations of untreated cells from the respective means of γH2AX IF of the same type cells that were exposed to the factors damaging their DNA (Huang et al. 2003). The differential (ΔγH2AX IF) provides an estimate of the damage-induced increase in intensity of γH2AX IF for a particular phase of the cell cycle.

Parallel with the doubling of DNA content, histone content also doubles throughout the cell cycle and therefore the ratio of histone to DNA content remains invariant in the cell (Marzluff & Duronio 2002). As a consequence of higher histone content, the cells in S and G2/M with the same degree of H2AX phosphorylation (the same per cent of phosphorylated H2AX molecules per total H2AX molecules) therefore have 1.5- and 2.0-fold higher integrated value of γH2AX IF compared to G1 cells. To assess the degree of H2AX phosphorylation, and thus to make γH2AX IF independent of histone doubling during the cycle, the data may be normalized by presenting it as γH2AX IF per unit of DNA (histone). This is accomplished by dividing the mean S-phase and G2/M-phase γH2AX IF by 1.5 and 2.0, respectively (Huang et al. 2003). After such normalization, the difference in H2AX IF during the cell cycle reveals the degree of γH2AX phosphorylation, i.e. the ratio of phosphorylated H2AX per total number of H2AX molecules within each cell. Similarly, by comparing H2AX phosphorylation in cells of different DNA ploidy, data should be standardized to express γH2AX IF per unit of DNA rather than per cell.

Figure 8. Induction of γH2AX foci in MCF-7 cells after exposure to 0.15 μm DNA topoisomerase I inhibitor topotecan (Tpt) for 4 h. The cells were stained with DNA fluorochrome DAPI and immunostained with FITC-tagged γH2AX Ab. (a) Emission of DAPI, (b) of FITC-labelled γH2AX and (c) of both (merged image). The nucleus of the cell in the upper left of (b) shows numerous typical γH2AX foci, each thought to represent a single DSB. The pattern of γH2AX-Ab IF of the cells below and to the right in (b) is typical of the intrinsic (‘programmed’) labelling. The cell with γH2AX Ab foci (upper left) most likely was in S-phase, as it is the collisions between DNA progressing replication forks and DNA topoisomerase I–DNA complexes stabilized by Tpt that induce DSBs (Hsiang et al. 1989; Del Bino et al. 1991).
Phosphorylation of γH2AX and of ATM kinase induced by genotoxic agents

As mentioned, induction of DSBs by genotoxic agents activates protein kinases that phosphorylate H2AX on Ser139. Figure 9 illustrates the cell cycle phase-related differences in response of individual cells to UV-B light irradiation. As it is evident, the exposure of HL-60 cells to UV light, regardless of the dose of radiation (57 J/m²−3.45 kJ/m²), led to induction of γH2AX predominantly in S-phase cells. At the lowest dose of exposure, the induction was distinctly more pronounced in early, compared with mid- or late-S-phase cell (Halicka et al. 2005). A large proportion of G1 and G2/M cells (below the marked threshold) showed no increase in expression of γH2AX, even at the highest doses of exposure to UV light. This pattern of cell response to UV is consistent with earlier reports describing formation of DSBs (H2AX phosphorylation detected by western blotting) in DNA replicating cells after exposure to UV radiation (Kaina 1998; McGregor 1999; Dunkern & Kaina 2002; Squires et al. 2004). The mechanism of DSB induction by UV involves a collision (stalling) of the replication forks at the sites of the UV-induced base adducts (Dunkern & Kaina 2002; Kaina 1998; McGregor 1999). This mechanism very much resembles that caused by DNA topoisomerase inhibitors, in which the collisions occurring at sites of stabilization of the DNA topoisomerase attached to DNA by the inhibitor (‘cleavable complexes’), trigger nuclease activation (Hsiang et al. 1989), and in turn, apoptosis (Del Bino et al. 1991). Suppression of DNA replication by the DNA polymerase inhibitor aphidicolin has prevented the UV-induced H2AX phosphorylation in these cells (Halicka et al. 2005). However, aphidicolin itself induced a moderate degree of H2AX phosphorylation in early S-phase cells.

It should be noted that the induction of γH2AX assayed by cytometry provides a sensitive and convenient means to measure the extent of DNA damage following exposure to X-irradiation (MacPhail et al. 2003a,b). The pioneering studies by Olive and her collaborators (Banath & Olive 2003; MacPhail et al. 2003a,b) provided evidence that DSBs induced by
X-radiation could be detected and conveniently measured using multiparameter flow and image cytometry. These authors proposed that this assay could be used as a surrogate for cell killing in viability tests for agents that generate DSBs (Banath & Olive 2003). Similar to our findings on response of cells to UV-B irradiation (Fig. 9; Halicka et al. 2005), X-irradiation also induced H2AX phosphorylation preferentially in S-phase cells (MacPhail et al. 2003a).

DSBs induced in cells that reproduce are potentially carcinogenic/mutagenic lesions. Thus, cytometric assays of H2AX phosphorylation can be used to assess the extent of genotoxic effects following cell contact with carcinogens. Figure 10 shows response of A549 human pulmonary adenocarcinoma cells to tobacco smoke. Whereas 10 min of exposure to whole smoke had little effect on the cells, longer exposure times led to increased DNA DSBs as detected by increased levels of γH2AX that showed little cell cycle phase specificity (Albino et al. 2004).

Inhibitors of DNA topoisomerase I and II (topo1 and topo2) are among the most clinically effective anti-tumour drugs. Most of them bind to DNA by intercalation between adjacent base pairs that leads to formation of a covalent link between topo1 or topo2 and DNA (Hsiang et al. 1989), thereby stabilizing otherwise cleavable complexes between DNA and topoisomerases. In DNA replicating cells, this causes the collision between the progressing DNA replication fork and such a stabilized complex and, in turn, to conversion of the complex into secondary lesions that consist of DSBs (Hsiang et al. 1989). Collisions with the cleavable complexes also occur during transcription, between the progressing RNA polymerase molecule and the inhibitor-stabilized topo1 or topo2 cleavable complex located on the template strand within the DNA region being transcribed (D’Arpa et al. 1990). The RNA polymerase collisions, similar to the collisions of the DNA replication fork, are also converted into DSBs (Wu & Liu 1997). In both instances, the secondary DSBs are presumed to be recognized by the cell as lethal and trigger apoptosis (Hsiang et al. 1989; D’Arpa et al. 1990; Wu & Liu 1997). Predominantly S-phase cells undergo apoptosis upon exposure to topo1 or topo2 inhibitors (Del Bino et al. 1990, 1991; Gorczyca et al. 1993c). Phosphorylation of H2AX in the cells treated with topo inhibitors reveals the presence of DSBs induced by these drugs, and therefore is expected to be predictive
of their cytotoxicity. Bivariate analysis of γH2AX expression vis-à-vis cellular DNA content can pinpoint the cell cycle phase that is the most sensitive in terms of induction of these lesions. Figure 11 illustrates the effect top1 inhibitor topotecan (Tpt) on H2AX phosphorylation in HL-60 cells. It is apparent that, compared with cells in G1 phase, the cells in S and G2M were much more sensitive in their response to Tpt by the induction of H2AX phosphorylation. It is also apparent that, in the presence of the protein (serine/threonine) phosphatase inhibitor calyculin A, the intensity of γH2AX IF was markedly elevated after 3 h, but was essentially unchanged after 1 h. There is an equilibrium between the rate of phosphorylation of histone H2AX after DNA damage, and its dephosphorylation that occurs as DNA repair progresses (Furuya et al. 1997). The data in Fig. 11 suggest that, while no significant dephosphorylation of H2AX took place during the first hour of treatment with Tpt, a significant degree of dephosphorylation occurred between 1 and 3 h in the absence of calyculin A. To assess the cumulative H2AX phosphorylation as a yardstick of the total number of DSBs generated by the treatment, one has to incubate the cells in the presence of the protein phosphatase inhibitor, to prevent γH2AX dephosphorylation. One has to be cautious in data interpretation, however, because inhibitors such as calyculin A or okadaic acid are cytotoxic and prolonged (> 3 h) incubation with them causes premature chromatin condensation followed by apoptosis (manuscript in preparation).

The capability to correlate the detection of γH2AX as well as the detection of apoptosis, each with respect to cell cycle phase as offered by multiparameter cytometry, makes it possible to reveal the potential correlation between induction of DSBs and apoptosis. Figure 12 shows such a correlation for HL-60 cells treated with the top2 inhibitor mitoxantrone (Mtx). It is quite evident that, unlike in the case of the top1 inhibitor Tpt (Fig. 11), cells in all phases of the cycle responded to the drug by H2AX phosphorylation. However, essentially only S-phase cells underwent subsequent apoptosis (Fig. 12). These data indicate that, in the case of treatment with Mtx, regardless of the extent of H2AX phosphorylation and thus most likely frequency of DSBs, DNA replicating cells are much more prone to undergo apoptosis than G1 or G2/M cells. Thus, it appears that, with comparable levels of DNA damage, the cells arrested at the G1 or G2/M
checkpoint remain at the checkpoint alive for an extended period of time, apparently in an attempt to repair the damage, while the S-phase cells succumb to apoptosis. However, both H2AX phosphorylation (Fig. 11) as well as apoptosis are selectively induced in S-phase cells after treatment with the DNA topo1 inhibitor Tpt (Huang et al. 2004).

As presented earlier in this review, apoptosis is associated with extensive DNA fragmentation and the apoptosis-associated DSBs also trigger H2AX phosphorylation (Huang et al. 2004). However, the degree of H2AX phosphorylation in response to formation of DSBs during apoptosis is many-fold higher compared with that in response to the primary DSBs, such as induced by radiation (Halicka et al. 2005) or DNA damaging drugs such as Tpt. This is evident from the bivariate distributions that illustrate expression of γH2AX versus caspase-3 activation (Fig. 13). The latter event, that is caspase-3 activation, is a reporter of apoptosis. Its immunocytochemical detection with an antibody that reacts with the epitope of the activated (cleaved) enzyme concurrent with detection of γH2AX makes it possible to identify both the non-apoptotic versus apoptotic cells that have phosphorylated H2AX. The bivariate distributions representing γH2AX IF versus activated caspase (caspase-3*) allows one to discriminate four cell populations as shown in the respective quadrants of the third panel in Fig. 13: (a) γH2AX positive–caspase-3* negative; (b) γH2AX positive–caspase-3* positive; (c) IF γH2AX negative–caspase-3* positive; and (d) γH2AX negative–caspase-3* negative. It is evident that the apoptotic cells (Ap), that is the cells with activated caspase-3 (quadrant b), have distinctly higher expression of γH2AX compared with cells that phosphorylated H2AX in response to the primary DSB induced by Tpt (pDSB; quadrant a). It should be noted, however, that, at later stages of apoptosis, expression of γH2AX declines and may be not much higher than that induced by the primary DSBs.

As mentioned earlier, H2AX phosphorylation in response to DSBs is being carried out by PI-3-like protein kinases, ATM- (Rogakou et al. 1998; Anderson et al. 2001; Burma et al. 2001;
Sedelnikova et al. (2002), ATR- (Furuta et al. 2003), and/or DNA-dependent protein kinase (DNA-PK) (Park et al. 2003; Wang et al. 2005). It recently has become possible to immuno-cytochemically detect activation of ATM kinase (the gene for which is located on chromosome 11q22.3), which in response to induction of DSBs undergoes autophosphorylation at Ser1981 (Bartkova et al. 2005). Similar to the pattern of the presence of DSBs, ATM is not phosphorylated in most normal tissues but undergoes phosphorylation in subsets of bone marrow lymphocytes and primary spermatocytes, that is the cells where DSBs are generated during physiological V(D)J recombination and meiotic recombination, respectively. As shown in Fig. 14, induction of DSBs by Tpt triggers both ATM autophosphorylation as well as phosphorylation of H2AX. In both instances, the phosphorylations are induced preferentially in S-phase cells. These data, thus, suggest that ATM is the kinase that phosphorylates H2AX after induction of DSBs by the DNA topo1 inhibitor Tpt. Studies are in progress to concurrently detect activated ATM and γH2AX in the same cells in order to compare kinetics of their phosphorylation, with respect to each other.

**FUTURE DIRECTIONS**

Future progress in the analysis of DNA damage by cytometry will be associated with development of antibodies that recognize chemically modified (phosphorylated, acetylated, methylated, ADP-ribosylated or ubiquinitylated) epitopes of proteins. Such antibodies will provide the means to detect functional changes (activation, inactivation, mutual interactions) of the proteins that respond to DNA damage and carry out repair. One example is ATM kinase, whose activation through auto-phosphorylation detected immunocytochemically (as illustrated in Fig. 14) reveals its involvement in response to drug-induced DNA damage. It also serves as a reporter of the damage itself. Thus, using function-associated protein modification-specific antibodies, the participation of individual proteins in the DNA repair process can be studied in individual cells in relation to cell cycle phase and also vis-à-vis induction of apoptosis.
Another functional marker of a particular protein is its translocation and interaction with other proteins. Intracellular translocations (for example, cytoplasm to the nucleus, local changes in distribution) can be detected using morphometric capabilities such as offered by laser scanning cytometry (Kamentsky 2001) or similar instruments. Using this approach, we have already been able to reveal activation of nuclear factor \( \kappa B \) (Deptala et al. 1998) by tumour necrosis factor \( \alpha \), or translocation of Bax protein to mitochondria to facilitate release of cytochrome \( c \) from mitochondria during induction of apoptosis (Bedner et al. 2000).

Fluorescence resonance energy transfer (FRET) is a further probe that reveals protein translocations and protein–protein interactions (Vereb et al. 2004), and will progressively be used in cytometric DNA damage assays, particularly to study participation of individual proteins in DNA repair. The probe that senses microenvironment of the fluorochrome, fluorescence lifetime microscopy (FLIM; Murata et al. 2001), when adapted more widely to cytometry (Sailer et al. 1997), is also expected to significantly contribute to a better understanding of the mechanism of DNA damage and repair.

Radio- and chemotherapy targeting DNA of tumour cells and the extent of DNA damage induced during the treatment certainly correlates with clinical response. One expects that sensitive cytometric assays that reveal the extent of the damage, particularly with respect to cell cycle phase, such as based on detection of H2AX phosphorylation or activation of the protein kinases that phosphorylate H2AX, will soon find application in the clinic to assess DNA damage early during therapy, as a possible prognostic marker.

ACKNOWLEDGEMENT

Supported by NCI CA 28 704.
REFERENCES


Kunitz M (1950) Crystalline desoxyribonuclease; isolation and general properties; spectrophotometric method for the measurement of desoxyribonuclease activity. J Gen Physiol. 33, 349.


Park EJ, Chan DW, Park JH, Oettinger MA, Kwon J (2003) DNA-PK is activated by nucleosomes and phosphorylated H2AX within the nucleosomes in an acetylation-dependent manner. Nucleic Acids Res. 31, 6819.


