BIOCHEMICAL KINETICS MODEL OF DSB REPAIR AND γH2AX FOCI BY NON-HOMOLOGOUS END JOINING

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ABSTRACT:

We developed a biochemical kinetics approach to describe the repair of double strand breaks (DSB) produced by low LET radiation by modeling molecular events associated with the mechanisms of non-homologous end-joining (NHEJ). A system of coupled non-linear ordinary differential equations describes the induction of DSB and activation pathways for major NHEJ components including Ku70/80, DNA-PKcs, and the Ligase IV-XRCC4 hetero-dimer. The autophosphorylation of DNA-PKcs and subsequent induction of γH2AX foci observed after ionizing radiation exposure were modeled. A two-step model of DNA-PKcs regulation of repair was developed with the initial step allowing access of other NHEJ components to breaks, and a second step limiting access to Ligase IV-XRCC4. Our model assumes that the transition from the first to second-step depends on DSB complexity, with a much slower-rate for complex DSB. The model faithfully reproduced several experimental data sets, including DSB rejoining as measured by pulsed-field electrophoresis (PFGE), quantification of the induction of γH2AX foci, and live cell imaging of the induction of Ku70/80. Predictions are made for the behaviors of NHEJ components at low doses and dose-rates, where a steady-state is found at dose-rates of 0.1 Gy/hr or lower.
INTRODUCTION

A mechanistic description of the processing of DNA double strand breaks (DSB) is important for the understanding of ionizing radiation effects leading to cell death, mutation, genomic instability, and carcinogenesis. Mathematical models of DSB repair are important for the description of radiation modalities not accessible by experimental means and for their possible predictive capabilities. Past mathematical models of ionizing radiation induced DSB repair have largely relied on phenomenological approaches, which did not consider specific molecular interactions involved in DSB repair (1-3). Previously, we had shown that a biochemical approach based on non-linear kinetics enjoys some special features in describing DSB repair, including the time delay caused by a DSB-repair enzyme intermediate complex (3). Application of biochemical kinetics models to describe molecular DSB repair experimental data is a goal of the present study.

Non-homologous end joining (NHEJ) is the primary pathway for DSB repair in eukaryotic cells (4-6), and defects in NHEJ increase radiation sensitivity and the risk of carcinogenesis (7, 8). Many of the steps involved in NHEJ have been characterized experimentally, including the initial recognition of DSB’s by the Ku70/80 heterodimer, subsequent recruitment of the DNA dependent protein kinase catalytic subunit (DNA-PKcs), and formation of the DNA dependent protein kinase (DNA-PK) (6-9). DNA-PKcs contains several serine-threonine residues which are auto-phosphorylated. Auto-phosphorylation of various subsets of these sites is thought to be important in regulating pathway choices between NHEJ or homologous recombination repair (HR) (6).
addition to DNA-PKcs, a number of other proteins have been implicated as being important in either NHEJ or HR. For example, Artemis in conjunction with both ATM and DNA-PKcs has been suggested to function in DNA end-processing of specific, difficult to repair, IR-induced damages (10-13), and both Ligase IV and XRCC4 have been shown to be important in the ligation step of NHEJ (14, 15).

DNA-PKcs is a member of the phosphoinositide-3-kinase-related protein kinase (PIKK) family, which includes ataxia-telangiectasia mutated (ATM), and ataxia-telangiectasia and Rad3-related (ATR) proteins, and these proteins play a role in sensing DNA damage (5). In addition to damage sensing, both ATM and ATR have been shown to have distinct roles from DNA-PKcs, consisting of G1/S, S and G2/M cell cycle checkpoints regulation (5, 16) and replication stress response (19), respectively. DNA-PKcs, ATM, and ATR share common features including a conserved carboxy-terminal motif (5), and a reliance on upstream activators, Ku70/80, the MRE-Rad50-Nbs1 complex (MRN), and ATRIP, respectively. ATR is believed to function largely in S-phase, whereas DNA-PKcs and ATM have important roles throughout the cell cycle (16-19). The activation step of DNA-PKcs and ATM is rapid occurring from a few to about 30-minutes as observed in recent studies (5, 9, 18). Both activated proteins have been shown to lead to the phosphorylation of the histone variant H2AX in a chromatin region corresponding to about 2-Mbp around the DSB, with the phosphorylated form denoted γH2AX (20, 21). Total numbers of γH2AX foci have been shown to be fairly representative of the total number of DSB (20, 22, 23). In addition, a correlation between γH2AX foci loss and radiation sensitivity has been noted (23-25).
The plethora of experimental studies involving NHEJ repair should facilitate the development of mathematical models of these processes. In this paper we have developed a systems biology approach to NHEJ repair that can be used to make predictions for other radiation modalities, including extrapolations to low doses and dose-rates. Systems biology seeks to describe emergent properties of biological systems from the interactions of molecules acting in specific pathways (26). We use this approach to describe DSB rejoining curves, and the kinetics of formation and loss of $\gamma$H2AX to gain insights into the kinetics of NHEJ repair pathway. A key component of a biochemical kinetics model is the role of DNA repair complex intermediates, which leads naturally to a non-linear kinetics description (3). We consider several intermediate complexes based on $\gamma$H2AX radiation induced repair foci (RIRF) data, and DNA-PKcs experimental studies, and relate their description to pulsed-field gel electrophoresis (PFGE) DSB rejoining curves.

Ionizing radiation produces DSBs that vary from simple to complex structures and are produced with equal proportions with increasing dose, and depend on radiation quality (27, 28). Clustered DNA damage sites are defined as two or more elemental lesions within one or two helical turns of DNA produces by a single radiation track (27, 29). Under this definition all DSB are clustered damages, however complex DBS’s are defined by the addition of other damage type such as base-damage, damaged ends, single-strand breaks near a DSB, or for two or more DSB in close proximity. Clustered non-DSB’s can lead to secondary DSB’s produced during damage processing (29, 30). For low LET radiation it has been estimated that 20-40% of the initial damage is complex
Closely space multiple DSB could inhibit the attachment of repair proteins to other nearby DSB, and this possibility increases with the ionization power or linear energy transfer (LET) of radiation. We hypothesize that damage processing of complex DSB involve additional NHEJ factors including Artemis (10-13), MRN (19) and ATM proteins (10).

**METHODS**

*DNA-PK Regulation and Repair Complexes*

We use the mass-action chemical kinetics approach to describe the binding of repair enzymes to DSB’s with several intermediate repair complexes leading to DNA rejoining: 1) an initial complex bound by the Ku\textsubscript{70/80} hetero-dimer, 2) Ku mediated DNA-PK\textsubscript{cs} binding, 3) The regulation of the DSB-DNA-PK\textsubscript{cs} complex through auto-phosphorylation by DNA-PK, and 4) a final repair complex involving the Ligase IV/XRCC4 heterodimer, denoted LiIV. **Figure 1** shows a schematic diagram of our model showing the sequence of proteins binding to the repair complex and the two activation steps considered; phosphorylation of DNA-PK\textsubscript{cs} and H2AX. The series of repair complexes are denoted $C_j$ or with super-scripts P for auto-phosphorylation in complex, for e.g. $C_j^P$. The first complex ($C_1$) is formed by Ku\textsubscript{70/80} binding to the DSB, and the second binding by DNA-PK\textsubscript{cs} to the first complex forming $C_2$ etc., through to the final ligation step. Because these proteins are post-transcriptionally regulated the total number of enzymes in free-form or complex form is assumed to be conserved.
DSB are assumed to be induced per unit dose-rate with efficiency, \( \alpha \) (Gy\(^{-1}\) per cell). The Ku\(_{70/80}\) hetero-dimer is highly abundant and rapidly attaches to the DSB (denoted as \( C_0 \)) leading to the mass-action equation

\[
\frac{d[C_0]}{dt} = \alpha \frac{dD}{dt} - k_1[Ku_{70/80}][C_0]
\]

forming the repair complex, \( C_1 \), which is followed quickly by DNA-PK\(_{cs}\) binding

\[
\frac{d[C_1]}{dt} = k_1[C_0][Ku_{70/80}] - k_2[DNAPK_{cs}][C_1]
\]

to form a second complex, \( C_2 \). Equations (1) and (2) follow the convention that symbols within brackets define for a given molecular species, the time-dependent number of copies per cell. The repair complex, \( C_2 \), is then modified by phosphorylation events that facilitate cleaning of the ends, signal transduction, and the translation of DNA-PK\(_{cs}\) away from the ends of the break to allow ligation by LigaseIV/XRCC4 complex. Auto-phosphorylation of a cluster of residues on DNA-PK\(_{cs}\), denoted ABCDE, is expected to be a gate-keeper regulating access to the break by other repair proteins (6). The phosphorylation of a second cluster of residues on DNA-PK\(_{cs}\), denoted PQR, has been suggested to promote HR (6), whereas phosphorylation of the ABCDE cluster is thought to inhibit HR (6). The PQR cluster has been noted to partially facilitate dissociation of DNA-PK from the ends, however it is expected that other phosphorylation sites are needed for complete disassembly (6). To date, phosphorylation of Ku\(_{70/80}\) has not been
implicated as being critical for the actual repair of DSB (31) shown and thus will not be considered in the model.

We consider a two-step model that depicts DNA-PKcs role in regulation of repair involving activation events controlled by auto-phosphorylation of DNA-PKcs. The exact nature of the auto-phosphorylation of DNA-PKcs is not known (6, 32, 33), autophosphorylation may occur in \textit{trans}, where one DNA-PKcs molecule phosphorylates a second molecule on opposing sides of a DSB; a second-order reaction. Alternatively, it may occur in \textit{cis}, by an intra-molecular mechanism; a first-order reaction. Both of these mechanisms may occur and could depend on the DSB end structure (32, 33). We have modeled the auto-phosphorylation of DNA-PKcs bound to the DSB ends as first-order for both steps in DNA-PKcs regulation of repair. We assume the second-step depends on the complexity of the DSB and may involve other proteins, including Artemis and other poorly defined repair proteins. Residual breaks are predicted at complex DSB sites through a competing first-order process that assumes not all complex DSB are successfully rejoined with the failure occurring before the transition to the ligation step of the reaction. The resulting equations are

\[ \frac{d[C_2]}{dt} = k_2[DNAPK_{cs}][C_1] - k_{r1}[C_2] \]

\[ \frac{d[C_2^p]}{dt} = k_{r1}[C_2] - k_{r2}[C_2^p] - k_{res}[C_2^p] \]
The rates, $k_{P2}$ and $k_3$ are assumed to depend on the complexity of the DSB, and $k_{res}$ set to zero for simple DSB.

Finally, the last step in our model involves ligation of the ends by the Ligase IV/XRCC4 complex, denoted $LiIV$, and enzyme release given by

(7) \[ \frac{d[C_3]}{dt} = k_3[LiIV][C_2^{pp}] - k_{Dx}[C_3] \]

The Ligase IV/XRCC4 complex is also regulated by covalent modifications (13), but this observation is not currently treated in our model.

\textit{γH2AX Foci Kinetics}

The histone variant H2AX is phosphorylated after DNA damage by each of the family of PIK3 phospho-proteins ATM, ATR, and DNA-PKcs (5). In the G1 phase of the cell cycle, ATM and DNA-PKcs phosphorylate H2AX with nearly equal efficiencies and in an overlapping manner (34). γH2AX foci appear at a distance from DSB corresponding to a region of 2 Mbp (20), and it is not known how many H2AX molecules are modified per
DSB or of the mechanism that leads to phosphorylation of a large number of H2AX molecules. We use Michaelis-Menten kinetics to describe the induction rate of H2AX by DNA-PKcs in its active forms as given by,

\[
\frac{d[\gamma H2AX]}{dt} = \frac{k_{py}[C_{DNA-PKcs}][H2AX]}{K_M + [C_{DNA-PKcs}]} - k_{dy}[\gamma H2AX]
\]

where \([C_{DNA-PKcs}]\) is the sum of active forms of DNA-PKcs (C_2^P, C_2^{PP}, and C_3). The mechanism of de-phosphorylation of \(\gamma\)H2AX foci has not been well studied. We assume this step follows a simple first-order decay law in Eq. (8).

**Scaling Variables**

In order to simplify the model solutions, we introduce new scaled-variables by considering the conservation relations for the total concentration of a given protein, and noting the sum of all repair complexes is equal to the initial number of DSB. The new scaled variables are introduced using the definitions,

\[
H_i = [E_i] + \sum_{j=1}^{n}[C_j] = const.; \quad h_i(t) = \frac{\sum_{j=1}^{n}[C_j]}{H_i}; \quad \kappa_i = H_i k_i
\]

and

\[
c_i(t) = \frac{[C_j]}{H_1}
\]

which after substitution leads to the system of equations
\[
\frac{dc_0(t)}{dt} = \frac{\alpha}{H_1} \frac{dD}{dt} - \kappa_0 c_0(t)(1-h_1(t))
\]

(10) \[
\frac{dc_1(t)}{dt} = \kappa_1 c_0(t)(1-h_1(t)) - \kappa_2 c_1(t)(1-h_2(t))
\]

(11) \[
\frac{dc_2(t)}{dt} = \kappa_2 c_1(t)(1-h_2(t)) - k_p c_2(t)
\]

(12) \[
\frac{dc_2^p(t)}{dt} = k_{p1} c_2(t) - (k_{p2} + k_{res}) c_2^p(t)
\]

(13) \[
\frac{dc_2^{pp}(t)}{dt} = k_{p2} c_2^p(t) - \kappa_3 c_2^{pp}(t)(1-h_3(t))
\]

(14) \[
\frac{dc_{res}(t)}{dt} = k_{res} c_2^p(t)
\]

(15) \[
\frac{dc_3(t)}{dt} = \kappa_3 c_2^{pp}(t)(1-h_3(t)) - k_{p3} c_3(t)
\]

All rate-constants are assumed to be independent of the type of initial DSB, except for \(k_{p2}\) and \(\kappa_3\), which are given distinct values for simple and complex DSB, respectively. For the solutions in terms of the scaled-variables, only the value of \(H_1\) enters as all other \(H_i\) are combined with the \(k_i\) to form the rate parameters, \(\kappa_i\) which are in units of \(\text{Hr}^{-1}\). The
functions $h_i(t)$ include contributions from repair complexes involving both simple and complex DSB’s.

The histone variant, H2AX content varies with cell lineage representing from 2 to 10% of all nucleosomes and there are about $2.0 \times 10^6$ H2AX molecules per cell (20). We reasoned that it was more useful to model the kinetics of the number of $\gamma$H2AX foci formed, rather than the number of activated molecules. For foci counting experiments the number of foci is limited by the model dependent initial number of DSB per cell. For low LET radiation the probability of more than one DSB within the spatial region of foci is small, however for high LET other considerations will be needed to be taken into account (Cucinotta et al., in preparation). Assuming $[\gamma$H2AX]$+[H2AX] = \text{constant}$, and denoting $\gamma(t)$ as the time dependent number of foci leads to

$$\frac{d\gamma(t)}{dt} = \frac{\kappa_p c_{DNA-PKc5}(t)(1 - \gamma(t))}{\kappa_M + c_{DNA-PKc5}(t)} - k_D \gamma(t)$$

where $\kappa_p = k_{p\gamma} / H_1$. For comparison to DSB rejoining kinetics in an acute irradiation measured using PFGE, the number of DSB’s remaining is given by

$$DSB_{\text{remaining}}(t) = H_1[\sum_{j=0}^{3} c_j(t) + c_{\text{res}}(t)]$$

For comparison to experimental data on relative Ku70/80 induction, which includes Ku70/80 in various DSB repair complexes the following sum is used
\[
C_{Ku_{70/80}}(t) = H_1 \sum_{j=1}^{3} c_j(t)
\]

The system of equations formulated above to represent NHEJ are non-linear ordinary differential equations, described as stiff equations describing equations were the values for the various parameters, \( k_i \) or \( \kappa_i \) vary over several orders of magnitude. These equations were solved numerically using the method of backward difference approximates. We note that the factors ‘\( l-h_i \)’ in our scaled equation have values close to unity at low doses where the initial number of DSB is \( << H_1 \).

**RESULTS AND DISCUSSION**

Our kinetics model of NHEJ consists of a system of 8 coupled non-linear ordinary differential equations for each class of DSB (simple and complex). This system of equations describe major components in the NHEJ repair pathway and the phosphorylation of H2AX by DNA-PKcs. Values for rate-constant were determined by comparing to experimental data with cell lineage specific values estimated for rate-constants and other parameters are listed in **Table 1**. Our scaling approach results in a significant reduction in parameter space since it avoids the need to estimate values for the total cellular concentration of Ku\(_{70/80}\), DNA-PKcs, LiIV, and XRCC4, which are effectively replaced by a single constant, \( H_j \). The value of \( H_j \) can be interpreted as the total number of copies of Ku\(_{70/80}\). However in the model other constants, \( H_j \), could be used as the scaling variable, and we prefer to interpret the value of \( H_j \) as the total.
number of DNA-repair complexes that could occur in a cell (3). We have fixed this value at a large number \( (H_I=3000) \), to ensure that the shape of the DSB rejoining curve is largely independent of dose, over the range from 1 to 40 Gy. To reduce the number of variable parameters, we fixed the peak time of the \([C_1]\) complex, corresponding to the binding of \( \text{Ku}_{70/80} \) to DSB, at about 1 min post-irradiation (35), and of the \([C_2]\) complex, corresponding to the binding of DNA-PK \(_{cs}\) complex, at about 3 min for all cell lineages considered using the values for \( \kappa_1 \) and \( \kappa_2 \) as listed in Table 1. In-vitro assays provide insights into rates for DNA-PK\(_{cs}\) activation occurring over times up to 30 min under different conditions (32, 36, 37). The remaining parameters are determined in a cell-lineage specific manner by comparing the model solutions to data for DSB rejoining, and the induction and loss of \( \gamma \text{H2AX} \) foci.

Figures 2 illustrates the model predictions for the time evolution for the sequence of repair complexes formed at an acute dose of 1 Gy for simple and complex damage processing. We compared the model prediction to recent results using live cell imaging of DSB induced by a near infrared laser (NIR) of \( \text{Ku}_{70/80} \) (35) in Figure 3. Our result using eq. (18), which represents the sum over different repair complexes containing the \( \text{Ku}_{70/80} \), is in excellent agreement with the live cell imaging observations where DSB’s are induced by a near infrared laser (NIR) (35). There will be differences in the initial number and types of breaks, perhaps due to higher DSB induction by NIR as compared to that of X-rays at 1 Gy, however the agreement found over the first few hours of repair lends support to the values for the rate-constants chosen.
We also compared our model to the rejoicing kinetics determined by PFGE, which is available in the literature for X-rays. DSB rejoicing kinetics measured by PFGE are made at high dose (>10 Gy) and must be corrected for the presence of heat-labile sites (29, 38, 39), which account for up to 50% of the fragment yields at early post-irradiation times (within 30 mins post-irradiation). To avoid the contribution of heat-labile sites, we compared PFGE data analyzed using the cold lysis method developed by Rydberg (38) to the data of Sternerlow et al. (39) for the GM5758 diploid fibroblast cells as shown in Figures 4. We have used experimentally determined values from Gulston et al. (29) for HF19 cells for the value of $\alpha$, the total number of DSB per Gy, of 25 and 16, respectively as initial conditions, and assume that 20% of the initial breaks repair with additional processing steps between the transition from $C_2^p$ to $C_2^{PP}$ and hence slower kinetic parameters. At moderate doses (<5 Gy) the model predicts a lack of rejoicing in the first few minutes post-irradiation as the multiple steps in NHEJ proceed. However, there may be some DSB rejoined by direct ligation independent of DNA-PKcs (35) leading to a faster component at early times, beyond those contributed by heat-labile sites.

Track structure calculations provide some estimates of the fraction of simple and complex DSB lesions. However, the bevy of mechanisms that would be available to repair the differential spectrum of DSB produced by ionizing radiation are not well understood and may utilize additional factors amongst these being Artemis (10-13), ATM (10), MRN (19, 40), Werner syndrome (41) proteins, and perhaps components in the nucleotide or base-excision repair pathways. In our model we assume just two average
components corresponding to so-called broad categories namely simple and complex DSB.

The fraction of residual breaks is easily modeled when the complex DSB are considered, if one assumes a first-order process results near the end of the cascade described above. We used a first-order rate-constant for residual break formation of $0.05 \, \text{h}^{-1}$ assuming a small fraction corresponding of the initial complex DSB are remain un-repaired at the $C_2^P$ complex and lead to residual DSB. The model presented here thus provides a framework to describe the dependence of residual breaks on radiation quality, dose-rate, and post-irradiation time.

We compared our model to data for the time courses and dose-response for $\gamma$H2AX foci. Leatherbarrow et al. (23) using confocal microscopy precisely measured the number of $\gamma$H2AX foci in V79 and HF19 cells. We find good agreement with their results as shown in Figure 5. Comparisons of the number of $\gamma$H2AX foci at 0.5 and 4 hr post-irradiation made by Short et al. (42) are shown in Figure 6. The model calculation shows a linear response at 0.5 hr post-irradiation. There is a concomitant induction of $\gamma$H2AX from active ATM (34) monomers, which has not been studied in the current model. ATM and DNA-PKcs are expected to induce these foci with nearly equal efficiency (34).

The understanding of dose-rate effects is an important consideration in radiation protection (43, 44). Since the processing of DSB after radiation is a determinant in mutation, chromosome aberrations, and carcinogenesis, we studied the induction of
various NHEJ components as a function of variable dose-rates and doses. Steady-state solutions for the systems equations can be found in closed form and compared with numerical solutions, and dose-rates where the steady-state, with foci counts independent of dose-rate, are obtained identified. The results of Figure 7 predict that the number of DSB repair complexes per cell becomes independent of dose-rate below about 0.1 Gy/hr. These observations can be tested with experiments. Also, for model building our description of NHEJ can be used as a starting point for mechanistic models of mutation and chromosomal aberrations. In addition, studying dose-rate dependencies for repair should be informative in understanding dose-rate effects for these other endpoints.

In summary, we have synthesized a large number of experimental observations into a biochemical kinetics model of the NHEJ repair pathway. The model is based on the current mechanistic understanding of molecular binding and kinase activity of major NHEJ components that have been described experimentally and is capable of describing the time-courses, and dose and dose-rate dependencies for major NHEJ components, the induction of $\gamma$H2AX foci upon activation of DNA-PKcs through auto-phosphorylation, and DSB rejoining curves as measured by PFGE. The model presented here can be modified as understanding on molecular mechanisms of NHEJ repair is obtained. The ability to describe the kinetics of DSB induction and repair and the various associated protein complexes will support models of chromosomal aberrations as a function of radiation quality, when descriptions of DSB complexity and spatial dependence of initial DSB are coupled to the present model (27, 28, 45). We plan on extending our work to include theoretical descriptions of the fractions of simple and complex initial DSB for
high LET radiation, and the resulting changes in DSB repair and foci kinetics and to include the description of the ATM signaling pathway in our model.

ACKNOWLEDGMENTS

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Table 1. Values of Rate-constants and other parameters in the Biochemical Model

<table>
<thead>
<tr>
<th>Rate Constant</th>
<th>V79 Cells</th>
<th>HF19 cells</th>
<th>T98G</th>
</tr>
</thead>
<tbody>
<tr>
<td>( \alpha ), Gy(^{-1} )</td>
<td>16</td>
<td>25</td>
<td>25</td>
</tr>
<tr>
<td>( \kappa_3 ), hr(^{-1} )</td>
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<td>8 (0.5)</td>
<td>8 (0.5)</td>
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<td>10</td>
<td>10</td>
</tr>
<tr>
<td>( k_{p2} ), hr(^{-1} )</td>
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<td>10 (0.5)</td>
<td>10 (0.5)</td>
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<td>900</td>
<td>1000</td>
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<td>0.5</td>
</tr>
<tr>
<td>( k_{res} ), hr(^{-1} )</td>
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<td>0 (0.05)</td>
<td>0 (0.05)</td>
</tr>
</tbody>
</table>

a) Values of \( \kappa_1 \), \( \kappa_2 \), and \( H_j \) are set at 100 hr\(^{-1} \), 100 hr\(^{-1} \), and 3000 per cell for all cell lineages considered. Values chosen correspond to a peak for a DSB-Ku\(_{70/80}\) complex at about 1 min post-irradiation (35), and assuming peak of DSB-Ku\(_{70/80}\)-DNA-PK\(_{cs}\) complex at about 3 min post-irradiation.

b) The initial number of breaks per Gy (\( \alpha \)) determined from experiments of Gulston et al. (34). We use the same values for GM5738 cells as HF19.
Figure Captions:

Fig. 1. Schematic of biochemical kinetics model of DSB repair by NHEJ with induction of $\gamma$H2AX by DNA-PKcs. The key components of the model and associated rate-constants are show. Not illustrated is the degradation of the $[C_3]$ complex after the ligation step nor distinction between simple and complex DSB including the formation of residual DSB when complex initial DSB do not proceed to the $[C_2^{PP}]$ complex.

Fig. 2. Model calculations of time course for sequence of DNA repair complexes in NHEJ pathway, and DSB rejoining curve (non-complex only) for 1-Gy gamma-ray exposures in normal human diploid fibroblast cells.

Fig. 3. Model calculations for the time-course of Ku70/80 hetero-dimers in complex with DSB and other NHEJ components compared to live cell imaging data from ref. (35) for EGFP-Ku80 induction after irradiation of CHO cells with a near infrared laser.

Fig. 4. Comparisons of model calculations to DSB rejoining determined by PFGE method for GM5758 (human diploid fibroblast cells) at 40 Gy (37). The solid line shows the contributions from simple and complex DSB. For comparison we show calculations of the rejoining curves for simple and complex DSB in our model normalize to unity as dash and dotted lines, respectively.

Fig. 5. Comparisons of model calculations to measurements of $\gamma$H2AX foci by Leatherbarrow et al. (23) with solid line for total (simple and complex DSB) induced $\gamma$H2AX foci, dash line foci from simple DSB alone, and dotted line the number of DSB remaining. Symbols with error bars are the experimental results (23).
   a) HF19 Cells at 1 Gy
   b) V79 Cells at 1 Gy

Fig. 6. Comparisons of model calculations for dose-response for $\gamma$H2AX foci at 0.5 (closed circles) and 4 hrs (open triangles) post-irradiation data of Short et al. (34). Model calculations shown are solid line at 0.5 hr, dash line at 4 hr post-irradiation.

Fig. 7. Predictions for the number of DSB repair complexes versus dose for various dose-rates in human fibroblast cells.
Ionizing Radiation

\[ [C_0] \xrightarrow{k_1} [C_1] \xrightarrow{k_2} [C_2] \xrightarrow{k_{p_1}} [C_{2'}] \xrightarrow{k_{p_2}} [C_{2''}] \xrightarrow{k_3} [C_3] \xrightarrow{k_{Dc}} \]

DSB

\[ k_{p_1}, k_{p_2}, k_{Dc} \]

H2AX

\[ k_{D_7} \]

\[ k_{u_{Ku70/80}} \]

DNAPKcs

LIH/XRCC4

\[ k_{P_1} ([C_{2'}]+ [C_{2''}]) \]

\[ \gamma H2AX \]

\[ H2AX \]
Fig. 2.

Post-Irradiation time, hr

Molecules per Cell

Post-Irradiation time, hr

[C₁]
[C₂]
[C₂P]
[C₂PP]
[C₃]
Fig. 3.

Biochemical Model
Live cell results

Post-irradiation time, hr

(%) Relative Ku Induction

0.0 0.5 1.0 1.5 2.0
Fig. 4

Fraction Unrejoined

Post-irradiation time, hr

Sternerlow et al.
Total DSB
Simple DSB
Complex DSB
Fig. 5a.

Post-irradiation time, hrs

Ave. Number of Foci per Cell

RAW TEXT
Fig. 5b.

The graph shows the average number of foci per cell over post-irradiation time in hours. The x-axis represents post-irradiation time in hours, ranging from 0 to 8. The y-axis represents the average number of foci per cell, ranging from 0 to 20. Several data points are plotted, each with error bars indicating variability. The data shows a decrease in the average number of foci per cell over time.
Fig. 6.
Fig. 7

Dose, Gy

Foci per Cell

100 Gy/hr
5
0.5
0.1
0.05
0.01