Rapid exchange of mammalian topoisomerase IIα at kinetochores and chromosome arms in mitosis

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A stable cell line (GT2-ŁPk) derived from LLC-Pk was created in which endogenous DNA topoisomerase IIα (topoIIα) protein was downregulated and replaced by the expression of topoIIα fused with enhanced green fluorescent protein (EGFP–topoIIα). The EGFP–topoIIα faithfully mimicked the distribution of the endogenous protein in both interphase and mitosis. In early stages of mitosis, EGFP–topoIIα accumulated at kinetochores and in axial lines extending along the chromosome arms. During anaphase, EGFP–topoIIα diminished at kinetochores and increased in the cytoplasm with a portion accumulating into large circular foci that were mobile and appeared to fuse with the reforming nuclei. These cytoplasmic foci appearing at anaphase were coincident with precursor organelles of the reforming nucleolus called nucleolus-derived foci (NDF). Photobleaching of EGFP–topoIIα associated with kinetochores and chromosome arms showed that the majority of the protein rapidly exchanges (t1/2 of 16 s). Catalytic activity of topoIIα was essential for rapid dynamics, as ICRF-187, an inhibitor of topoIIα, blocked recovery after photobleaching. Although some topoIIα may be stably associated with chromosomes, these studies indicate that the majority undergoes rapid dynamic exchange. Rapid mobility of topoIIα in chromosomes may be essential to resolve strain imparted during chromosome condensation and segregation.

Introduction

DNA topoisomerase II (topoII)* is essential in proliferating cells and is a major target for many anticancer drugs (Bakshi et al., 2001; Wang et al., 2001). In mammals, two genes code for isoforms of topoisomerase II, termed α and β, and alternative splicing confers further diversity (Petruiti-Mot and Earnshaw, 2000). TopoIIα has been proposed to play both catalytic and structural roles in mitotic chromosome segregation. Genetic studies in yeast and inhibitor studies in mammalian cells suggest that topoIIα is required to resolve sister chromatid catenations during separation of the chromatids (Uemura et al., 1987; Holm et al., 1989; Gorbsky, 1994). In chromosomes that have been isolated from cells arrested in M phase, the bulk of topoIIα is tightly associated, suggesting that topoIIα forms a stable structural component or scaffold of chromosome architecture (Earnshaw et al., 1985). A study of rhodamine-labeled topoII in Drosophila embryos challenged this model with evidence that much topoIIα diffuses from the chromosomes at progressive stages of mitosis (Swedlow et al., 1993). The stability of topoIIα protein is cell cycle regulated, high during G2/M phases, and becoming unstable in the subsequent G1 phase (Heck et al., 1988).

Some immunolocalization and electron microscopy studies show a distribution of topoII in an axial core extending the length of the chromosome (for review see Warburton and Earnshaw, 1997). However, in both Drosophila embryos and condensed chromosomes formed in vitro in Xenopus extracts, topoII shows more uniform distribution on the chromosome arms (Hirano and Mitchison, 1993; Swedlow et al., 1993). In some immunolabeling studies, the enzyme was reported to be concentrated at kinetochores (Taagepera et al., 1993; Gorbsky, 1994; Rattner et al., 1996; Sumner, 1996). In interphase mammalian cells, various groups report differences in the subnuclear distribution of topoIIα with some but not all studies noting a concentration in the nucleoli (Meyer et al., 1997; Khelifa and Beck, 1999; Mo and Beck, 1999).

To investigate the dynamics of topoIIα in living cells, we produced a stable cell line expressing EGFP–topoIIα. FRAP

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*Abbreviations used in this paper: EGFP, enhanced green fluorescent protein; NDF, nucleolus-derived foci; topoIIα, topoisomerase IIα.

Key words: DNA topoisomerase II; cell division; cell cycle proteins; kinetochores; nucleolus
experiments show that most topoII exchanges rapidly between cytoplasmic and kinetochore/chromosome-bound pools, and thus does not constitute a static structural chromosome scaffold. We also report a novel localization of topoII in late anaphase and telophase to discrete cytoplasmic foci that appear to incorporate into the reforming nucleoli during telophase.

Results and discussion
Establishment of a stable cell line expressing EGFP-topoII
To track the localization and dynamics of topoII in unperturbed living cells, we constructed a stable cell line, called GT2-LPk, that constitutively expresses EGFP–topoII. The overexpression of active topoII is cytotoxic, and although transient expression is possible, it has not previously been possible to obtain stable lines that constitutively express tagged forms of the enzyme (Mo et al., 1998; Mo and Beck, 1999). We compared the expression levels of endogenous topoII in the parental LLC-Pk and GT2-LPk lines. We found that expression of endogenous topoII was diminished in the GT2-LPk line, presumably accounting for the ability of the GT2-LPk line to escape cytotoxicity from topoII overexpression (Fig. 1 A). Immunoprecipitated EGFP–topoII efficiently catalyzed decatenation of kinetoplast DNA (Fig. 1 B). EGFP–topoII bound to protein A beads showed equivalent or greater catalytic activity compared with purified human topoII, a gift from Dr. Neal Osheroff (Vanderbilt University, Nashville, TN) (unpublished data).

EGFP–topoII localization in living cells
In living cells in interphase, EGFP–topoII was present diffusely in the nucleoplasm and concentrated in the nucleoli (Fig. 1 C). Nucleolar labeling persisted through early prophase when concentration of EGFP–topoII on chromosomes and at kinetochores became apparent. In living cells during prometaphase and metaphase topoII localized to thin lines running down the lengths of the chromosome arms (Fig. 1 C). Higher resolution images in fixed cells revealed that EGFP–topoII was concentrated along the central axis of each chromatid arm (Fig. 1 D). This distribution is consistent with the axial distribution of topoII observed in immunolabeling studies of fixed mammalian cells and isolated chromosomes (Earnshaw and Heck, 1985; Gorbsky, 1994; Rattner et al., 1996; Sumner, 1996). In anaphase, centromere concentration diminished while the lo-
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In anaphase, some of the cytoplasmic EGFP–topoIIα concentrates into distinct foci (closed arrows) that are motile. At telophase, the foci appear to fuse with the reforming nucleus (open arrows), whereas nucleoli become more apparent. (Image frames in this sequence were individually adjusted for contrast to optimize visualization of the cytoplasmic foci; Video 1, available at http://www.jcb.org/cgi/content/full/jcb.200202053/DC1) (B) EGFP–topoIIα foci (arrows) in telophase cells colocalize with NDFs identified by labeling with antibody to nucleolar B23 protein, a gift from Dr. Mirek Dundr (National Cancer Institute, Bethesda, MD). (The EGFP–topoIIα image is oversaturated for the nuclear fluorescence to clearly visualize the cytoplasmic foci.) (C) EGFP–topoIIα foci do not colocalize with reforming nuclear envelope identified by RL1 antibody to nuclear pore proteins, a gift from Dr. Bryce Pascal (University of Virginia, Charlottesville, VA). Bars, 10 μm.

Table I. Recovery of EGFP–topoIIα after photobleaching at kinetochores and chromosome arms

| Structure            | t1/2 s (SD) | Range     | % recovery (SD) | Range     | n  |
|----------------------|------------|-----------|-----------------|-----------|----|
| Kinetochores         | 15.7 (4.7) | 9.0–22.4  | 61.9 (14.7)     | 42.8–86.7 | 8  |
| Chromosome arm       | 15.5 (3.6) | 9.9–22.5  | 75.9 (13.0)     | 52.4–90.0 | 10 |

Kinetochores and chromosome arms of GT2-LPk cells were photobleached with a nitrogen dye laser. Recovery of fluorescence was measured in the photobleached area from images taken at intervals after photobleaching. After correcting for background and loss of fluorescence due to image capture, measurements were used to calculate halftime recovery (t 1/2) and the percentage of recovery.
skeletal role in maintaining the organization of the kinetochores or chromosome arm, then recovery should be slow. We found that recovery of the majority of the EGFP–topoII at kinetochores and chromosome arms occurs rapidly (Fig. 3 and Table I). Because the average recovery was <100%, there may be a subpopulation of kinetochore and chromosome-associated topoII that is more stably associated (for kinetochores an average of 38%; for chromosome arms an average of 24%). We found that the exchange of topoII occurred at all stages of mitosis and did not differ markedly from prophase through anaphase (Fig 3). Recovery of fluorescence likely reflects rapid exchange between the pools of topoII bound at chromosomes and kinetochores with the pool of cytoplasmic topoII.

The rapid exchange of the majority of topoII in vivo contrasts to the tight association of topoII in chromosomes isolated from mitotic cells. In isolated chromosomes, topoII is resistant to DNAse treatment and extraction with high salt, and has thus been proposed to function as part of a stable structural scaffold for the mitotic chromosome. Although there may be a minor population of topoII that is stably associated with chromatin, we find the majority to exchange rapidly with topoII in the cytoplasm. Thus, in vivo, it appears unlikely that the bulk of topoII serves a static nucleoskeletal role in maintaining mitotic chromosome structure.

Rapid exchange of topoII requires catalytic activity

To determine whether catalytic activity of topoII was required for the rapid exchange observed in our FRAP analyses, we used a chemical topoII inhibitor, ICRF-187. ICRF-187 is an inhibitor of the bisdioxopiperazine class that blocks the enzyme by trapping it in the postcleavage closed clamp form (Roca et al., 1994). Applied to cells in mitosis, this inhibitor inhibits chromosome condensation and induces massive failure of chromosome segregation at anaphase in LLC-Pk cells, the parental line of the GT2-LPk cells (Gorbsky, 1994). Similarly, we found that ICRF-187 inhibits normal chromosome condensation and chromosome segregation in GT2-LPk cells (Fig. 4, A and B). In mitotic cells treated with ICRF-187, we detected only minimal recovery of EGFP–topoII into the bleached areas over a 10-min period (Fig. 4 C).

To corroborate the effects of ICRF-187 on the dynamics of topoII in mitotic cells, we also tested its effects in interphase nuclei. Treatment of cells with ICRF-187 greatly diminished the level of EGFP–topoII concentrated in the nucleolus. When tested by FRAP analysis of interphase cells,
again ICRF-187 treatment was found to cause a marked decrease in the rate and extent of fluorescence recovery when compared with nondrug-treated interphase cells (Fig. 4, C and D). Together, these results suggest that the rapid exchange noted for EGFP–topoIIα in unperturbed cells requires catalytic activity. Moreover, ICRF-187 treatment slows the exchange rate of EGFP–topoIIα, lending further support to the idea that the EGFP–topoIIα protein is functional in vivo.

**Rapid exchange of chromosome-associated and cytoplasmic pools of topoII**

To further test whether the rapid exchange of topoIIα was somehow restricted to the protein associated with the chromosomes or occurred by exchange with a soluble cytoplasmic pool, we used fluorescence loss in photobleaching. We repeatedly photobleached a small area in the cytoplasm (Fig. 5 A) or on one region of the chromosomes of cells treated with a microtubule inhibitor to inhibit chromosome movement (Fig. 5 B; Video 2, available at http://www.jcb.org/cgi/content/full/jcb.200202053/DC1). Loss of fluorescence of EGFP–topoIIα from unbleached mitotic chromosomes occurred upon repetitive bleaching at the distant area (Fig. 5). These data demonstrate that topoIIα mobility is not regionally confined. TopoIIα associated with chromosomes and kinetochores is mobile and exchanges with cytoplasmic pools of the enzyme.

Another study recently appeared analyzing GFP derivatives of topoIIα and topoIIβ in stable lines of 293 cells (Christensen et al., 2002). In general, the results from these authors and ours are consistent in describing the overall localization of topoIIα in interphase and mitotic cells. Both studies also agree that most topoIIα undergoes rapid exchange with the cytoplasm, and the studies concur on the necessity for topoIIα catalytic activity in rapid exchange. The studies do differ with regard to certain conclusions regarding topoIIα in mitotic chromosomes. Whereas Christensen et al. (2002) report that nearly 100% of topoIIα turns over rapidly, our results indicate that a population of topoIIα associated with the kinetochores and chromosome...
arms turns over more slowly. Moreover, whereas Christensen et al. (2002) conclude that in living cells topoII \textsubscript{H9251} is uniformly distributed across the width of the chromosome arms, our evidence favors the idea that topoII \textsubscript{H9251} concentrated toward the axes of the arms. There are several potential sources for the differences in the two studies. Apart from inherent differences between the two parental cell lines (LLC-Pk vs. 293), the GT2-LPk derivative line used in our work has downregulated levels of endogenous topoII \textsubscript{H9251} that is replaced by EGFP–topoII \textsubscript{H9251}. The 293 cell derivatives of Christensen et al. (2002) did not show evidence of downregulation of the endogenous enzyme. In addition, the photobleaching studies of mitotic chromosomes performed by Christensen et al. (2002) were carried out on cells arrested at M phase by treatment with the microtubule stabilizer paclitaxel. Apart from the cell shown in Fig. 5 B, our studies were done on cells not treated with drugs. In preliminary studies, we have noted greater recovery of EGFP–topoII \textsubscript{H9251} after photobleaching GT2-LPk cells treated with either paclitaxel or nocodazole (unpublished data). Full resolution of the differences between the two studies will require further investigation.

Conclusions
Cell fractionation studies originally suggested that the bulk of topoII\textsubscript{x} in mitotic cells was stably associated with the mitotic chromosomes and formed a structural scaffold. Although our evidence of rapid exchange of the bulk of chromosome-associated topoII does not rule out a structural role for the enzyme, any such role must accommodate the fact that most of the protein is highly dynamic, exchanging with the soluble pool in seconds. Consistent with the earlier findings on the single isoform of topoII in \textit{Drosophila} embryos (Swedlow et al., 1993), we find in mammalian cells a net movement of topoII\textsubscript{x} from the chromosomes to the cytoplasm in anaphase. However, two-way exchange between the chromosome arms and cytoplasm persists during anaphase. We report a novel association of topoII\textsubscript{x} with NDFs in late mitosis. These organelles may serve to accumulate proteins to newly forming nucleoli in the daughter cells. The rapid dynamics of topoII\textsubscript{x} throughout the mitotic chromosomes may be essential in allowing the enzyme to reach and rapidly relieve strain before torsional stresses imparted by chromosome condensation and chromosome movements cause breaks to the DNA.

Materials and methods
Cell culture and immunofluorescence
LLC-Pk were grown in DME supplemented with 10% FBS and antibiotics. To produce a stable cell line expressing EGFP–topoII, LLC-Pk cells were transfected using Lipofectamine Plus according to the manufacturer’s instructions. Cells were selected for resistance to 2 \mu g/ml G418 and cloned by dilution in microwell plates. Cells were processed for immunofluorescence using methods described previously (Kallio et al., 1998).

Immunoprecipitation and decantation assays
GT2-LPk cells were lysed in high salt buffer (20 mM Tris, pH 8.0, 0.75 M KCl, 0.75% NP40) and immunoprecipitated with anti-EGFP antibody using previously described methods (Kallio et al., 1998). Decatenation assays were performed using a kit supplied by Topogen according to the manufacturer’s directions.

Western blotting
Proteins were separated by SDS polyacrylamide gel electrophoresis using 4–20% gradient acrylamide gels. Proteins were transferred to Immobilon-P
membrane. Anti-topoII was used at 1:1,000. Blots were then incubated with HRP-conjugated goat anti-rabbit and proteins visualized by chemiluminescence and imaged with a digital camera.

**Laser photobleaching**

Cells were observed on a warm stage using a Zeiss Axioplan II microscope equipped with the ORCA II CCD camera (Hamamatsu) and controlled with MetaMorph software (Universal Imaging Corporation). A nitrogen laser-pumped dye laser (Photonic Instruments) delivered 4 ns laser pulses at 440 nm attenuated with a neutral density slider. Typically, we bleached for 1 s at a repetition rate of 30 Hz. For each time-lapse series in Figs. 3, 4, and 5, the individual frames were imaged and adjusted for contrast using identical conditions.

**Data analysis**

Metamorph software was used for data collection and analysis. Data were analyzed essentially as described (Gorbsky et al., 1990; Howell et al., 2000; Phair and Misteli, 2000). Briefly, an area slightly larger than the target area was used for local cytoplasmic background subtraction. Integrated intensity of the target and background regions and their associated area get area was used for local cytoplasmic background subtraction. Integrated normalized relative intensity values were exported to GraphPad Prism software and analyzed by nonlinear regression. The rate constant k was determined using the perturbation-relaxation equation and half time of recovery was determined using 1/2 = ln2/k. Percent recovery was calculated according to the method described by Howell et al. (2000) using normalized relative intensity values.

**Online supplemental material**

Videos 1 and 2, corresponding to Figs. 2 A and Fig. 5 B, respectively, are available online as Quicktime movies at http://www.jcb.org/cgi/content/full/jcb.200202053/DC1.

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