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14-3-3 σ is required to prevent mitotic catastrophe after DNA damage

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14-3-3 σ is a member of a family of proteins that regulate cellular activity by binding and sequestering phosphorylated proteins. It has been suggested that 14-3-3 σ promotes pre-mitotic cell-cycle arrest following DNA damage, and that its expression can be controlled by the p53 tumour suppressor gene¹. Here we describe an improved approach to the generation of human somatic-cell knockouts, which we have used to generate human colorectal cancer cells in which both 14-3-3 σ alleles are inactivated. After DNA damage, these cells initially arrested in the G2 phase of the cell cycle, but, unlike cells containing 14-3-3 σ , the 14-3-3 σ ^{-/-} cells were unable to maintain cell-cycle arrest. The 14-3-3 σ ^{-/-} cells died ('mitotic catastrophe') as they entered mitosis. This process was associated with a failure of the 14-3-3 σ -deficient cells to sequester the proteins (cyclin B1 and cdc2) that initiate mitosis and prevent them from entering the nucleus. These results may indicate a mechanism for maintaining the G2 checkpoint and preventing mitotic death.

Many cell types treated with DNA-damaging agents arrest in the G2 phase of the cell cycle. The 14-3-3 σ gene is transcriptionally activated by p53 after DNA damage, and exogenous overexpression of 14-3-3 σ can block cells in G2, indicating that 14-3-3 σ might be a component of the G2 checkpoint¹. To test this hypothesis, we created cell lines deficient in 14-3-3 σ by homologous recombination. The human 14-3-3 σ genomic locus was cloned and fully sequenced, and subclones were used to construct a targeting vector containing a geneticin-resistance gene in place of genomic 14-3-3 σ sequences. Two loxP sites were introduced into the construct, one immediately 5' and the other directly 3' to the geneticin-resistance gene. A primer site for polymerase chain reaction (PCR) derived from deleted genomic sequences was placed between the 5' loxP site and the 5' end of the selection marker². The two loxP sites and the primer-containing construct enabled a relatively rapid and robust approach to screening clones for correctly targeted alleles, and for sequentially generating clones with both alleles disrupted (see Methods).

The human colorectal cancer cell (CRC) line HCT116 was used for these experiments because it expresses wild-type p53 and 14-3-3 σ , has intact DNA-damage checkpoints and is suitable for targeted homologous recombination³. Two independently derived 14-3-3 σ ^{+/-} and three 14-3-3 σ ^{-/-} clones were used for the studies described below (Fig. 1a–c). All clones of the same genotype behaved identically.

We investigated the function of 14-3-3 σ in human cells following DNA damage by adriamycin, a commonly used chemotherapeutic agent, as well as by ionizing radiation. The disruption of 14-3-3 σ had a marked effect on the responses of the cells to these agents. After either treatment, 14-3-3 σ ^{+/-} and 14-3-3 σ ^{-/-} cells increased in size, with a corresponding nuclear enlargement and DNA content characteristic of cells arrested in G2 (Fig. 2a). Although 14-3-3 σ ^{-/-} cells appeared to enter into a similar G2 block following DNA damage, they failed to maintain this arrest and eventually underwent 'mitotic catastrophe' (Fig. 2a). Mitotic catastrophe is an apoptosis-like process that begins in prophase, after dissolution of the nuclear membrane, and is associated with the entry of cdc2 and cyclin B1 into the nucleus^{4,5}. This process began ~24 h after

treatment and was complete after 72–96 h (Fig. 3a). Although chromatin condensation and micronucleation occurred during mitotic catastrophe, this process was distinguished from more common forms of apoptosis by a relative lack of DNA degradation, indicated by both DNA laddering (not shown) and TdT-mediated dUTP nick end labelling (TUNEL) staining for nicked DNA (compare with ceramide-induced apoptosis in Fig. 2b).

Roughly 75% of parental cells and 14-3-3 σ ^{+/-} heterozygote cells arrested after DNA damage with a G2 DNA content, whereas the remaining 25% of cells arrested in G1 (Fig. 3b). A similar fraction (~25%) of 14-3-3 σ ^{-/-} cells arrested in G1, but a relative decrease in the G2 fraction was evident as early as 24 h after adriamycin treatment (Fig. 3b). At later times, the 14-3-3 σ ^{-/-} cells showed a marked decrease in cells arrested in G2 and a corresponding increase in the number of sub-G1 cells, whereas the fraction of G2-arrested cells remained constant in both 14-3-3 σ ^{+/+} and 14-3-3 σ ^{+/-} cells

(Fig. 3b). The number of G1-arrested cells remained constant in cells of all three genotypes, indicating that the cells were probably undergoing catastrophe directly from the G2/M phase rather than from all parts of the cell cycle.

To study the expression of 14-3-3 σ following DNA damage, we generated an antibody specific for 14-3-3 σ using an amino-acid sequence found in 14-3-3 σ but not in the other six 14-3-3 family members. The specificity of this antibody was verified by the detection of a protein of the expected size upon western blotting of parental cells treated with DNA-damaging agents but not of 14-3-3 σ ^{-/-} cells (Fig. 1d). The 14-3-3 σ protein was induced as early as 6 h after exposure to adriamycin, with kinetics similar to those of the p53-induced gene *p21* in the same cells (Fig. 3c).

The 14-3-3 σ antibody was used to study the protein *in situ*. There was no detectable staining in most exponentially growing 14-3-3 σ ^{+/-} cells, although a small population of large cells stained

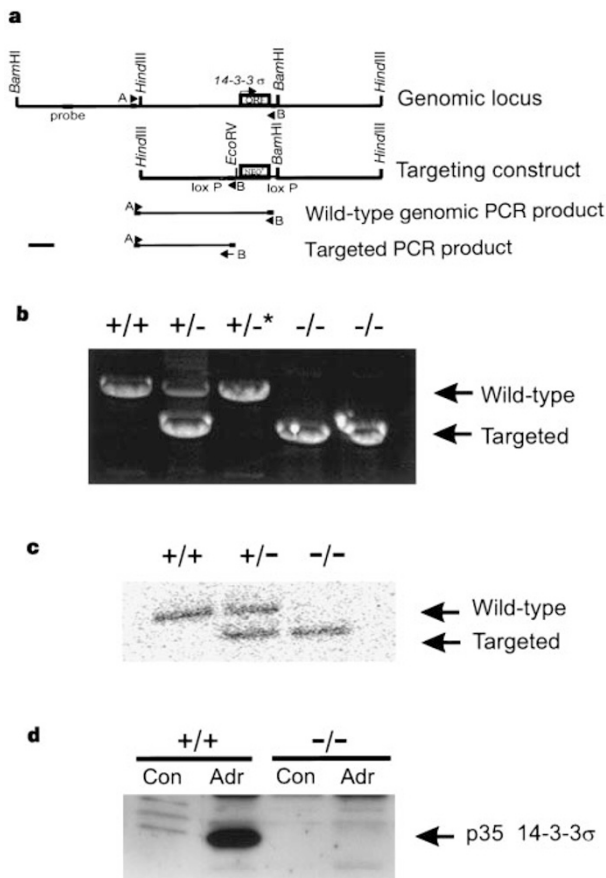


Figure 1 Generation of human cells deficient in 14-3-3 σ . **a**, Genomic structure of the human 14-3-3 σ gene and targeting construct. The box designated 'probe' represents the region used for Southern blotting. Primers at sites A and B were used in the PCR screen to identify targeted clones. The neomycin-resistance gene within the targeting construct is flanked by two loxP sites. After expression of *cre* recombinase to excise the selection cassette, the same targeting construct was used to disrupt the second 14-3-3 σ allele. Primer site B and an *EcoRV* site were incorporated directly upstream of the neomycin-resistance gene. The PCR products expected from wild-type and targeted alleles are shown at the bottom. Scale bar, 1 kb. **b**, PCR analysis of DNA from targeted cells of the indicated genotypes, using primers A and B. The 14-3-3 σ ^{+/-*} clone was derived from a 14-3-3 σ ^{+/-} clone that was infected with a recombinant adenovirus encoding the *cre* recombinase to remove the neomycin-resistance gene and primer B sequences from the targeted allele. **c**, Southern blot analysis of genomic DNA from cells with the indicated 14-3-3 σ genotype. Genomic DNA was digested with *Bam*HI and *EcoRV* and probed with the labelled 200-bp fragment shown in **a**. **d**, Western blot analysis. Cells with the indicated 14-3-3 σ genotype were cultured in the absence (Con) or presence (Adr) of adriamycin and subsequently lysed in sample buffer. Extracts were fractionated by SDS-PAGE and probed with an antibody specific for 14-3-3 σ .

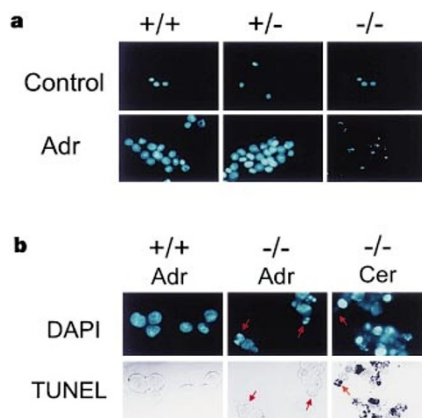


Figure 2 Mitotic catastrophe in 14-3-3 σ ^{-/-} cells. **a**, Nuclear morphology after adriamycin treatment for 72 h and staining with the DNA-specific dye DAPI. 14-3-3 σ ^{+/+} and ^{+/-} cells arrested and became enlarged when treated with adriamycin. 14-3-3 σ ^{-/-} cells developed condensed, fragmented chromatin when treated with the drug. Similar results were obtained after γ -irradiation (data not shown). **b**, TUNEL staining. 14-3-3 σ ^{+/-} cells treated with adriamycin underwent cell-cycle arrest but their chromatin remained uncondensed, and they did not stain with TUNEL. 14-3-3 σ ^{-/-} cells treated with adriamycin developed condensed chromatin (red arrows) but did not stain with TUNEL. Cells treated with C2-ceramide underwent micronucleation but did stain with TUNEL. The peroxidase reaction products of TUNEL staining significantly quenched DAPI fluorescence (orange arrow).

intensely (Fig. 3d). The size and morphology of the cells expressing 14-3-3 σ in the absence of DNA damage suggested that they were arrested in G2 and perhaps senescent. When cells were treated with γ -ionizing radiation or adriamycin, all the cells expressed 14-3-3 σ (Fig. 3d). As expected, 14-3-3 $\sigma^{-/-}$ cells did not stain for 14-3-3 σ either before or after treatment with adriamycin (Fig. 3d), confirming the specificity of the antibodies for immunohistochemical analysis.

A key step in regulating the progression of cells from G2 into mitosis is the activation of the protein kinase cdc2 (ref. 6). Cdc2 and cyclin B1 are cytoplasmic during interphase and are translocated to the nucleus in late G2 to initiate mitosis^{4,7}. The DNA damage checkpoint prevents the activation of cdc2–cyclin B1 complexes and thereby prevents cells from entering a potentially lethal mitosis when their DNA is damaged⁸. When we treated parental cells or 14-3-3 $\sigma^{+/-}$ cells with adriamycin or ionizing radiation, cdc2 and cyclin B1 remained in the cytoplasm throughout the duration of the experiment (Fig. 4a). In identically treated 14-3-3 σ -deficient cells, cdc2 and cyclin B1 were initially cytoplasmic, as in the parental cells; however, cdc2 and cyclin B1 soon migrated to the nucleus in most of the cells, and mitotic catastrophes occurred soon after (Fig. 4a, b). Normally, the entry of cyclin B1, cdc2, and cdc25C into the nucleus occurs simultaneously⁴; however, cdc25C remained localized in the cytoplasm before nuclear-membrane dissolution, despite the fact that cyclin B1 and cdc2 were in the nucleus (Fig. 4a). Double-staining with antibodies specific for cdc2 and 14-3-3 σ in DNA-damaged cells revealed a striking colocalization of the two proteins in the cytoplasm of parental cells (Fig. 4c). This may indicate that 14-3-3 σ normally sequesters cyclin B1 and cdc2 in the

cytoplasm, keeping cdc2–cyclin B1 from entering the nucleus and initiating mitosis following DNA damage. To investigate the molecular determinants of this sequestration, we carried out immunoprecipitation experiments using anti-14-3-3 σ antibodies. Western blots of the immunoprecipitates showed that cdc2 and cyclin B1 were bound to 14-3-3 σ , and that this binding markedly increased following adriamycin treatment (Fig. 4d; and data not shown). Wee1 kinase was also found in the immunoprecipitates (Fig. 4d); it has already been shown that cdc2 and cyclin B1 can bind to each other, and that wee1 binds to cdc2–cyclin B1 (ref. 9). No cdc25C could be detected (Fig. 4d), indicating that other 14-3-3 family members, but not 14-3-3 σ , may be responsible for the reported cdc25C interactions¹⁰.

Thus, it appears that 14-3-3 σ normally sequesters cdc2–cyclin B1 complexes in the cytoplasm during G2 arrest, and that the absence of 14-3-3 σ eventually allows cdc2–cyclin B1 complexes to enter the nucleus, resulting in mitotic catastrophe. This idea is consistent with several previous experiments which show that the cytoplasmic localization of cdc2–cyclin B1 is a critical regulator of the G2/M transition⁸, and that mitotic catastrophes occur if mitosis is experimentally induced in the presence of unreplicated or damaged DNA⁴. Our results also support the idea that the initiation of G2 arrest is distinct from its maintenance¹¹. Notably, we observed identical mitotic catastrophes in DNA-damaged parental cells after treating them with leptomycin B, an agent that inhibits nuclear export and results in a similar lack of cytoplasmic sequestration of cdc2–cyclin B1 (data not shown). These results, in combination with previous studies, suggest a simple but redundant set of mechanisms for preventing lethal mitosis following exposure of cells to DNA-

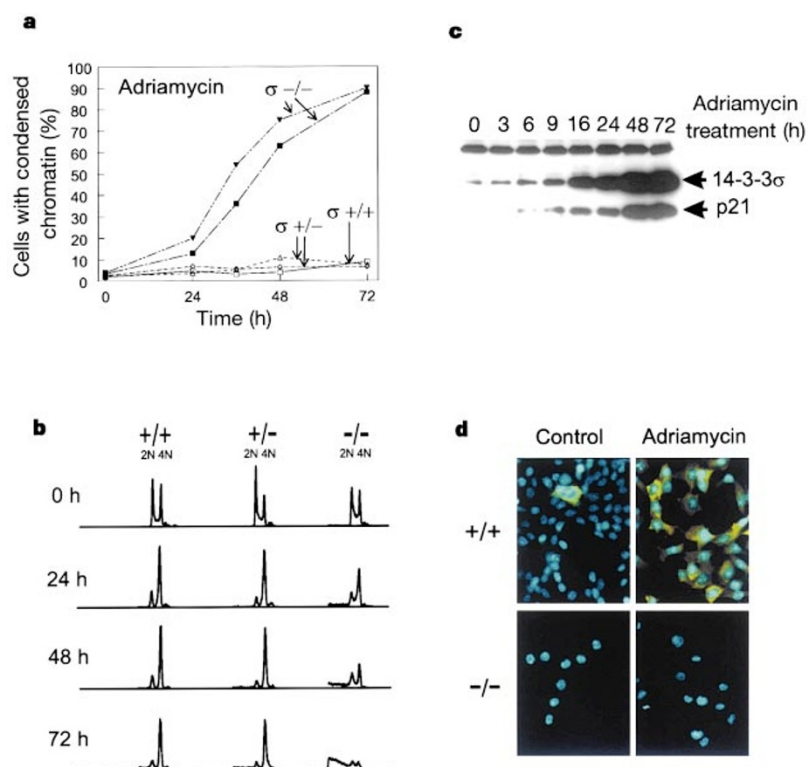
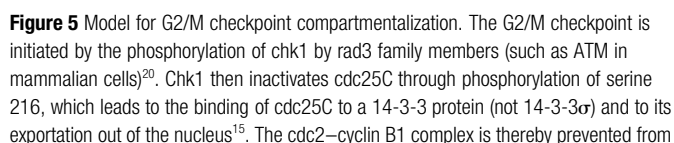
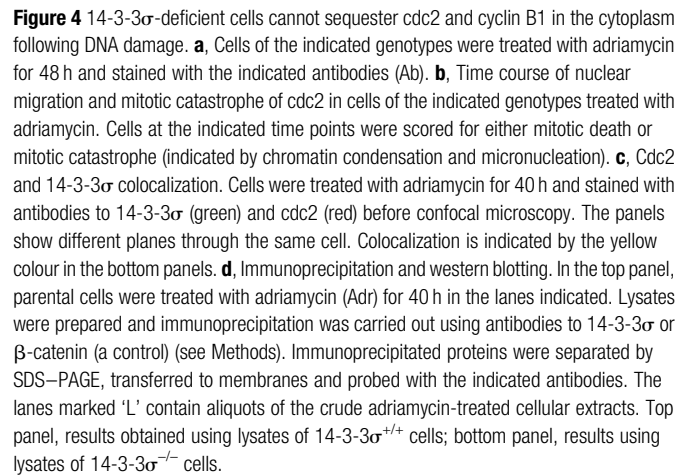


Figure 3 Cells deficient in 14-3-3 σ are sensitive to DNA-damage. **a**, Cells with the indicated 14-3-3 σ genotypes were treated with adriamycin for various time periods, stained with DAPI and scored for chromosome condensation. Two independent clones of homozygous (14-3-3 $\sigma^{-/-}$) and heterozygous (14-3-3 $\sigma^{+/-}$) cells were tested. **b**, Cells were adriamycin treated for the indicated times, stained with Hoechst 33258 and analysed by flow cytometry. The peaks labelled 2N and 4N represent cells with DNA contents characteristic of those in the G1 and G2 phases of cell cycle, respectively. **c**,

Kinetics of 14-3-3 σ induction. HCT116 cells were treated with adriamycin for the indicated time periods, and the extracts were used for western blot analysis, using antibodies specific for 14-3-3 σ and p21. **d**, Immunostaining for 14-3-3 σ . Cells of the indicated genotypes were incubated in the presence (adriamycin) or absence (control) of adriamycin, stained with a fluorescein-labelled anti-14-3-3 σ antibody (green) and counterstained with DAPI (blue).

in a cytoplasmic complex with cdc2 during G2 arrest, and localization is dependent both on 14-3-3 σ (Fig. 4) and on continued nuclear transport by the *crml*-dependent nuclear-export complex¹²⁻¹⁴. In the absence of either 14-3-3 σ or nuclear transport, cdc2 and cyclin B1 escape to the nucleus and initiate a catastrophic mitotic process⁴. Thus, two different 14-3-3 proteins appear to



becoming activated and initiating mitosis, and the cells arrest in G2. DNA damage also leads to stabilization of p53, which is required for maintenance of the G2 arrest through the transactivation of the *p21* and *14-3-3σ* genes. 14-3-3σ is required to sequester cdc2–cyclin B1 complexes in the cytoplasm and prevent mitotic catastrophes. p21 may prevent any cdc2–cyclin B1 that enters the nucleus from becoming activated.

ensure that mitosis does not occur in the presence of DNA damage, one by sequestering cdc25C¹⁵ and the other by sequestering cdc2–cyclin B1. It is becoming apparent that it is not only the enzymatic activities of cyclin-dependent kinase complexes but also their spatial compartmentalization that is critical for proper control of the cell cycle⁵. □

Methods

14-3-3 σ targeting construct

A BAC clone containing 14-3-3 σ was obtained as described¹. The BAC clone was digested with *Bam*HI, and two fragments, one 4.7 kilobases (kb) and the second 3.8 kb, were used to construct the 5' and 3' arms of the targeting vector, respectively. The 4.7-kb subclone contained the region immediately 5' of the initiating codon of the 14-3-3 σ coding region. The 3.8-kb subclone contained a region beginning 900 base pairs (bp) distal to the initiating codon. A synthetic *Eco*RV site plus the sequence 5'-CGTGGAGAGGGACTGGCAG-3', derived from a region of the 14-3-3 σ locus deleted by the targeting construct, were ligated to the 5' end of a geneticin-resistance gene. This product was placed into the pBluescript plasmid (Stratagene). To facilitate knockout of both alleles, *loxP* sites surrounding the geneticin-resistance gene were incorporated into the vector. Details of the constructs are available upon request. The construct was linearized by digestion with *Not*I and used for transfection. Southern blot analysis was carried out using standard techniques.

Cell culture and transfection

HCT116 cells were obtained from the American Type Culture Collection (ATCC). The HCT116 p21^{-/-} line has been described³. Cells were cultured in McCoy's medium supplemented with 10% fetal bovine serum (Gibco). We carried out transfections with Lipofectamine as directed by the manufacturer (Gibco). Clonal selection following transfection with the knockout construct was carried out in McCoy's medium with 10% fetal bovine serum and 0.4 mg ml⁻¹ geneticin (Gibco). Following transfection, cells were diluted in selection media and plated out in 96-well plates. After selection, we prepared genomic DNA from the drug-resistant clones using the QiaAmp column system (Qiagen). Identification of clones with successful targeting events was achieved using a PCR-based screen with the primers 5'-AGTGTCTGGGATCTCCAGC-3' and 5'-CTGCCAGTCCCCTCTCCAGC-3' and Taq Platinum (Gibco). PCR products were resolved by electrophoresis in 1% agarose gels. Knockout clones were confirmed by Southern blot and western blot analysis. Irradiation was performed using a 137Cs γ -irradiator at 1 Gy min⁻¹ for 12 min. Adriamycin was used at a concentration of 0.2 μ g ml⁻¹ (ref. 16). Leptomycin B was a gift from M. Yoshida. Time-lapse microscopy was done as described¹⁷.

Flow cytometry

Cells were trypsinized, washed with HBSS (Gibco) and resuspended in 40 μ l HBSS. The cells were then added to 360 μ l of a solution containing 1% NP-40 (Sigma), 4.7% formaldehyde (J. T. Baker), and 11 μ g ml⁻¹ Hoechst 33258 in PBS. The fixed and stained cells were stored at 4 °C and analysed within three days by flow cytometry.

Immunoprecipitation and western blot analysis

Immunoprecipitations were performed as described^{9,18}. 14-3-3 σ antibody was conjugated to beads using an Affi-Gel kit (Bio-Rad). Samples of protein from equivalent numbers of cells were fractionated on SDS-polyacrylamide gels (Novex). The proteins were then transferred to Immobilon P (Millipore) and incubated with either the p53-specific DO1 monoclonal antibody, the p21-specific EA10 monoclonal antibody (Calbiochem), a 14-3-3 σ -specific polyclonal antibody, anti-cdc2 polyclonal antibody (Santa Cruz), anti-wee1 antibody (Santa Cruz), or anti-cdc25C antibody (Santa Cruz). Polyclonal antibodies against 14-3-3 σ were generated in rabbits using a KLH-conjugate of the peptide SNEEGSEKGPVEV and were affinity purified using the same conjugate. The membranes were then washed with phosphate buffered saline (PBS) and incubated with the appropriate horseradish-peroxidase-coupled secondary antibody (Jackson Labs). Proteins were visualized with ECL (Pierce).

Immunohistochemistry

Cells were rinsed twice with PBS and then fixed with Histochoice (Amresco), permeabilized with 1% NP40 in PBS, and blocked in goat serum for 1 h. Antibodies specific for cdc2, cyclin B, cdk4, cyclin D, α -tubulin (all from Santa Cruz), 14-3-3 σ (generated as described above) and p21 (Calbiochem) were applied in GT (goat serum containing 0.05% Tween 20). After washing in PBST (PBS with 0.05% Tween 20), fluorochrome-labelled secondary antibody (Molecular Probes) was applied in GT for 1 h. Cells were washed for 5 min in PBST 3 times. In some cases, cells were counterstained with 4,6 diamidino-2-phenylindole (DAPI). Slides were mounted in DAPCO/glycerol and analysed with a Nikon Eclipse E800 microscope equipped with a CCD camera (Photometrics). Images were pseudocoloured using the software program IPLab (Signal Analytics Cooperation). TUNEL analysis was performed as described¹⁹. Cdc2 kinase assays were performed as described¹⁷.

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