Transcription-associated recombination is independent of XRCC2 and mechanistically separate from homology-directed DNA double-strand break repair

Linda Savolainen¹ and Thomas Helleday¹,²,*

¹Department of Genetics, Microbiology and Toxicology, Arrhenius Laboratory, Stockholm University, S-106 91 Stockholm, Sweden and ²Gray Institute for Radiation Oncology & Biology, University of Oxford, Old Road Campus Research Building, Roosevelt Drive, Headington, Oxford, OX3 7DQ, UK

Received July 29, 2008; Revised October 23, 2008; Accepted November 17, 2008

ABSTRACT

It has previously been shown that transcription greatly enhances recombination in mammalian cells. However, the proteins involved in catalysing this process and the recombination pathways involved in transcription-associated recombination (TAR) are still unknown. It is well established that both the BRCA2 protein and the RAD51 paralog protein XRCC2 are required for homologous recombination. Here, we show that the BRCA2 protein is also required for TAR, while the XRCC2 protein is not involved. Expression of the XRCC2 gene in XRCC2 mutated irs1 cells restores the defect in homologous recombination repair of an I-SceI-induced DNA double-strand break, while TAR is unaffected. Interestingly, the XRCC2-deficient irs1 cells are also proficient in recombination induced at slowed replication forks, suggesting that TAR is mechanistically linked with this recombination pathway. In conclusion, we show that TAR depends on BRCA2 but is independent of XRCC2, and that this recombination pathway is separate from that used to repair a two-ended DNA double-strand break.

INTRODUCTION

Transcription-associated recombination (TAR) is conserved in all cellular organisms investigated, from bacteria to mammals (1). The mechanisms and underlying causes of TAR are still largely unknown, as are the proteins catalysing this process. Studies in Saccharomyces cerevisiae has shown that a number of factor influence TAR; for instance DNA damage appears to have a synergistic effect with transcription on the levels of recombination (2). It has also been shown in S. cerevisiae that RNA polymerase I-dependent transcription can result in collision with the replication machinery leading to replication fork blockage and recombination in rDNA repeat copies (3). RNA polymerase II transcription can also impair the replication fork progression, which results in an increased recombination (4). A similar increase in recombination levels can be observed in S. cerevisiae strains with impaired transcription elongation owing to mutations in the THO/TREX complex (5,6). The THO/TREX complex is active at the interface between transcription and messenger ribonucleoprotein (mRNP) metabolism, and as a consequence of the mRNP biogenesis defect in THO/TREX mutants an impaired replication fork progression could be observed, which appear to stimulate TAR (7). Nickoloff and Reynolds (8) were first to show that transcription stimulated homologous recombination in mammalian cells, using heteroallelic neomycin genes. TAR in mammalian cells has been shown to also be associated with replication and restricted to cells in the S phase of the cell cycle (9). The available data thus suggest that TAR is likely involved in bypassing an active RNA polymerase, but details of the recombination mechanisms and proteins involved in the process remain elusive.

Homologous recombination (HR) can be induced by DNA double-strand breaks (DSBs) or at replication forks (10–12). There are two major pathways by which DSBs can be repaired; non-homologous end-joining (NHEJ) or homologous recombination (HR). NHEJ is a fast and error-prone repair pathway that involves ligation of free ends (13), while homologous recombination is slow and error-free if an intact DNA molecule, usually the sister chromatid, is used in the repair (14,15). Several proteins, e.g. BRCA2, RAD51 and five RAD51 paralogs,
have been shown to be essential for efficient homologous recombination repair of DSBs in mammalian cells (16–19), and mutations in these genes often results in cellular sensitivity to ionizing radiation. Chinese hamster cells sensitive to ionizing radiation have been isolated (20) and it was later found that one of the five RAD51 paralog genes, XRCC2, correct the ionizing radiation sensitive hamster cell line irs1 (21). The precise function of XRCC2 is unknown, but it has been shown to associate with three other RAD51 paralogs; RAD51B, RAD51C and RAD51D (22). This complex is called BCDX2 and has been shown to bind single-stranded DNA as well as single-stranded regions of DNA and to facilitate RAD51 filament formation (22). Cell lines deficient in XRCC2 are viable, but exhibit chromosomal aberrations, sensitivity to cross-linking agents, a mild sensitivity to γ-radiation (20) and defective RAD51 foci formation (18).

Here, we investigated the connection between homologous recombination and TAR using well-characterized Chinese hamster cell lines, irs1 and V-C8, deficient in XRCC2 and BRCA2, respectively (21,23). We find that BRCA2 defective cells are deficient in TAR, showing that TAR employs homologous recombination proteins. Surprisingly, the XRCC2 defective irs1 cells are still able to carry out TAR, in spite of being defective in homologous recombination of a DSB induced by ionizing radiation or a restriction endonuclease. This genetically separates TAR from DSB-induced homologous recombination. Furthermore, we show that XRCC2-deficient irs1 cells are also proficient in thymidine-induced recombination, which altogether suggest that TAR is employing a similar recombination mechanism to bypass replication blocks as for lesions produced by thymidine treatment.

### MATERIALS AND METHODS

#### Cell culture

All cell lines used in this study are derived from V79 Chinese hamster cells, with an additional mutation in BRCA2 (V-C8 and V-C8TofZM4), XRCC2 (irs1TofZM14 and irs1TofZM15) or with a partial duplication in the hprt gene S8TofZM5 (Table 1). The cells were cultured in Dulbecco’s Modified Eagle Medium with 10% fetal bovine serum and 1% PEST (penicillin–streptomycin). To select for the desired clones and to keep the inserted genes in the cells, 0.25 mg/ml of zeocin and 120 U/ml hygromycin were added to the medium. In order to keep the transcription of the recombination substrate off during growth, 1 µg/ml of doxycycline was also added to the medium. The cells were cultured in an incubator at 37°C with 5% CO2.

#### Transfection

The Chinese hamster cell lines were stably transfected with a recombination substrate using electroporation. The plasmids were purified from *Escherichia coli*. Fifteen micrograms of plasmid DNA were used for each transfection. The plasmid DNA was diluted in 50 µl H2O and mixed with 7.5 x 10^6 cells in an electroporation cuvette. The cells were transfected using the voltage 2.5 kV/cm and the capacitance 25 µF. The electroporated cells were aliquoted in the amounts 20, 50 and 100 µl on Petri-dishes and incubated for 2 days before the appropriate selective agent was added. After the colonies had formed, 30 colonies of varying sizes were picked and transferred to culture plates for further cultivation. Transient transfection was performed using Lipofectamine 2000 from Invitrogen according to the manufacturer’s protocol.

#### Luciferase assay

For measuring luciferase activity individual clones were trypsinised and counted and 2 x 10^5 cells from each clone were incubated with and without doxycycline for 24 h prior to lysis. After the incubation the cells were rinsed twice with Dulbecco’s PBS w/o Ca and Mg. All PBS was removed and 500 µl of lysis buffer was added to each well. The plates were shaken for 20 min in order to lyse the cells and the luciferase activity was measured using an illuminator. Clones exhibiting low background and high inducibility in the luciferase assay were selected for further experiments.

#### Recombination assay

For measuring recombination 1 x 10^6 cells were seeded onto four Petri-dishes. To two of the dishes, 10 µl (1 mg/ml) of doxycycline was added to repress expression from the Pbi-1 promoter. In the case of I-SceI-induced recombination, the cells were transiently transfected using Lipofectamine after 24 h. After an additional 24 h the cells were plated on cloning and selection dishes to determine survival and recombination, respectively. On the cloning dishes, 500 cells were seeded and on the selection dishes 300 000 cells were seeded. After 24 h, 100 µl of G418 was added. When colonies had formed (10 days for cloning and 15 days for selection), the cells were stained, using methylene blue in methanol (4 g/l), and counted. The recombination frequency was calculated as the number of recombinants formed in relation to survival. Thus, differential cloning efficiencies are compensated for in the recombination assay. Recombination assays while

| Table 1. Genotype and origin of Chinese hamster cell lines used in this study |
|-----------------|-----------------|-----------------|-----------------|
| Cell line       | Genotype        | Defect/modification | Origin References |
| irs1TofZM14,15  | XRCC2<sup>+</sup> | deficient in homologous recombination, carrying TAR substrate | V79 (37) |
| S8TofZM5        | WT              | Wild-type Chinese hamster, partial duplication in hprt gene, carrying TAR substrate | V79 (38) |
| V-C8            | BRC<sub>2α</sub> | BRC<sub>2α</sub>, deficient in homologous recombination | V79 (23) |
| V-C8TofZM4      | BRC<sub>2α</sub> | BRC<sub>2α</sub>, deficient in homologous recombination, carrying TAR substrate | V79 (23) |
| V79             | WT              | Wild-type Chinese hamster | Lung (23) |
over-expressing wild-type XRCC2 was also performed. For these assays, 20 μg of XRCC2 plasmid (24) was used for each 10 cm Petri-dish. One microgram of 1-SceI plasmid was used for each Petri-dish in order to induce a DSB in the recombination substrate. Transient transfections were performed using Lipofectamine 2000 according to the manufacturer’s protocol.

**RESULTS**

**BRCA2 is required for TAR**

We have previously constructed a substrate to investigate the effect of transcription on homologous recombination (9). Briefly, the construct contains two non-functional neomycin resistance genes; one neo repeat has a 18-bp long recognition site for I-Sce1 inserted, which introduce a stop codon that truncates the gene product, and the second neo repeat has a 3’ deletion and is called 5’neo (Figure 1A). A functional neoR gene can be regained either through gene conversion (GC) or sister chromatid exchange (SCE), but not through single-strand annealing. The truncated neo repeat is under the control of a bi-directional inducible promoter based on a Tet-Off gene expression system. Using this approach, the levels of transcription over this neo repeat can be measured using the expression levels of the luciferase gene, simultaneously expressed in the opposite direction in the vector (9).

Here, we transfected wild-type, XRCC2 and BRCA2 mutated Chinese hamster cells with both the Tet-regulatory vector pTetOffZeo and the recombination construct pBI-LMScI and selected for individual clones resistant to zeocin and hygromycin, to obtain cells with both vectors stably integrated into the genome. Withdrawal of doxycycline from the media resulted in increased luciferase activity in both wild-type (S8TofZM5) and BRCA2 defective (V-C8TofZM4) cells (Figure 1C), showing that BRCA2 does not influence the inducibility of transcription on the recombination substrate.

Transcription on the recombination substrate enhanced recombination levels in S8TofZM5 cells 3.7-fold (Figure 1C), which is in agreement with what was reported earlier for other wild-type hamster cells (9). However, transcription did not induce recombination in BRCA2 defective V-C8TofZM4 cells (Figure 1C). This is expected as the BRCA2 protein is vital for RAD51-mediated recombination (17), and in particular the gene conversion events produced by transcription (9, 25). Here, we confirm the homologous recombination defect in BRCA2 defective V-C8 cells and show that RAD51 foci cannot form following either ionizing radiation [which has been shown before (16)] or following thymidine treatments (Figure 1D).

**Western blot**

To confirm that transient transfection with wild-type XRCC2 increased the levels of the XRCC2 protein in the cells, western blots were performed. An antibody against XRCC2 diluted 1:200 was used. An antibody against α-tubulin diluted 1:1000 was used as a loading control. The proteins were extracted using lysis buffer and the protein concentration was measured by using the Coomassie (Bradford) Protein Assay Kit from Pierce. A standard western blot protocol was used and the proteins were separated on a NuPage NoveX 10% Bis–Tris gel from Invitrogen and then blotted onto a PVDF membrane. The proteins were visualized using SuperSignal Western blotting kit from Pierce.

**Transcription associated recombination is independent of XRCC2**

We also studied TAR in XRCC2 mutated irs1 cells carrying the Tet-regulatory vector pTetOffZeo and the recombination construct pBI-LMScI. Transcription was efficiently increased over the recombination substrate following removal of doxycycline from the media, as determined by measuring the luciferase activity (Figure 2A). Surprisingly, both the irs1TofZM14 and irs1TofZM15 clones showed a 3.8- and 3.3-fold increase in TAR following removal of doxycycline, respectively (Figure 2B), indicating a functional recombination pathway. This was unexpected as the XRCC2-defective irs1 clone earlier has been shown to be defective in homology directed repair of
[Text extracted from the image]
DSBs and are at the same time proficient in TAR. Thus, there might be a sub-pathway of homologous recombination repair in irs1 cells that is still functional. It was previously reported that irs1 cells are proficient in thymidine-induced RAD51 foci, but defective in hydroxyurea and γ-ray-induced RAD51 foci (30). Thymidine is an agent that depletes only the (dCTP) pool in cells, as a consequence of a negative feedback mechanism of the R1 subunit of ribonucleotide reductase that follows high (dTTP) levels (31). The consequence is that the progression of the replication fork is slowed down during replication, which results in a unique replication lesion, with no DSBs, that is separate from those produced by hydroxyurea. Hydroxyurea directly inhibits ribonucleotide reductase, depleting all (dNTP) pools resulting in stalled replication forks and DSB formation (32). Thymidine efficiently induces homologous recombination at replication forks (32), which likely involves a template switching mechanism (33).

**DISCUSSION**

TAR is a phenomenon present in all investigated cellular organisms but, in spite of this, the proteins involved in catalysing TAR are unknown. Here, we show that...
Cells containing >g type (S8TofZM5) or XRCC2 defective (irs1TofM14) cells 5 h following transcription and XRCC2 on homologous recombination triggered by an I-SceI-induced DSB following transient transfection of the pCMV3xnlsI-Sce I nuclease likely is a rare event in vivo two-ended DSB formed by ionizing radiation or an endonuclease. These experiments clearly show that the recombination induced by an I-SceI-induced DSB is distinct from DSB-induced homologous recombination.

BRCA2 is required for TAR, which strongly support that TAR involves RAD51-mediated strand invasion (34). This is an expected finding and therefore, it is more surprising to find that the XRCC2 protein is not required for TAR. The XRCC2 protein was earlier found to be important in catalysing DSB-induced homologous recombination and RAD51 foci formation after ionizing radiation (18,19,27). Here we report that the irs1 cell line is able to catalyse TAR and that overexpression of a wild-type XRCC2 protein does not influence TAR levels, which altogether show that XRCC2 is not involved in TAR. As irs1 cells are functional for TAR, while defective for DSB-induced homologous recombination, these experiments clearly show that the recombination induced following transcription is functionally different than homologous recombination induced by an I-SceI-induced DSB. This finding is of biological importance as the two-ended DSB formed by ionizing radiation or an endonuclease likely is a rare event in vivo. However, the discrepancy of the XRCC2 gene involved in one pathway, but not another, is anticipated as homologous recombination is involved in repairing several different types of lesions (33).

Using the irs1TofZM14 and irs1TofZM15 cell lines, we now have a system to genetically separate TAR from ordinary DSB-induced homologous recombination repair. Interestingly, it was reported that the irs1 cell line is partially proficient for thymidine-induced homologous recombination, while defective for DSB or hydroxyurea-induced homologous recombination (30), which we can confirm to be the case also in the irs1 cells used here. In speculation, it is possible that the thymidine-induced and transcription-induced homologous recombination occur with similar mechanisms in mammalian cells, a mechanism that appears to be largely distinct from DSB-induced homologous recombination. We have shown in several reports that thymidine causes a unique substrate for homologous recombination, which may involve template switching to bypass a lesion (33,34,35,36). The DNA polymerase is about 20 times faster than RNA polymerase II and would need to overtake the RNA polymerase not to be slowed down. The model for thymidine-induced recombination may also explain how the RNA polymerase could be over taken by the DNA polymerase, as well as explaining how the XRCC2 allele in irs1 cells are proficient for both thymidine and transcription-induced recombination.

Using the irs1TofZM14 and irs1TofZM15 cell lines, we now have a system to genetically separate TAR from ordinary DSB-induced homologous recombination repair. Interestingly, it was reported that the irs1 cell line is partially proficient for thymidine-induced homologous recombination, while defective for DSB or hydroxyurea-induced homologous recombination (30), which we can confirm to be the case also in the irs1 cells used here. In speculation, it is possible that the thymidine-induced and transcription-induced homologous recombination occur with similar mechanisms in mammalian cells, a mechanism that appears to be largely distinct from DSB-induced homologous recombination. We have shown in several reports that thymidine causes a unique substrate for homologous recombination, which may involve template switching to bypass a lesion (33,34,35,36). The DNA polymerase is about 20 times faster than RNA polymerase II and would need to overtake the RNA polymerase not to be slowed down. The model for thymidine-induced recombination may also explain how the RNA polymerase could be bypassed during replication (Figure 5). There is already strong support for TAR being connected with replication in both mammals and yeast (3,9) and it has been
shown in yeast that recombination is induced when a replication fork hits an elongating RNA polymerase (4). Also, in mammalian cells TAR is restricted to the S-phase of the cell cycle and relies on a rapidly moving replication fork (9).

In conclusion, we show a differential involvement of the BRCA2 and XRCC2 proteins in catalysing TAR, demonstrating that homology directed DSB repair and TAR employ distinct recombination pathways.

ACKNOWLEDGEMENTS

We thank John Thacker, Mark Meuth and Malgorzata Zdziennicka for materials.

REFERENCES


