Telomere Dynamics and Homeostasis in a Transmissible Cancer

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Abstract

Background: Devil Facial Tumour Disease (DFTD) is a unique clonal cancer that threatens the world's largest carnivorous marsupial, the Tasmanian devil (Sarcophilus harrisii) with extinction. This transmissible cancer is passed between individual devils by cell implantation during social interactions. The tumour arose in a Schwann cell of a single devil over 15 years ago and since then has expanded clonally, without showing signs of replicative senescence; in stark contrast to a somatic cell that displays a finite capacity for replication, known as the “Hayflick limit”.

Methodology/Principal Findings: In the present study we investigate the role of telomere length, measured as Telomere Copy Number (TCN), and telomerase and shelterin gene expression, as well as telomerase activity in maintaining hyperproliferation of Devil Facial Tumour (DFT) cells. Our results show that DFT cells have short telomeres. DFTD TCN does not differ between geographic regions or between strains. However, TCN has increased over time. Unlimited cell proliferation is likely to have been achieved through the observed up-regulation of the catalytic subunit of telomerase (TERT) and concomitant activation of telomerase. Up-regulation of the central component of shelterin, the TRF1-intercating nuclear factor 2 (TINF2) provides DFT a mechanism for telomere length homeostasis. The higher expression of both TERT and TINF2 may also protect DFT cells from genomic instability and enhance tumour proliferation.

Conclusions/Significance: DFT cells appear to monitor and regulate the length of individual telomeres: i.e. shorter telomeres are elongated by up-regulation of telomerase-related genes; longer telomeres are protected from further elongation by members of the shelterin complex, which may explain the lack of spatial and strain variation in DFT telomere copy number. The observed longitudinal increase in gene expression in DFT tissue samples and telomerase activity in DFT cell lines might indicate a selection for more stable tumours with higher proliferative potential.

Introduction

The world's largest carnivorous marsupial, the Tasmanian devil (Sarcophilus harrisii) has recently become threatened with extinction due to a unique transmissible cancer, Devil Facial Tumour Disease (DFTD) [1,2,3]. Prior to the emergence of the disease, devils were common throughout Tasmania. However, since the first sighting of DFTD in 1996, the disease has spread across the island state, resulting in population declines of up to 90% [3]. The disease now occurs in over 80% of the devil’s geographic range, and the rapid population decline has led to the Tasmanian devil being listed as endangered by international (International Union for Conservation of Nature [4]) as well as national and state authorities [5].

DFTD is transmitted between individuals by biting during social interactions [6] and manifests in gross malignant tumours around the oral cavity, with frequent metastases to other organs [7,8]. Due to starvation, secondary infections and organ failures, devils usually succumb to the disease within 6 months of tumour emergence [1,7]. Cytogenetic analyses have revealed that DFTD is caused by a rogue clonal cell line [9], that is likely derived from cells of the neural crest lineage (Schwann cells) [8,10]. Although DFTD possesses a highly rearranged genome, and is characterised by tumour specific complex translocations and chromosomal rearrangements, the cell line is remarkably (chromosomally) stable [9]. Recently however, four, closely related but karyotypically distinct DFT strains have been identified, suggesting that the tumour is evolving [11,12]. Despite the four distinct DFT strains, genetic studies using microsatellite and immune-gene markers have demonstrated that Devil Facial Tumour (DFT) cells are genetically identical [10,13,14,15].

Since their emergence in 1996 [9] DFT cells have undergone continuous division and propagation in thousands of devils without...
exhausting their capacity for replication and compromising their genomic stability. In contrast, normal human somatic cells display a finite capacity for replication, known as the “Hayflick limit”[16]. That is, after a given number of divisions, the cells exhaust their replicative potential due to shortened telomeres and enter a state known as replicative senescence. In hyperproliferative diseases, such as tumourgenesis, when telomere attrition reaches a critical level, cells enter a stage of growth arrest referred to as “crisis” [17,18,19]. By up-regulating or reactivating the telomere terminal transferase enzyme (telomerase), cancer cells are able to emerge from the “crisis” state and maintain telomeres that are slightly longer than those observed during “crisis” [17,20].

Telomeres are ribonucleoprotein complexes at the ends of eukaryotic chromosomes essential in regulating cell lifespan [18]. Their primary functions are to ensure correct chromosome segregation during mitosis, and to prevent chromosome fusion and concomitant cell-cycle arrest, caused by the end of the chromosomes being treated as DNA double-strand breaks [21]. In vertebrates, including Tasmanian devils, telomeres consist of variable numbers of tandem repeats (TTAGGG nucleotides) bound by a specialised multiprotein complex known as shelterin [22,23]. Telomere length homeostasis in germ line and tumour cells is achieved through the negative feedback loop of the shelterin complex and the telomere terminal transferase enzyme [24]. Telomerase is activated in pluripotent embryonic, and adult stem cells, to arrest the progressive telomere attrition through the addition of TTAGGG repeats to the 3’ strand of chromosomes [24]. Most human tumour cell lines have stable telomere settings, which are achieved by the negative regulation of the telomerase by the shelterin complex [25]. The shelterin complex consists of three shelterin subunits: TRF1, TRF2 and POT1, which are interconnected by three additional proteins TPP1, RAP1 and TINF2. TINF2 (TRF1-interacting nuclear factor 2, or also called TRFI)-Interacting Nuclear protein 2 (TIN2) occupies a central position in the protein complex, by providing a bridge between the subcomponents of shelterin [for review see [26]]. It has been shown that low expression of TINF2 has a destabilising effect on shelterin [27,28]. Due to the central and critical role of TINF2 (TIN2) in shelterin stability we chose to measure the expression of this gene, as a proxy of shelterin activity.

The accumulation of shelterin along the telomeric repeat array prevents further telomerase induced telomere elongation [23]. Human cancer studies have shown that the joint up-regulation of telomerase expression and the genes of the shelterin complex may facilitate in stabilising the cancer cells by preventing the activation of DNA damage responses, such as apoptosis[27]. In approximately 85% of human cancers, telomerase activity has been shown to facilitate malignant transformation by maintaining replicative potential [29,30]. In the remaining 10–15% of cancers, prevention of telomere loss is achieved in the absence of telomerase activity, through a recombination-mediated template switching mechanism known as alternative lengthening of telomeres (ALT) [31]. Consequently, tumour cells are able to escape apoptosis and hence maintain infinite replication capacity.

The DFTD cell line has been continuously dividing and adapting to the microenvironment of each different host for over 15 years. Therefore this clonally transmitted disease provides an unprecedented opportunity to study cancer cell evolution and progression in vivo. Increased knowledge of telomere homeostasis in this transmissible cancer may provide novel insights into how DFT cells achieve and maintain their hyperproliferative potential and may help us to understand the origins, somatic evolution and extraordinary success of this parasitic clonal lineage. Furthermore, both TERT and TINF2 have been suggested as potential therapeutic targets in human cancer [32,33] and increasing our understanding of the role of these genes in Devil Facial Tumour Disease may open novel avenues for disease treatment.

In the present study we focused on the role of telomere length, quantified as Telomere Copy Numbers (henceforth TCN) in hyperproliferation of DFT cell samples. As proxies for telomerase activity in tumour tissue samples we investigated the expression of the catalytic subunit of telomerase (TERT) and one of the main components of shelterin, the TRFI-interacting nuclear factor 2 (TINF2). Additionally, temporal changes in telomerase activity were quantified in five DFT cell lines.

**Results**

(a) Telomere Restriction Fragment length analyses

Telomere restriction fragment (TRF) length was analysed in both primary and metastatic tumours, as well as spleen samples from four Tasmanian devils (a total of 12 samples). We were unable to assign telomere length in all of the 12 samples as the restriction digest produced several repeated TRF-smears at various lengths (ranging from <2 kbps up to ~18 kbps) (Figure 1).

(b) Relative telomere repeat copy number

Altogether 65 tissue samples, collected from 17 locations across Tasmania (Bothwell, Bronte Park, Buckland, Fentonbury, Forestier, Freycinet, Hamilton, Mt William, Narawntapu, Raitlon, Ravenswood, Reedy Marsh, Sorell, St. Marys, Weegena, Wisedale and West Pencil Pine, Figure 2), were included in the relative telomere repeat copy number analysis. Spleen, lung and tumour samples exhibited a significant TCN variation (Kruskal Wallis test: $T = 17.1$, $P = 0.0007$, $DF = 3$); with tumours (both primary and metastatic) showing the lowest (mean = 3.21±3.28) and spleen the highest (mean = 12.52±4.62), whereas lung samples showed intermediate TCN (mean = 8.03±2.04, Figure 3). A posthoc Conover-Inman test (available in StatsDirect) revealed no significant difference in TCN between lung and spleen ($P = 0.52$), between lung and metastasis ($P = 0.08$), between primary tumours and metastasis ($P = 0.52$). The same test did, however, reveal a significant difference in TCN between lung and primary tumours ($P = 0.006$), between spleen and tumour ($P = 0.0001$), and between spleen and metastasis ($P = 0.01$).

(c) Temporal (longitudinal) geographical and strain variation in TCN

A Kruskal-Wallis test revealed a significant temporal variation in TCN of samples collected in 2006, 2007 and 2010 ($T = 7.66$, $P = 0.02$, $DF = 2$) and a posthoc and a Conover-Inman test revealed significant differences in TCN between years 2006 and 2007 ($P = 0.03$) and 2006 and 2010 ($P = 0.01$), but no significant difference in TCN was observed between years 2007 and 2010 ($P = 0.6$). The post hoc test thus suggests a temporal increase in TCN (Figure 4).

We did not however, observe any significant difference in TCN among the three geographic regions (East, Central, North-West) (Kruskal Wallis test: $T = 1.75$, $P = 0.42$, $DF = 2$), nor among the four different strains (Kruskal Wallis test: $T = 2.1$, $P = 0.56$, $DF = 3$).

(d) TERT and TINF2 expression

Devil TERT and TINF2 expression was significantly up-regulated in primary tumours compared to spleen by a mean factor of 14.63 $P<0.0001$ (Std. Error (SE) ranging between 4.5 and 37.8), and 37.86 $P<0.0001$ (SE ranging between 4.6–272.9), respectively (Figure 5). TERT and TINF2 expression showed...
substantial variation across tumour samples. We did not, however, observe any significant association between TCN and TERT or TINF2 expression in the tumour samples (Spearman rank correlation, $R = 0.31$, $P = 0.36$, $N = 11$; $R = 0.05$, $P = 0.88$, $N = 11$, respectively).

In the tumours, the expression level of TINF2 was significantly lower than that of TERT (Two-sided Mann-Whitney U-test; $U = 27$, $P = 0.05$, median $TINF2 = 0.51$, median $TERT = 3.58$). Despite the difference in expression level we observed a significant association between TERT and TINF2 (Spearman rank correlation $R = 0.83$, $P = 0.0017$, $N = 11$). We also detected a significant temporal variation in TERT and TINF2 expression levels as both TERT and TINF2 showed significantly increased expression levels in 2010 compared to 2007 (Two sided Mann-Whitney U-test, $U = 28$, $P = 0.0173$ and $U = 28.5$, $P = 0.013$, respectively; TERT median 4.77 and 2.44, respectively; TINF2 median 2.84 and 0.47, respectively, Figure 6).

Discussion

Like many human cancers [34,35], Devil Facial Tumours have short telomeres. TERT gene expression is up-regulated 15-fold in DFT cells compared to spleen cells, and telomerase activity is present in DFT cell lines. This telomerase activity prevents DFT cells from entering replicative senescence, and taken together with the lack of extrachromosomal telomeric DNA (Pearse pers. com) in DFT karyotypes, points towards telomerase up-regulation, not alternative lengthening of telomeres (ALT), as the primary mechanism for DFT immortality [31].

High expression of TINF2, a negative regulator of telomerase activity [23], in DFT cells suggests that telomere elongation is highly regulated in this cancer. DFT cells appear to monitor and regulate the length of individual telomeres i.e. shorter telomeres are elongated by telomerase activity; longer telomeres are protected from further elongation by the shelterin complex [27].

Increased TERT and TINF2 expression most likely explain the lack of spatial variation in DFT TCN. Also, TCN does not differ between DFTD strains. However, the temporal increase in TERT and TINF2 gene expression and enzyme activity may be linked...
with growth advantage and increased tumour progression in DFT, as it is in human cancers [34,36,37].

The short telomeres and up-regulation of telomerase likely counteract each other. The short telomeres lead to increased genetic instability but the telomerase activation facilitates tumour growth by either inhibiting further chromosomal instabilities or by
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Figure 6. TERT and TINF2 gene expression increases with time in DFT samples. Open bars depict TERT expression, black bars depict TINF2 expression. Number of samples used in the analysis: tumours collected in 2007: N = 5 and 2010: N = 6. * depicts significant differences (P = 0.0173 and P = 0.013, respectively).

Materials and Methods

(a) Samples
Tissue samples were collected from 17 locations across Tasmania (Bothwell, Bronte Park, Buckland, Fentonbury, Forestier, Freycinet, Hamilton, Mt William, Narawntapu, Raitlon, Ravenswood, Reedy Marsh, Sorell, St. Marys, Weegena, Wisedale and West Pencil Pine, Figure 1) by the members of the Department of Primary Industries, Parks, Water and Environment (DPIPWE) from euthanised DFTD affected devils and stored at the Animal Health Laboratories (DPIPWE). The research was carried out with approval from the DPIPWE (Department of Primary Industries, Parks, Water and Environment, Tasmania) animal ethics comittee, Animal Ethics No: 101 2010/11. We obtained tissue samples from 48 devils. We had access to spleen and primary tumour, as well as metastasis samples from four devils. 51 primary tumours, five metastases, four lung and five spleen DNA samples were used in the analyses (Figure 2).

In order to investigate geographical/spatial variation in telomere copy number, the samples were divided into three geographical regions (East = distribution prior to 2003, Central = distribution between 2003–2005 and North-West = distribution between 2005–2007) based on the temporal/spatial progression of DFTD across Tasmania [40]. We had information about the specific strains of 45 tumour samples and used these samples to investigate telomere copy number variation between DFT strains.

Temporal variation in telomere attrition rates was based on copy numbers observed in samples collected in 2006, 2007, and 2010 (N = 51). Due to sample collection procedures we were only able to extract RNA from five spleen and 11 (5 from 2007 and 6 from 2010) primary tumour samples which were subsequently analysed with the Quantitative Real-Time PCR.

The telomerase activity assays were performed on five lysed DFT cell line samples obtained from DPIPWE. Tumour cell lines were generated and maintained at DPIPWE according to the descriptions of Pearse et al 2012 [11]. The five cell lines originated from tumour samples collected in 2003, 2006, 2007, 2010 and 2011.

(b) DNA extraction, telomere fragment length measurements and telomere copy number quantitation
Genomic DNA was isolated from tissue samples by phenol-chloroform extraction. Sample DNA quantity and quality was...
measured using a NanoDrop Spectrophotometer (NanoDrop Technologies, Wilmington, DE).

(c) Telomere Restriction Fragment Length analyses (TRFL)
Telomere restriction fragment (TRF) length was quantified by Southern blot hybridisation following the protocol outlined in the Telo TAGGG TL assay kit (Roche, Indianapolis, IN), using constant field electrophoresis. After digesting genomic DNA with a mixture of HindIII and RsaI restriction enzymes to remove sequence-diverse DNA from the centromeric side of the telomeres, telomere length was analysed on agarose gels, which were run for 4 hours at 5 V/cm. The TRF fragments were labeled with a digoxigenin labeled probe, and the TRF images were subsequently developed on high performance chemiluminescence film (Amersham Biosciences, Waukesha, WI).

(d) Quantitative PCR of relative telomere copy number
Relative telomere repeat copy number was analysed by quantitative PCR (Q-PCR) as described by Cawthon [41]. Telomere specific primers were adopted from Cawthon [41], Tel1: 5’-GGTTTTTGGAAGGTAGGGTTAGGGGTAGGGGT-3’, Tel2: 5’-TCCCGACTATTCTATCCCTATCCCTATTCCATCTCTACTCTGA-3’. RPLP0 (also called 36B4) gene was chosen as single copy gene following the methodology of Cawthon [41], and the single copy presence of this gene in the Tasmanian Devil genome [42] was confirmed by sequencing the genome for alternative copies of the gene. No alternative RPLP0 copies or pseudogenes were found. RPLP0 gene specific primers were designed based on the Tasmanian Devil genome sequence [42], using the Primer3Plus website (http://www.bioinformatics.nl/cgi-bin/primer3plus/primer3plus.cgi). RPLP0 F: 5’-CTTCCCGTTTACCAAAAGAG-3’ and RPLP0 R: 5’-TGTGTTCTGAAGTGGGAAGTG-3’. The Q-PCR reactions were performed on the RotorGene6000 (Qiagen, Germantown, MD) in 15 µl total volume, containing 7.5 µl of Qiagen 2xQuantiFast Sybr Green PCR master mix (Qiagen, Germantown, MD), 0.5 µM forward and reverse primers (the optimal primer concentrations) and 1 µl of gDNA (1 ng/µl concentration). Q-PCR conditions were established according to the manufacturer protocol; 95°C for 5 min denaturation followed by 40 cycles of 95°C for 15 s and 60°C for 30 s (annealing temperature, AT). Fluorescence signal was acquired at the AT. To evaluate the specific amplification a final melting curve analysis (from AT up to 99°C) was added under continuous fluorescence measurements. Standard curves were generated using serial 1:5 dilutions of a composite sample containing equal parts of DNA samples generated from spleen and tumour tissue RNA extracts. All dilutions were run in triplicate. Standard curves had an $R^2>0.99$ (GUSB reaction; $R^2=0.998$, TERT reaction: $R^2=0.990$ and TINF2 reaction: $R^2=0.993$) and contained at least four dilutions from the dilution series with a linear dynamic range of at least 3 orders of magnitude and had PCR efficiencies between 0.98 and 1.4 ($GUSB$ 1.1, $TERT$: 1.4 and $TINF2$: 0.98). All samples were run in quadruplicate, and all Cq values for unknowns fell within the linear quantifiable range of the appropriate standard curves. The program Rest [43] was used to calculate the normalized fold change of the target gene compared to the reference gene. This program package also corrects for the different reaction efficiencies. Statistical significance (P<0.05) was determined by a Pair Wise Fixed Reallocation Randomisation Test® as described by Pfaffl et al. [43].

(e) RNA extraction and quantifying telomerase expression by quantitative RT-PCR
RNA was extracted from tissue samples using a combination of Trizol (Sigma, St. Louis, MO) and Qiagen RNeasy mini kit (Qiagen, Germantown, MD). RNA quality and quantity were quantified on an Agilent 2100 BioAnalyzer (Agilent, Santa Clara, CA). Genomic DNA was removed from the RNA samples by the DNAse I AMPD1 kit (Sigma, St. Louis, MO) and cDNA was synthesized with the QuantiTect Reverse Transcription Kit (Qiagen, Germantown, MD). Telomerase gene specific primers spanning exon boundaries were designed in the catalytic protein subunit of devil TERT gene, using the Primer3Plus website (http://www.bioinformatics.nl/cgi-bin/primer3plus/primer3plus.cgi). TERT-F: 5’-TGCTGTTACTGCAAGAGAATGTC-3’, and TERT-R: 5’-TGCAAGGAAGAGGTCTTCT-3’. Tel1: 5’-GGATCCTGGAAAACGTGGTC-3’, and TINF2-R: 5’-GGATCCTGGAAAACGTGGTC-3’. Two genes, GUSB (gGUSB) and GUSB (gGUSB) were used as normaliser genes following the description of Murchison et al.[10,14]: gGAPDHf: 5’-GACTCAACCGATGTCCGATTCTC-3’ and gGAPDHR: 5’-ATAATGGTACCCCATGCAAGCC-3’. gGUSBf: 5’-CTGCTGCTATTATTTGGAGAC-3’ and gGUSB: 5’-CAAGATCCATTCGAGGTT-3’. The Q-PCR reactions were performed on the RotorGene6000 (Qiagen, Germantown, MD) in 15 µl total volume, containing 7.5 µl of Qiagen 2xQuantiFast Sybr Green PCR master mix (Qiagen, Germantown, MD), 0.5 µM forward and reverse primers (the optimal primer concentrations) and 1 µl of cDNA (5 ng/µl concentration). Reverse transcriptase negative and cDNA negative samples were run alongside the cDNA samples as controls to detect genomic DNA contamination and primer-dimer formations. Q-PCR conditions were established according to the manufacturer protocol; 95°C for 5 min denaturation followed by 40 cycles of 95°C for 15 s and 60°C for 30 s (annealing temperature, AT). Fluorescence signal was acquired at the AT. To evaluate the specific amplification a final melting curve analysis (from AT up to 99°C) was added under continuous fluorescence measurements. Standard curves were generated using serial 1:5 dilutions of a composite sample containing equal parts of cDNA samples generated from spleen and tumour tissue RNA extracts. All dilutions were run in triplicate. Standard curves had an $R^2>0.99$ (GUSB reaction; $R^2=0.998$, $TERT$ reaction: $R^2=0.990$ and $TINF2$ reaction: $R^2=0.993$) and contained at least four dilutions from the dilution series with a linear dynamic range of at least 3 orders of magnitude and had PCR efficiencies between 0.98 and 1.4 ($GUSB$ 1.1, $TERT$: 1.4 and $TINF2$: 0.98). All samples were run in quadruplicate, and all Cq values for unknowns fell within the linear quantifiable range of the appropriate standard curves. The program Rest [43] was used to calculate the normalized fold change of the target gene compared to the reference gene. This program package also corrects for the different reaction efficiencies. Statistical significance (P<0.05) was determined by a Pair Wise Fixed Reallocation Randomisation Test® as described by Pfaffl et al. [43].

(f) Telomerase assay
Telomerase activity was measured using the TRAPEZE-RT telomerase detection kit (Millipore, Bedford, MA). Cells were lysed in 200 µl of CHAPS buffer, and protein content was quantified by using the Pierce BCA Protein Assay Kit (Thermo Scientific, Rockford, IL). Aliquots of cell lysate (250 ng of protein/well) were assayed in triplicate. Standards, inactivated samples, and non-template reactions were also included in the assay as quality controls. Real-time amplifications were performed with a RotorGene6000 multicolor real-time PCR detection system (Qiagen, Germantown, MD). Standard curve was generated from
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Author Contributions

Conceived and designed the experiments: BU KB. Performed the experiments: BU CF SG. Analyzed the data: BU TM ATP. Contributed reagents/materials/analysis tools: AMP RT SP ATP. Wrote the paper: BU TM KB.

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