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EVOLUTION OF CHROMOSOMAL ABERRATIONS AND TELOMERES AFTER A SINGLE SCAN IN NON-CANCER PATIENTS

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SUMMARY

Recent epidemiological investigations demonstrate an increased risk of cancer in children and adolescents following exposure to low-dose ionizing radiation from diagnostic were computed tomography scans with a cumulative dose of approximately 50 mSv. Peripheral blood lymphocytes from 50 non-cancer patients before and 24 hours after a CT scan were obtained. Chromosomal and telomeric aberrations were performed after staining by fluorescence hybridization of telomeres and centromeres. The frequency of these aberrations was compared to the calculated effective radiation dose using a computational dosimetry system and a dose-length product in a scanner. A significant increase in DSB resulting from all chromosomal aberrations after CT exposure was observed. A significant increase in telomere aberrations was observed after CT exposure. However, no correlation was observed

between the effective radiation dose and the frequency of chromosomal and telomeric aberrations. It should be noted that the increase in chromosomal and telomeric aberrations was age-dependent. We were demonstrated in this study for the first time the significant increase in telomere aberrations after CT exposure. This loss of telomere functionality is played a major role in the continuation of chromosomal instability. These results could be used in the monitoring of populations exposed to low doses.

KEYWORDS: Scanner, Dicentric, DSB, Dose-length product, Age, Low-dose.

INTRODUCTION

Among the uses of x-rays in diagnosis, computed tomography has been established itself as one of the most informative and accurate diagnostic radiology examinations (Thomas F. Burker MD *et al.,* 1994). However, the delivered dose of computed tomography examinations is approximately 50 mSv (Cynthia *et al.,* 2015). This exposure poses a problem in the event of repeated scanning and especially if the subject is young (Heidi *et al.,* 2014). An epidemiological study has demonstrated the increased risk of brain tumors and leukemia in children exposed to CT scans. The genotoxic effect of low dose exposure by CT Scan has been demonstrated after in vitro and in vivo exposure. Several approaches have been applied such as gH2AX test, dicentric chromosomal test (Venkateswarlu *et al.,* 2021), FISH translocations, CBMN test (Dayton *et al.,* 2018) and PCC combined with FISH test (Pouget *et al.,* 2004). It is now well documented that CT exposure induces DSB and interindividual variation has been shown particularly in young patients (Volodymyr *et al.,* 2022). The introduction of telomere and centromere staining with short hybridization times and high specificity and signal intensity in the analysis of induced chromosomal aberrations not only allows the reliable and accurate scoring of all chromosomal aberrations, but also possible analysis of telomere aberrations such as telomere loss and telomere doublet formation after expsoure. Telomeres protect the ends of chromosomes, ensuring the stability and integrity of the genome. Dysfunction of the telomere nucleoprotein complex can be exposed the free ends of chromosomes to the DNA double-strand break repair machinery. Thus, the consequences of telomere loss or dysfunction can be promoted chromosomal instability, leading to the progression of malignant transformation. The impact of exposure to high, moderate or low doses on telomere functionality is even less studied. Genotoxic stress after exposure to ionizing radiation was generally carried out using cultures of T lymphocytes. This is the reference technique recognized by the IAEA and the OECD. Currently, the introduction of

genomic approaches in the analysis of genotoxic stress allows the use of other samples such as saliva samples. Nevertheless, the detection of chromosomal aberrations induced in other cells are made it was possible to be validated the data, was obtained with T lymphocytes. B lymphocytes are key cells in the immune response with the production of antibodies and immunoglobulin molecules. The analysis of DNA damage in B lymphocytes after exposure to be lowed doses allows the best appreciation of the inflammatory reaction.

MATERIALS AND METHODS

1. Patients CT scans:

The samples and medical records was used in our study were approved by the ethics committee of the Ministry of Hospitals of Congo Brazzaville (n° 0011/MSP/CAB/DGSSa/DH/SH-22) and the University of Congo Brazzaville (No. 398/MESRSIT/IRSSA-CERSSA). Written informed consent was obtained from all participants for the analysis of blood samples. The study was involved 50 non-cancer patients aged 7 to 70 who underwent medical CT scans. Three hospitals were participated in this study. No prior exposure to ionizing radiation or administration of chemotherapy was reported (Table 1-A). A validation cohort of 20 young patients (Table 1-A).

Table 1-A: Distribution of patients and healthy donors by age.

Age group	Workforce	Percentage
7 – 18	19	38
19 – 32	16	32
33 – 46	03	6
47 – 60	08	16
61 – 72	04	8
Total	50	100%

Total 50 100% Let m be the average age of our sample.

m = ∑nixi / n; with ni the frequency corresponding to each class, xi the class centers and n the total number of patients.

$$m = \frac{38x12.5 + 32x25,5 + 6x39,5 + 16x53,5 + 8x66,5}{50} = 58,32$$

Our study sample has been an average age of 58 years. Its modal class is: [47-60[. While the ages of healthy donors are distributed as follows:

Table 1-B: Distribution of healthy donors by age.

N°	ages of healthy donors	Workforce
1	17	01
2	18	01
3	19	03
4	23	02
5	24	02
6	30	01
7	31	01
8	35	02
9	40	01
10	42	01
11	44	01
12	48	01
13	51	01
14	52	02

Let m_2 be the average age of our sample.

$$m_2 = \frac{17+18+3x19+2x23+2x24+30+31+35x2+40+42+44+48+51+2x52}{20} = 32,3$$

Our sample of healthy donors has an average age of 32 years.

2. Contributions / Progress of work (Computed tomography)

Computed tomography of the brain, Thoraco-abdominal-pelvic or Abdomino-pelvic were performed with and without contrast medium. This was performed using a SOMATOM EMOTION ECO CT scanner with a tube voltage of 80–140 kV, mAs=70–120 and pitch=0.8–1.5 mm. The effective radiation dose was calculated by the EDEREX computer dosimetry system. Furthermore, it has been defined according to methodical guidelines using data regarding age, sex, initiation and final CT scan position.

The dose-length product was calculated based on the CT dose index (CTDI), which was set uniformly in the CT scanner with the length of the CT axial scan range of a body, as below: DLP = CTDI (mGy) × L (cm). Furthermore, it has been defined according to methodical guidelines using data regarding age, sex, initiation and final CT scan position. The dose-length product (DLP) was calculated based on the CT dose index (CTDI), which was set uniformly in the CT scanner with the length (L) of the CT axial scan range of a body , as below: DLP = CTDI (mGy) × L (cm). For the thorax, the doses varied between 1.5 and 3 mSv; for the abdomen, they were varied between 2.5 and 5 mSv; and for the brain, they were varied between 2 and 3 mSv.

3. Peripheral blood lymphocyte Cultures and Plating in metaphase:

In this study, chromosomal and telomeric aberrations were investigated in T and B lymphocytes. Peripheral blood lymphocytes before and 24 h after CT were cultured with RPMI 1640 medium supplemented with 10% fetal bovine serum in the presence of phytohaemagglutinin for T cell stimulation and TPA for B cell stimulation. Bromodeaoxyuridine (1%) was added at 5 mg/ml in culture medium. After 46 h of culture, the cells were exposed to colcemid (0.1 µg/mL) (Gibco KaryoMAX,) for 2 h at 37° C., 5% CO2, in a humidified atmosphere to stop the dividing cells in metaphase. After harvesting cells, they were centrifuged for 7 min at 1400 rpm at room temperature, supernatant removed, cell pellet was resuspended in warm 0.075M and incubated for 20 min in a 37°C water bath. Cells were prefixed by adding approximately five drops of fixative to each tube with shaking and the tubes were centrifuged for 7 min at 1400 rpm at room temperature. The supernatant was removed and the cells were suspended in fixative solution followed by centrifugation using the same parameters. After two more cycles of these fixation steps, the cells were stored in the fixative solution at 4°C overnight and the metaphases were plated on cold moist slides the next day. Slides were dried overnight at room temperature and stored at -20°C until further use.

4. Telomere-Centromere staining technique

Telomeres and centromeres were stained with a Cy-3-labeled PNA probe specific for TTAGGG for telomeres and a FITC-labeled probe specific for centromere sequences, as previously was described. Briefly, slides were washed with 1X PBS and were fixed with 4% formaldehyde at room temperature. After three rinses with PBS, they were treated with pepsin at 37°C for 5 min. After additional rinsing three times with PBS, slides were sequentially dehydrated with 50%, 70%, and 100% ethanol and air-dried.

The telomere and centromere probes were added to the slides then denatured on a hot plate at 80° C, for 3 min and then incubated in the dark for 1h at room temperature. Slides were then rinsed in 70% formamide /10 mM Tris pH 7.2 three times for 15 min was followed by 50 mM Tris pH 7.2/150 mM NaCl pH 7.5/0.05% Tween-20. After a final rinse in PBS, the slides were counterstained with DAPI and were mounted in PPD at the appropriate pH. Automatic metaphase capture with telomere and centromere staining was performed.

5. Digitization of Slides and Metaphase acquisition:

Images of an average of 100 metaphases were captured using the Automated Acquisition Module Autocapt software and a ZEISS Plan-Apochromat 63x/1.40 oil and camera CoolCube 1 high-resolution digital CCD with constant settings for exposure and gain. . Automatic scoring of these aberrations was performed using ChromoScore software and an operator was validated and was excluded false aberrations (Figure 1-A).

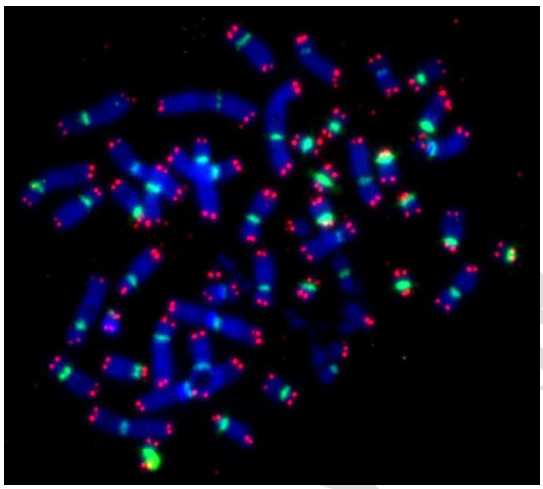

Figure 1-A: Image Capture of 100 Metaphases.

6. Scoring of Chromosomal and Telomeric aberrations:

Two slides per sample were used to analyzing unstable chromosomal aberrations after telomere and centromere staining. Only metaphases at 46 centromeres were analyzed. Chromosomal aberrations were scored based on the presence or absence of telomere and centromere sequences. We were detected dicentrics, centered and acentric rings, as well as four-telomere fragments, resulting from a fusion event usually accompanied by the formation of a dicentric chromosome or a ring center.

We were also detected two-telomere fragments, representing terminal deletions, as well as acentric fragments without telomeres, representing interstitial deletions (Figure 1). Telomere deletions have also been detected. The combined information was noted by telomere and centromere staining was allowed us to accurately calculate the number of unrepaired or poorly repaired double-strand breaks that generated the chromosomal aberrations: dicentric chromosomes and centered rings with a fragment containing four telomeres were considered two DSBs. Excess acentric fragments were considered to result from one DSB for terminal deletions with only two telomeres and two DSBs for interstitial deletion fragments with no telomere sequences. Telomere deletion has been defined as the loss of two telomere signals

on the same arm, an aberration thought to represent double-strand breaks, leading to activation of DNA repair mechanisms. Telomere deletion has been considered to be the result of DSB. Telomere aberrations were assessed using the following criteria: (i) telomere loss was defined as a signalless end at a single chromatid, an aberration that results in telomere-end-fusion and rupture-fusion-bridge cycles; (ii) telomere doublets or telomere fragility was defined as more of a single arm telomere signal, an aberration signaling inadequate telomere replication and shelterin protein dysfunction.

7. Statistical analysis:

A script in R® has been developed according to the recommendations of the IAEA. Data were analyzed using the Wilcoxon-Mann-Whitney rank sum test or the nonparametric Kruskal-Wallis test. The null hypothesis was one that considered the subgroups to be identical populations. A value of $p < 0.05$ was considered statistically significant, rejecting the null hypothesis.

RESULTS AND DISCUSSION

1- Frequency of unstable chromosomal aberrations after CT exposure:

Unstable chromosomal aberrations have been noted in circulating lymphocytes of non-cancer patients before and 24 hours after computed tomography examinations. Analysis of unstable chromosomal aberrations was also performed in circulating lymphocytes from healthy donors of similar age and ethnicity. The results were obtained for chromosomal aberrations before and after CT scans in patients and in the control group show that some of the typical aberrations founded in circulating lymphocytes have been shown in Figure 2. No dicentric chromosomes were observed in lymphocytes blood circulation of patients before the CT scan as well as in the control group.

After computed tomography, a significant is increased in the dicentric chromosome rate was observed, but this increase was significant. Interestingly, some radial formations were observed after CT scan in B cells. The frequency was significantly higher after CT compared to that observed before. However, the main chromosomal aberrations noted after CT scan were chromosomal acentricity and chromosomal deletion (Figure 2)

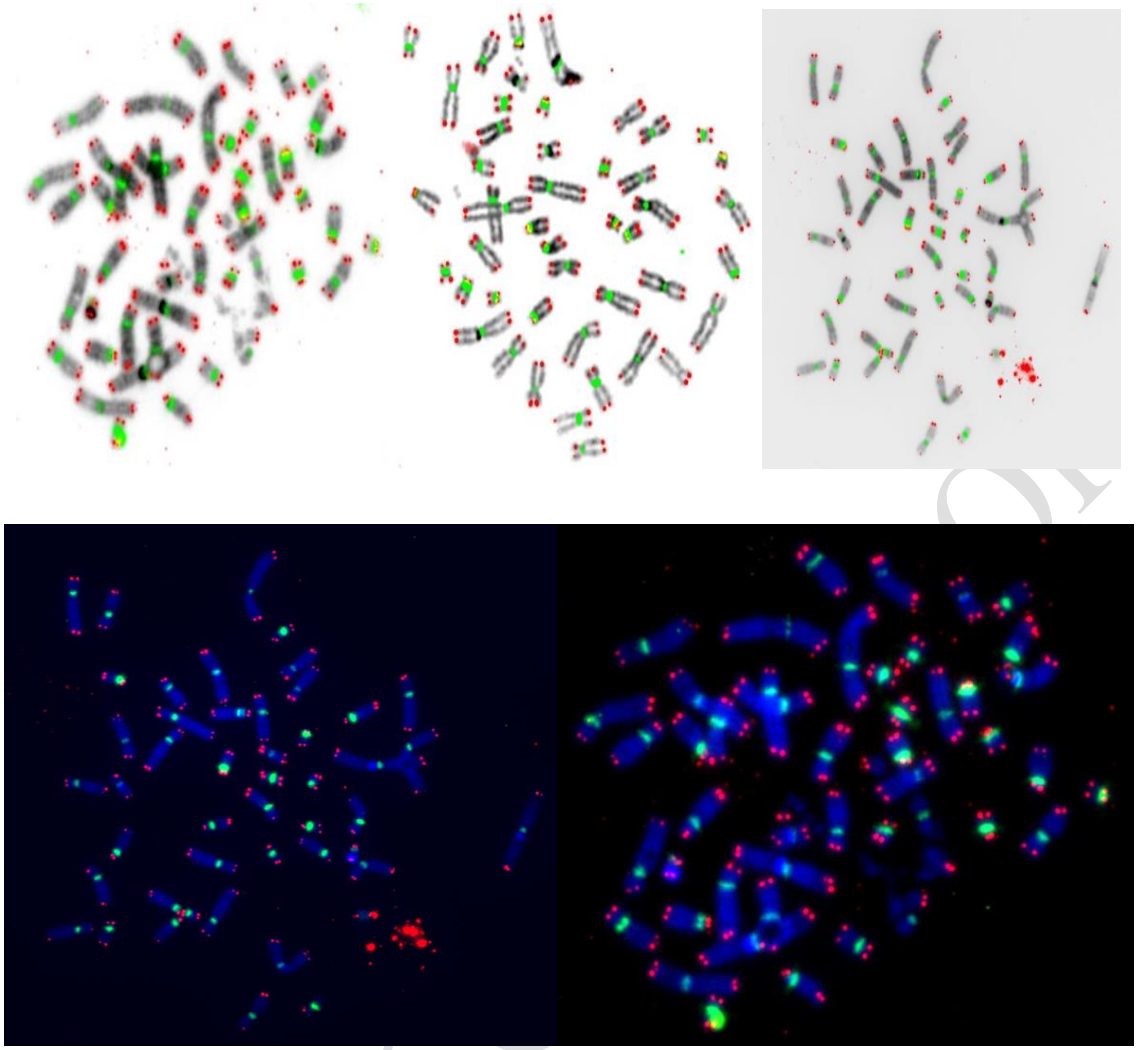

Figure 2: Image captures of chromosomal Acentricity and Chromosomal deletion.

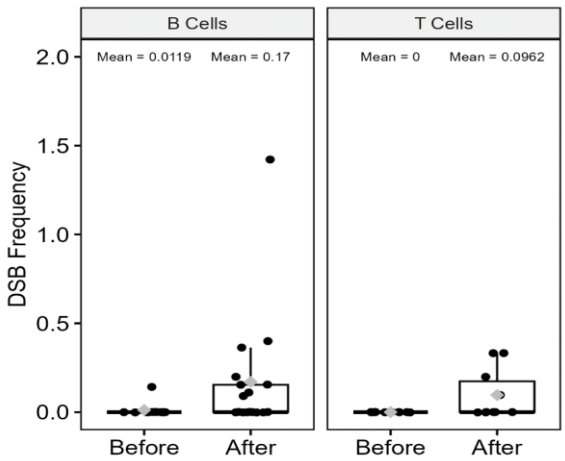

Figure 3: The frequency of total DSBs before and after CT in B and T lymphocytes.

Taking into account all the chromosomal aberrations were induced for the calculation of DSBs, the frequency of total DSBs after CT scan is increased significantly, compared to that

estimated before CT scan in B and T lymphocytes (respectively p<2.2 10-16 and p< 2.0210-8) (Figure 3). The frequency of chromosomal aberrations were induced after CT sacn in B lymphocytes was significantly higher than that was served in T lymphocytes.

2- **Frequency of telomere aberrations after CT exposure:**

Telomere structural aberrations is abolished the presence of a functional telomere leading to chromosomal instability. In this study, we were analyzed telomere loss and telomere doublet formation before and after CT exposure. Note that telomere deletion was considered DSB and their frequency has been introduced into the estimation of total DBS. After CT scan, the rate of telomere loss was significantly higher in B and T cells were compared to their rate before CT scan exposure (Figure 4).

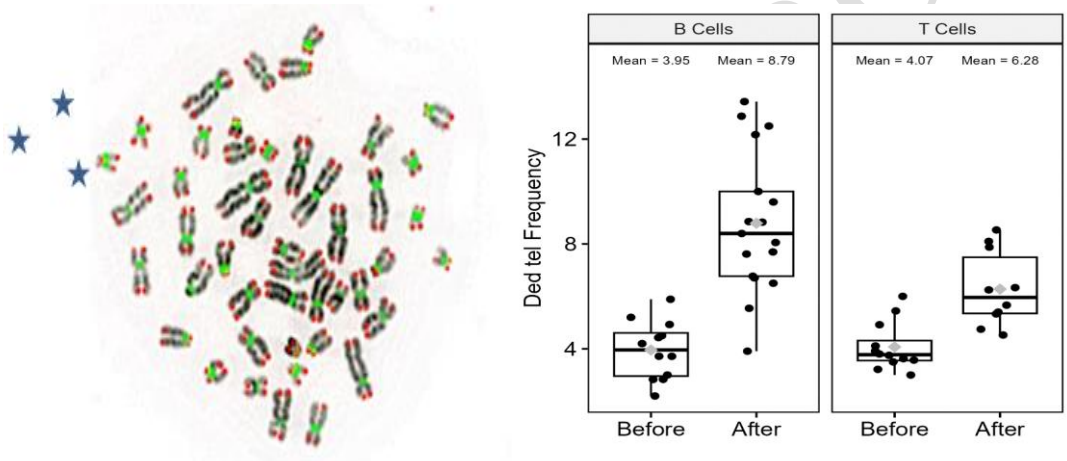

Figure 4: Frequency of telomere aberrations after CT exposure.

Similar results were obtained for telomere doublet formation after CT scan was compared to that seen before CT exposure (Figure 5).

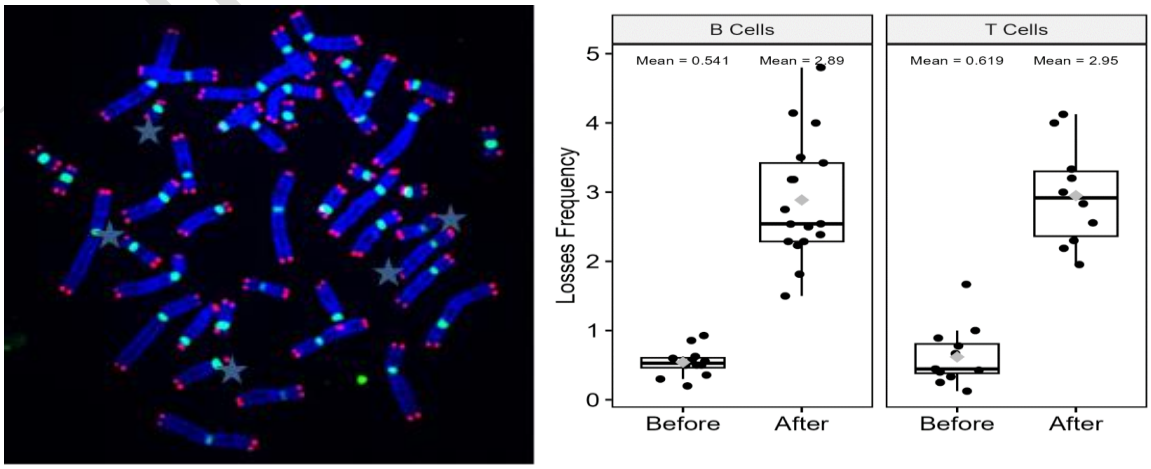

Figure 5: Formation of telomere doublets after computed tomography.

It should be noted that the telomere doublet rate in B cells was significantly higher than the rate observed in T cells (p<10-3).

3- Confounding factors in the formation of chromosomal aberrations after CT:

Many confounding factors were tested such as age, gender, dose delivered and changes in hematological parameters. Telomere dysfunction is one of the hallmarks of aging and is used as a biomarker in the prognosis of several age-related chronic diseases. The intimate is linked between telomere length and male and female infertility has been previously reported. Telomere length has been proposed as a new and important biomarker to elucidate the formation of chromosomal and telomeric aberrations in patients after CT examinations in Congo-Brazzaville. Indeed, chromosomal and telomeric aberrations were realized after staining by fluorescence hybridization of telomeres and centromeres. Thus, the frequency of these aberrations were compared to the effective radiation dose was calculated using a computational dosimetry system and a dose-length product in a scanner. This first was deduced a significant was increased in DSB resulting from all chromosomal aberrations after CT exposure. Then, the results of the analyzes was also showed a significant was increased in telomere aberrations after the exposure to the scanner. However, no correlation has been inferred between the effective radiation dose and the frequency of chromosomal and telomeric aberrations.

It is urgent to be noted that the increase in chromosomal and telomeric aberrations were depended on age. Here, we were demonstrated, for the first time, the presence of telomere aberrations after CT exposure, in addition to telomere shortening, in patients and that telomere were lossed and/or the short telomere ratio is less of a diagnostic tool for identifying damaged cells than conventional measurements of telomere length. This loss of telomere functionality is played a major role in the continuation of chromosomal instability. Considering all the chromosomal aberrations were induced for the calculation of DSBs, the frequency of total DSBs after CT scan is increased significantly compared to that estimated before CT scan in B and T lymphocytes (respectively p<2.2 10-16 and p<2, 0210-8). What explains telomere dysfunction can be affected B and T cells and be compromised chromosome pairing, causing recombination defects. These events will be eventually leaden to very low frequencies of unstable chromosomal aberrations. As a logical next step, we were used circulating lymphocytes to study telomere shortening and aberrations in patients as part of the analysis of chromosomal aberrations, a standard test was used in the medical care of

these patients. The primary outcome of this study was the identification of increased telomere aberrations. However, studies of telomere dysfunction in these patients are limited. Quantification of telomere length from a control cohort, with ages ranging from 17 to 52 years, is showed that telomere length is age-dependent and decreased at a rate of 79 bp / year. This rate of telomere loss, linked to natural aging, is consistent with previous reports. telomere length which is varied between individuals (Gilson *et al.,* 2007; Hernandez *et al.,* 2015), is depended on the different cell types in a single individual, but also on the arms of chromosomes in a single is given cell (Pommier *et al.,* 2002) naturally decreases continuously with each cycle of cell replication (Harley *et al.,* 1990). This telomere shortening can be accelerated either by exposure to ionizing radiation or by an increase in cell proliferation with the aim of replacing dead cells after exposure, or by radiation-induced telomeric damage preventing thus maintenance of telomeres. Was accelerated telomere shortening will be prolonged by continued exposure to other endogenous and exogenous DNA-damaging agents over the life of the cell (d'Adda di Fagagna *et al.,* 2003; Jackson and Bartek *et al.,* 2009 ; Lin *et al.,* 2012; Price *et al.,* 2013). Considering that heterogeneity in telomere length on each arm of individual chromosomes are maintained during telomere shortening at each cell cycle, the shorter telomeres will be eventually become critical and dysfunctional. In normal cells with intact cell cycle checkpoints, these dysfunctional or unprotected telomeres are detected as DNA damage; DNA damage response mechanisms are activated thus forming TIFs (Takai *et al.*, 2003).

A major study was suggested that normal human cells are able to tolerate a small number of dysfunctional telomeres and continue to proliferate until a threshold of five TIFs per cell was reached. In normal cells with intact cell cycle checkpoints, senescence or apoptosis was triggered when this threshold of five dysfunctional telomeres is reached. In immortalized cells, which are incapable of senescence due to loss of cell cycle checkpoint proteins (such as p53 or p16), senescence is temporarily bypassed, and cells continue to proliferate while accumulating chromosomal instabilities. , FITs, and telomeric shortening, until a “telomeric crisis” is reached. In cells undergoing this crisis, more than five dysfunctional telomeres were found (Kaul *et al.,* 2012), with massive chromosome fusion and cell death (Counter *et al.,* 1992 ; Counter *et al.,* 1994 ;Ducray *et al.,* 1999), probably due to extreme telomere shortening and loss of shelterin proteins. We are deduced that this cell death due to “too much” genomic instability stops the process of carcinogenesis, but is responsible for the increased risk of cell death-related diseases. Exposure to ionizing radiation also induces a

variety of other DNA and cellular damage, most notably double-strand breaks and mitochondrial dysfunction. Double-strand is broken in DNA can be leaden to the formation of chromosomal aberrations. Stress signals can be transmitted to progeny of irradiated cells, but also to non-irradiated bystander cells and their progeny, leading to continued oxidative stress, prolonged cell injury, and propagation of genomic instability; telomeres themselves may play a role in the long-term transmission of chromosomal instability (Shim *et al.*, 2014). As presented in this thesis, there are inter-individual variations in radiosensitivity, measured in terms of radiation-induced double-strand breaks, which may be related to age, sex, and intrinsic telomere lengths and their radiological changes. In addition, radio-induced mitochondrial dysfunction produced by an excess of reactive oxygen species can be caused further damage to the genome. This mitochondrial dysfunction can be also spread into bystander cells and their progeny, leading to be prolonged oxidative stress producing more DNA damage long after exposure. Prolonged oxidative stress can be therefore exacerbate genomic instability (Azzam *et al.*, 2012 ; Shim *et al.*, 2014; Morgan and Sowa *et al.*, 2015). All of these factors can also be related to telomeres, as their dysfunctions can be caused and propagated genetic instability and lossed of heterozygosity. Thus, telomeres can be considered as key players in the process of radiation-induced diseases. Several characteristics of telomeres and the mechanisms of their maintenance make telomeres a promising candidate as a predictive biomarker (Shim *et al.*, 2014).

In agreement with the article (Shim *et al.*, 2014), a recent article (Mirjolet *et al.*, 2015) highlights the potential of telomeres and their maintenance as key players in the prediction of individual radiosensitivity which can be applied to personalize radiotherapy protocols. Key points supporting telomeres as a predictive biomarker of individual radiosensitivity are summarized here:

- The length of telomeres varies between individuals and within the same individual, including within a given cell. The length of telomeres in somatic proliferative tissues naturally decreases during each cycle of cell replication, and therefore with age. Natural telomere shortening can be accelerated by endogenous factors and by external environmental and lifestyle stressors that cause DNA double-strand breaks or poor telomere replication. Telomere length can be therefore being considered as a prognostic marker taking into account a set of all past events.
- Reduced telomere length reflects the accumulation of previous insults from various damaging conditions and has been associated with many chronic diseases that are

generally considered diseases of aging, such as diabetes, cancer, and the diseases heart disease (M'Kacher *et al.*, 2015). (Armanios *et al.*, 2012; Holohan *et al.*, 2014). Telomerase is up-regulated in approximately 85% of human cancers, suggesting its important role in the process of cell immortalization and tumorigenesis. This shows that telomeres and their maintenance mechanisms play important roles at different stages in the initiation and development of cancer and other human pathologies.

- Telomeric regions are particularly sensitived to radiation-induced oxidative stress and are more prone to DNA double-strand breaks, perhaps due to their inappropriate treatment: the presence of damage to DNA in telomere sequences interferes with telomere replication, leading to telomere shortening or loss. Impaired repair of DNA double-strand breaks near telomeres has been suggested to play a role in the chromosomal instability associated with human cancers. This is made telomeres more sensitive to exposure to ionizing radiation than the rest of the genome, and therefore to radiotherapy.
- There is a bidirectional and co-dependent relationship between telomeres and DNA damage repair mechanisms. As dysfunctional telomeres are recognized as double-strand breaks and trigger DNA damage repair pathways, proteins of which are also involved in the maintenance and protection of telomeres. As DNA damage repair processes are also closely related to radiosensitivity, telomere maintenance could also likely be closely related to radiosensitivity.

All this evidence indicates that telomeres and their maintenance could be sensitived and reliabled biomarkers of exposure to ionizing radiation, and could be a new parameter to be predicted individual radiosensitivity (Shim *et al.*, 2014; Mirjolet *et al.*, 2015). As we were found that radiosensitivity could indeed be predicted by a combination of age and gender, as well as the combination of intrinsic telomere length and their radiation-induced is changed with TC-FISH analysis. In view of all the above, it would be important for these factors to be able to be adapted in order to establish a clinical method for the identification of radiosensitive persons. The ability to reliably predict individual radiosensitivity would be allowed the refinement of radiation protection protocols to identify and protect highly radiosensitive individuals in particular. Although the analysis of telomeres and their length, using TC-FISH may be too complex to be used as a biomarker to provide dose estimates for use in biodosimetry, prior knowledge of an individual's radiosensitivity could be aid in medical triage appropriate for these individuals. TC-FISH analysis of telomeres and their length to be predicted individual radiosensitivity could, however, be used ful in the context of

radiotherapy. Nevertheless, there are remained the question of how to effectively measure and runk individuals according to their radiosensitivity. at the point of 4 hours post-irradiation allows the creation of these sorting categories independently of individual radiosensitivity it is allowed to overcome the question of classifying individuals according to their radiosensitivity. Although this method is fast and capable of high-throughput analysis, this analysis is hampered by the time-sensitive nature of the γH2AX measurement. In the context of radiotherapy, as pointed out (Mirjolet *et al.*, 2015), the ability to be reliably predicted individual radiosensitivity could be allowed the personalization of treatment. Furthermore, since radiosensitivity has been associated with telomere length and telomerase activity, the management of telomere lengths and telomerase could be used ful in radiotherapy. In general, shorter telomere lengths have been linked to increasing radiosensitivity in several in vivo and in vitro studies in mice and telomerase-deficient human cells. Downregulation or inhibition of telomerase has been shown to compromise cancer cell viability while minimizing the effect on normal cells; thus, the use of telomerase inhibitors during chemotherapy or radiotherapy can be made cancer cells more sensitive to treatments. On the other hand, radioresistant cancer cells show upregulation of telomerase activity and longer telomeres (Genesca *et al.*, 2006; Ayouaz *et al.*, 2008; Shim *et al.*, 2014). In the context of personalized radiotherapy treatments was based on individual radiosensitivity, the authors Mirjolet et al are proposed that the lengths of telomeres and shelterin is proteined in cancer cells and in normal cells can be used.

Telomere length can be used to adjust doses per fraction, which would be improved the efficacy and safety of radiotherapy using pharmacological treatments that interfere with telomere biology in tumor cells (Mirjolet *et al.*, 2015).

CONCLUSION

During this study, we were recorded on the one hand, the loss of telomeres, was defined as an end without signal at the level of a single chromatid then an aberration resulting in telomere-end-fusion and rupture-fusion-bridge cycles. On the other hand, it has been found the occurrence of telomere doublets or telomere fragility has been defined as more of a single arm telomere signal, an aberration signaling inadequate telomere replication and protein dysfunction. shelterins Indeed, telomeres, long was considered the guardians of the genome, can be indicated the general state of health of an individual, as they can be represent all exposures to various DNA-damaging agents, including ionizing radiation of a lifetime.

Telomeres and the mechanisms for their maintenance could be therefore have been important implications for long-term human health. As human beings are constantly exposed to ionizing radiation via natural and artificial sources, it is important to be determined if and how is telomeres played a role in the mechanisms of direct and indirect radiation-induced biological effects, as well as their role in the transmission of these radiation-induced effects during cell proliferation. These roles are perhaps critical for determining long-term radiation-induced effects on human health, and may be contributed to a better understanding of radiation-induced cancers associated with other human pathologies. Scientific studies have been found that a diet high in whole grains, vegetables, fruits, seaweed, seafood, dairy products and coffee is positively associated with good telomere length in white blood cells. This should be then being recommended to patients.

Competing interests

The authors declare that they have no competing interests.

Authors' contributions

All the authors' participle in writing, giving feedback on this manuscript, have read and approved the final manuscript.

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