DNA damage-induced cellular senescence is sufficient to suppress tumorigenesis: a mouse model

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Tumor suppressor p53–dependent apoptosis is critical in suppressing tumorigenesis. Previously, we reported that DNA double-strand breaks (DSBs) at the V(D)J recombination loci induced genomic instability in the developing lymphocytes of nonhomologous end-joining (NHEJ)–deficient, p53–deficient mice, which led to rapid lymphomagenesis. To test the ability of p53–dependent cell cycle arrest to suppress tumorigenesis in the absence of apoptosis in vivo, we crossed NHEJ–deficient mice into a mutant p53R172P background; these mice have defects in apoptosis induction, but not cell cycle arrest. These double-mutant mice survived longer than NHEJ/p53 double-null mice and, remarkably, were completely tumor free. We detected accumulation of aberrant V(D)J recombination–related DSBs at the T cell receptor (TCR) locus, and high expression levels of both mutant p53 and cell cycle checkpoint protein p21, but not the apoptotic protein p53–upregulated modulator of apoptosis. In addition, a substantial number of senescent cells were observed among both thymocytes and bone marrow cells. Cytogenetic studies revealed euploidy and limited chromosomal breaks in these lymphoid cells. The results indicate that precursor lymphocytes, which normally possess a high proliferation potential, are able to withdraw from the cell cycle and undergo senescence in response to the persistence of DSBs in a p53–p21–dependent pathway; this is sufficient to inhibit oncogenic chromosomal abnormality and suppress tumorigenesis.

The tumor suppressor p53 is one of the most extensively studied proteins (1, 2). At the cellular level, p53 acts as a “gatekeeper” to eliminate potentially tumorigenic cells by inducing programmed cell death, inhibiting the proliferation of damaged cells through cell cycle arrest (3), or inducing cells to withdraw from the cell cycle, referred to as cellular senescence (4, 5). The ability of p53 to induce apoptosis is considered the primary means by which p53 suppresses tumor growth (6–9). However, experiments have shown that p53 deficiency does not necessarily translate into an interruption in the apoptotic response (10, 11). We hypothesize that the ability of p53 to induce cell cycle arrest or senescence, in some cases, could play a central role in tumor suppression.

At the molecular level, activated p53 functions as a transcription factor by transactivating genes that are important for inducing apoptosis or cell cycle arrest and senescence (12, 13). Therefore, gene expression profiles can be used as markers of apoptosis or senescence. The levels of proapoptotic proteins, such as p53–upregulated modulator of apoptosis (PUMA), are elevated in cells programmed to undergo apoptosis (14, 15), whereas the cyclin–dependent kinase (CDK) inhibitor p21, a well-studied downstream target of p53, is highly expressed in cells undergoing cell cycle arrest and senescence. p21 directly inhibits CDK2 and plays a pivotal role in p53–induced cell cycle arrest (16). It is also an important molecule in one of the mechanisms leading to senescence (17).

The term senescence refers to the finite replicative lifespan of cultured human cells that enter a stable growth-arrested state (18). Currently, senescence is recognized as the final phenotypic state adopted by a cell in response to various stimuli. Senescent cells show a characteristic flattened and enlarged morphology and...
are positive for acidic β-galactosidase (β-gal) activity (19). Senescent cells also undergo dramatic chromatin remodeling and express proteins that are characteristic of transcriptionally silent heterochromatin. An example of these proteins is the heterochromatin protein 1 (HP1) family member HP1γ, which has been established as a marker for senescence-associated heterochromatin foci (SAHF) (20) in human (21) and murine cells (22). Numerous studies suggest that a major cause of senescence in human cells is telomeric shortening (23), which triggers cellular responses that are identical in many aspects to a DNA damage response (24, 25). Additionally, DNA damage could be considered an extrinsic factor contributing to cellular senescence. Because of its essential property of cell growth arrest, senescence is proposed as a potent tumor suppressor mechanism (26).

DNA damage occurs in the developing lymphocytes when these cells begin to rearrange antigen receptor genes in a process termed V(D)J recombination. This genetically programmed DNA rearrangement process involves the cleavage of DNA double-strands at the recombination signal sequences by the Rag nucleases, which generate two kinds of DNA breaks—signal ends and coding ends (27). Signal ends are blunt and 5′–phosphorylated, whereas coding ends are covalently sealed to form a hairpin structure requiring further processing by the DNA-dependent protein kinase (DNA–PK) and the repair factor Artemis complex before ligation (28). Both signal and coding ends are joined by the nonhomologous end-joining (NHEJ), which is a major DNA repair pathway that is generally responsible for the repair of DNA double-strand breaks (DSBs). The participating factors in this pathway are the DNA–PK complex, which includes the DNA-binding subunits Ku70 and Ku80 and the catalytic subunit of DNA–PK, the repair factor Artemis, and the DNA ligase complex, which is composed of DNA ligase IV, XRCC4, and XLF/Cernunnos (29, 30). All of the NHEJ factors are essential for V(D)J recombination; a severe combined immunodeficient phenotype results from impaired V(D)J recombination in mice deficient in each of the joining factors (31, 32).

In NHEJ-deficient mice, Rag-mediated DNA breaks accumulate because the breaks cannot be joined by other nonspecific end-joining activity. However, the stalled V(D)J recombination breaks induce a p53-dependent apoptosis in developing lymphoid cells. Therefore, NHEJ-deficient mice do not usually develop early lymphomas. In contrast, Rag-mediated DSBs lead to massive genomic instability in the absence of both p53 and NHEJ activity, including chromosomal translocations and oncogenic gene amplifications (33, 34). As a result, double-null mice succumb to early pro-B lymphomas with chromosomal translocation at chromosome 12 at the immunoglobulin locus and chromosome 15 near the protooncogene c-Myc. The involvement of Rag nucleases in tumorigenesis has been confirmed by the lack of lymphoma development in Rag, NHEJ, and p53 triple-deficient mice (35, 36).

A unique p53 mutation, p53R172P (the human equivalent of murine R172P), which was originally identified from human tumor samples (37, 38), provides an excellent model to study the role of p53-dependent cell cycle arrest and senescence in tumor suppression. Although p53R172P lacks the ability to induce apoptosis in response to various stimuli, it retains its partial ability to induce cell cycle arrest through its ability to transactivate key molecules such as the CDK inhibitor p21 (10, 37). In this study, we crossed NHEJ-deficient mice into a p53R172P mutant background to establish an in vivo model to examine the involvement of the p53–p21 pathway in the induction of cell cycle arrest and senescence in response to DNA damage and the consequent suppression of genomic instability and tumorigenesis.

RESULTS

Mutant p53R172P rescues embryonic lethality caused by DNA ligase IV deficiency and suppresses tumorigenesis

To determine whether the p53R172P mutant was sufficient to suppress tumorigenesis, we crossed heterozygous DNA ligase IV–deficient mice (Lig4+/−) with p53R172P/R172P mice (p53R172P/p53R172P) to generate Lig4+/−/p53R172P/p53R172P mice. These animals were subsequently interbred to generate Lig4+/−/p53R172P/p53R172P mice, which were viable and fertile. Next, Lig4+/−/p53R172P/p53R172P mice were generated from crossing Lig4+/−/p53R172P/p53R172P mice. 24% (67 out of 279) of pups from the Lig4+/−/p53R172P mice breeding were genotyped as Lig4+/−/p53R172P (Table S1, available at http://www.jem.org/cgi/content/full/jem.20062453/DC1). This number was very close to the expected Mendelian segregation ratio. This indicates that the mutant p53R172P successfully rescued the embryonic lethality caused by the DNA ligase IV deficiency, and the embryonic lethality of Lig4+/− was caused by p53-dependent apoptosis (39, 40). Similar to Lig4+/−/p53−/− mice (Fig. S1), Lig4+/−/p53−/− mice were smaller than their Lig4+/−/p53−/− littermates (Fig. 1 A). 6 out of 25 Lig4+/−/p53R172P/p53R172P mice died shortly after weaning. These mice had difficulty ingesting solid food, and the necropsy of a 4-wk-old Lig4+/−/p53R172P/p53R172P mouse revealed the cause of death was starvation and not tumor-related (unpublished data).

Figure 1. Phenotype, survival curve, and lymphoma incidence. (A) Lig4+/−/p53R172P (top) and Lig4+/−/p53−/− (bottom) mice. (B) Survival curve of Lig4+/−/p53R172P mice (black) and Lig4+/−/p53−/− mice (red). Lig4+/−/p53R172P survival is significantly different from Lig4+/−/p53−/− mice (P = 0.0000204 by log rank test). (C) Lymphoma incidence in Lig4+/−/p53R172P and Lig4+/−/p53−/− mice.
After the malnourishment problem was corrected by simply providing soft food, all Lig4−/− p53+/p mice survived far beyond the weaning age and significantly longer than the Lig4−/− p53−/− mice (Fig. 1 B; P < 0.001, log rank test). The median survival age of Lig4−/− p53+/p mice was ~120 d, compared with 65 d for the Lig4−/− p53−/− mice. Of particular note, 2 of the mice survived beyond 6 mo of age (Fig. 1 B), which was never observed in Lig4−/− p53−/− mice. Remarkably, Lig4−/− p53+/p mice were free of lymphomas and any other types of tumor, whereas 14 out of 15 Lig4−/− p53−/− mice died of pro-B lymphomas (Fig. 1, B and C; one Lig4−/− p53−/− mouse died around the weaning age with enlarged incisor teeth). These results clearly demonstrated that the p53R172P mutation successfully rescued the embryonic lethality of Lig4-deficient mice and suppressed the development of lymphomas in Lig4−/− p53+/p mice.

In the absence of apoptosis, Lig4−/− p53+/p precursor lymphocytes enter senescence

To confirm the defective apoptosis in p53R172P mice, we performed a TUNEL assay and a hematoxylin and eosin (HE) staining of thymic sections from Lig4−/− p53+/p, Lig4−/− p53−/−, and NHEJ-deficient mice (Artemis−/−). As predicted, apoptosis was not observed in thymic sections from Lig4−/− p53−/− or Lig4−/− p53+/p mice, whereas apoptosis was readily detected in thymic sections from Artemis−/− mice (Fig. S2, available online).

Figure 2. Developing lymphoid cells undergo senescence. β-gal staining for thymic sections (A) and bone marrow cells (B) of Lig4−/− p53+/p, Lig4−/− p53−/−, and Lig4+/+ p53+/p mice showing positive staining only in Lig4−/− p53+/p mice. Anti-HP1γ staining of thymic sections (C) and bone marrow cells (D) of Lig4−/− p53+/p, Lig4−/− p53−/−, and Lig4+/+ p53+/p mice; positive staining was observed only in Lig4−/− p53+/p mice. (E) Bone marrow cells from Lig4−/− p53+/p mice, positive for β-gal staining, were costained with the B cell marker CD19 (dark brown cells); arrows show double-positive cells and an example of bone marrow cells from Lig4−/− p53+/p mice that are positively stained for CD19 and HP1γ (F), showing single channel of green fluorescence (HP1), red (CD19) and blue (DAPI), and merged image; (G) thymocytes staining positive for HP1γ (green), CD25 (red), and DAPI (blue). Images with wider views of both stainings are shown in Figs. S5 and S6, available at http://www.jem.org/cgi/content/full/jem.20062453/DC1.
at http://www.jem.org/cgi/content/full/jem.20062453/DC1. These results confirmed that Rag-mediated DNA DSBs induce a p53-dependent apoptosis in NHEJ-deficient mice, but is completely absent in the p53R172P mutant background. HE staining of thymic sections from Lig4−/− p53+/p mice showed decreased cellular density compared with wild-type (WT) and Lig4−/− p53−/− mice (Fig. S3), but the density was similar to that of Artemis−/− mice. In addition, the cellularity of thymus from a 4-wk-old Lig4−/− p53+/p mouse is only 1.3 million cells, compared with 202 million cells from a Lig4+/+ p53+/p littermate. Analysis by flow cytometry indicated a severe developmental blockage in both thymocytes and bone marrow cells at early stages (Fig. S4). This confirms that the mutant p53R172P is not capable of rescuing V(D)J recombination, but is able to inhibit tumorigenesis in developing lymphoid cells, possibly by responding to the V(D)J recombination-associated breaks and inhibiting genomic instability.

Given that cellular senescence is proposed to be an anticancer mechanism (4), we thought the Lig4−/− p53+/p mice served as an excellent in vivo model for investigating this potential antitumor activity. To determine whether the mutant p53R172P protein was able to induce senescence in response to Rag-mediated DNA breaks, lymphoid cells from Lig4−/− p53+/p mice were examined using the senescence-associated β-gal assay. β-gal staining of thymic sections revealed a large number of Lig4−/− p53+/p thymocytes had entered a senescent state, whereas no β-gal–positive thymocytes were observed in Lig4+/+ p53+/p littermates or age-matched Lig4−/− p53−/− mice (Fig. 2 A). Because Lig4−/− p53−/− mice succumb to pro-B lymphomas at an early age (35), we examined the extent to which cellular senescence occurs in developing B lymphocytes. Bone marrow cells were isolated and stained for β-gal activity. As shown in Fig. 2 B, bone marrow cells from Lig4−/− p53+/p, but not cells from Lig4+/+ p53+/p littermates or age-matched Lig4−/− p53+/p mice, were stained positive for β-gal. Furthermore, similar results were obtained when thymic sections (Fig. 2 C) and bone marrow cells (Fig. 2 D) were stained with HP1γ, which is a different marker for senescence. To verify that these β-gal–positive bone marrow cells were precursor B cells, the cells were also stained with the anti-CD19 surface marker. The results revealed that most of the β-gal–positive cells were, indeed, CD19 positive (Fig. 2 E), thereby confirming their B cell lineage. Similarly, HP1γ-positive cells in the bone marrow and thymus of Lig4−/− p53+/p were also stained positive for the surface markers CD19 and CD25, respectively (Fig. 2 F and G; and Figs. S5 and S6, available at http://www.jem.org/cgi/content/full/jem.20062453/DC1) and HP1γ staining was not detected in Lig4−/− p53−/− thymocytes (Fig. S5). These results indicate that both Lig4−/− p53+/p T and B precursor lymphoid cells undergo senescence in a p53-dependent pathway. This strongly suggests that un-repaired Rag-mediated DSBs are able to activate p53R172P and that its residual activity is sufficient to induce senescence, which successfully blocks tumorigenesis in the lymphoid precursor cells.

Accumulation of aberrant V(D)J recombination breaks in Lig4−/− p53+/p thymocytes

Cleavage of DNA by the Rag nucleases generates blunt signal ends and hairpin coding ends. Signal ends are protected in the postcleavage complex and are persistent in WT lymphoid precursor cells (41), whereas hairpin coding ends are usually resolved. As a result, coding ends never accumulate in WT mice. However, hairpin coding ends were previously detected in the thymocytes of DNA–PKcs–deficient, Artemis-deficient, and Ku80-deficient mice (42–44) because of a defect in processing and opening the hairpins. Because DNA ligase IV functions in the last step of V(D)J recombination and the DNA–PKcs–Artemis complex (45, 46), which is the same methodology used in this study. Our LMPCR assay revealed that signal ends were clearly present at the TCR D62 site in WT and Lig4−/− p53+/p samples (Fig. 3, A and B). ApaLI digestion cut the perfect signal ends and reduced the fragment size from 123 bp to 98 bp (Fig. 3 B, left). However, in Lig4−/− p53+/p, but not in WT thymocytes, DNA breaks in addition to the signal ends were clearly detected. These were potential coding ends. This was further demonstrated by the increased intensity of bands in those DNA samples treated with DNA polymerase or mung bean nuclease. Because LMPCR assays can only detect DNA breaks with open blunt termini, treatment with DNA polymerase

Figure 3. Accumulation of open coding ends in Lig4−/− p53+/p thymocytes. (A) Diagram of VDJ recombination activity at the TCRδ locus. Cleavage by Rag nucleases generates a blunt signal end (se) and hairpin coding end (ice), which can be further processed by the DNA–PK–Artemis complex. (B) LMPCR assay of WT and Lig4−/− p53+/p (LP) thymocytes. Signal ends can be digested by ApaLI to reduce the PCR products from 123 to 98 bp. The residual species are coding ends, which was confirmed by cloning and sequencing (Fig. S6). MBN, mung bean nuclease; T4 Pol, T4 DNA polymerase. Fig. S6 is available at http://www.jem.org/cgi/content/full/jem.20062453/DC1.
(which does not open hairpin coding ends) converts those ends with single-strand overhangs to blunt ends. On the other hand, mung bean nuclease opens the hairpin ends, thus allowing the detection of these sealed ends. Our results revealed that both treatments enhanced the extent to which potential coding ends were detected, suggesting the presence of coding ends with a single-strand overhang and hairpin ends. This is the first report of the direct detection of processed (open) coding ends in the mouse, mechanistically implicating a stepwise processing of hairpin coding ends by the DNA–PKcs–Artemis complex.

To confirm that these ends were coding ends, we cloned and sequenced the PCR products that were resistant to ApaLI digestion. Three individual PCR products of the DNA polymerase- treated samples were performed, and the products were cloned into Escherichia coli and screened for ApaLI-resistant colonies. Sequencing analyses revealed that these were indeed coding ends. We found perfect coding ends containing the entire Dβ2 coding sequences, as well as coding ends with 3–6 nucleotide deletions (Fig. S7, available at http://www.jem.org/cgi/content/full/jem.20062453/DC1). Our results indicate that in Lig4 deficiency, Rag–liberated coding ends cannot be joined, but they can still be processed by the DNA–PK and Artemis complex. However, whereas aberrant ends normally induce a p53-dependent DNA damage response that leads to apoptosis, these ends instead induce mutant p53 response in Lig4−/− p53−/− mice that drives cells with these aberrant ends to undergo cell cycle arrest and become senescent.

Euploid profile of Lig4−/− p53−/− cells with limited chromosomal breaks

Our previous study conducted in NHEJ/p53−/− mice indicated that Rag–mediated DSBs formed during V(D)J recombination and, if not properly controlled during the cell cycle, lead to genomic instability and tumorigenesis (35). Because Lig4−/− p53−/− mice do not succumb to lymphomas, we compared the extent of genomic instability in precursor lymphoid cells from these two genotypic backgrounds. To ensure a fair comparison, liver cells from newborn mice of both genotypes before the onset of tumors were examined. 50 metaphases were analyzed in cells of each genotype; typically metaphase spreads with telomeric probes are shown in Fig. 4 (A and B). Each chromosomal spread was examined using confocal microscopy to identify telomeric signals. A chromosomal arm without a telomeric signal was scored as a chromatid break (47). Most of the Lig4−/− p53−/− metaphases contained one or two chromatid breaks, and the majority of metaphases were euploid (46 out of 50 metaphases had the normal 40 chromosomes). In contrast, Lig4−/− p53−/− metaphase spreads predominantly had one or two chromosomal breaks, and only 7 out of 50 metaphases (14%) had a normal number of chromosomes (Fig. 4, C and D). These results suggest that aberrant V(D)J recombination breaks result in chromatid breaks in cells of each genotype. However, the effects of these breaks differ between the two different genotypes; in the absence of the tumor suppressor p53, these breaks lead to genomic instability and the activation of oncogenes, possibly via abnormal chromosomal replication related to aneuploidy. In contrast, the mutant p53R172P induces cell cycle arrest and senescence, which is sufficient to block genomic instability and inhibit tumorigenesis. These results underscore the important role of abnormal chromosomal/centromere duplication in tumorigenesis by inducing chromosomal translocation and amplification under the effect of p53 deficiency.

DNA damage response in Lig4−/− p53−/− thymocytes: stabilized mutant p53 and activation of p21 protein leads to cell cycle arrest and senescence

To understand the p53 activation occurring in Lig4−/− p53−/− mice, thymocytes were harvested and examined for the expression of the mutant p53 by Western blot analysis. A significant increase in the p53R172P protein level was observed in Lig4−/− p53−/− thymocytes (Fig. 5, lane 2). This p53 level was comparable to that observed in Lig4−/− p53−/− thymocytes (Fig. 5, lane 1). Our results indicate that both treatments enhanced the extent to which potential coding ends were detected, suggesting the presence of coding ends with a single-strand overhang and hairpin ends. This is the first report of the direct detection of processed (open) coding ends in the mouse, mechanistically implicating a stepwise processing of hairpin coding ends by the DNA–PKcs–Artemis complex.
also confirmed by immunohistochemistry (Fig. S8, available at http://www.jem.org/cgi/content/full/jem.20062453/DC1). To further rule out any involvement of this pathway, Western blot analysis did not show any change in the expression of the pRB protein in Lig4−/− p53p/p thymocytes compared with WT and Lig4+/p53p/p thymocytes (Fig. S11). Thus, although the p16–pRB pathway may induce senescence in some instances, V(D)J recombination breaks mainly induce a p53–p21 pathway in Lig4−/− p53p/p thymocytes that in turn, cause the cells to enter senescence.

DISCUSSION

In this study, we have successfully established and characterized an in vivo model showing that the mutant p53R172P induces cell cycle arrest and senescence, rather than apoptosis, most likely through a p21-dependent pathway in response to persistent DNA damage. This response is sufficient to inhibit genomic instability and suppress tumorigenesis. We report for the first time the detection of aberrant V(D)J recombination intermediates (open coding ends) in thymocytes of Lig4−/− p53p/p mice. We also detected stabilized mutant p53 and high level of p21 in thymocytes, which coincides with large numbers of senescent cells in CD25-positive (DN) thymocytes and CD19-positive bone marrow cells. Consistent with the finding of senescence in precursor lymphoid cells, we found a very low level of the proapoptotic protein PUMA in thymocytes. In addition, cyogenetic analysis of the lymphoid cells of Lig4−/− p53p/p mice showed normal chromosomal counts with few chromosomal breaks, suggesting that the p53–p21 pathway was able to suppress genomic instability and inhibit tumorigenesis. This was unexpected, taken into consideration a previous study in which DNA ligase IV–p53 double-deficient mice succumbed to aggressive pro-B cell lymphomas in a Rag-dependent manner, with chromosomal translocation and oncogenic amplification (35).

Based on the findings of this study in Lig4−/− p53p/p mice, we propose the model shown in Fig. 6. When V(D)J recombination–induced DSBs remain unrepaird as a result of a deficiency in the NHEJ pathway, p53 is activated, leading to apoptosis. In the absence of p53 activity, these DSBs may induce senescence in some instances, V(D)J recombination breaks mainly induce a p53–p21 pathway in Lig4−/− p53p/p thymocytes that in turn, cause the cells to enter senescence.
found in the Lig4\(^{-/-}\) p53\(^{-/-}\) thymocytes, which is consistent with previous studies of the inability of the mutant p53 protein to transactivate another crucial proapoptotic protein, BAX (38, 49). We suggest the inability of p53\(^{R172P}\) to activate apoptosis-related genes explains at least partially why the p53\(^{R172P}\) mice are deficient in apoptosis, confirming the essential function of the transactivation activity of p53 in inducing apoptosis. Our results also implicate the critical role of p53 in determining cell cycle arrest versus apoptosis, in addition to the upstream signaling. It is intriguing, however, that the mutant p53 is able to transactivate p21 to a very high level. Previous studies have indicated that p53\(^{R175P}\) was able to activate p21 in irradiated cells, but at a reduced rate (10, 37, 38). Although we cannot discard the possibility that p53R172P may function independently of p21 in preventing genomic instability, it is improbable because we observed increased levels of both p53 and p21 in only Lig4\(^{-/-}\) p53\(^{-/-}\) lymphoid cells, and because recent evidence showed that p21 deficiency accelerates the tumor onset and chromosomal aberrations in p53\(^{-/-}\) mice (52). We interpret a high p21 level found in Lig4\(^{-/-}\) p53\(^{-/-}\) thymocytes as likely caused by a combination of persistent unrepaired DNA breaks resulting from the deficiency of DNA ligase IV and the failure of p53 to transactivate other effector genes key to inducing apoptosis, such as PUMA and BAX (38). Perhaps this activation of p21 serves as a “backup” pathway in the event that the primary goal, apoptosis, cannot be achieved. Another possibility is the accumulation of senescent cells with high levels of p21 to maintain their senescent status in thymus and bone marrow.

Our previous study of mice with the Lig4\(^{-/-}\) p53\(^{-/-}\) genotype convincingly demonstrated that the tumorigenic process requires chromosomal translocation and rounds of replication to amplify the oncogene c-Myc by means of breakage–fusion–bridge cycles (35). In this study, our data suggest that in the absence of an apoptosis pathway, persistent DNA breaks activate the p53–p21 pathway, which blocks DNA replication and cell cycle, thereby inhibiting further genomic instability, which is a key event for tumorigenesis. Our study further reveals a strong correlation between aneuploidy and oncogene activation, implying that p53 has an essential tumor suppressor role in preventing chromosomal abnormality. Aneuploidy is characteristic of p53-deficient cells and can result from a failure of controlling centrosome duplication, which is normally coordinated with other cell cycle events, such as DNA replication. Indeed, centromere dysregulation is commonly found in p53-deficient cells, but normal centrosome duplication can be restored through the reintroduction of p53 (53). Furthermore, the main control mechanism of centromere duplication occurs through the CDK2, where the kinase can be inhibited by p21, which is a major p53 effector expressed at high levels in Lig4\(^{-/-}\) p53\(^{-/-}\) thymocytes. These observations lead us to further hypothesize that the V(D)J recombination–mediated DNA DSBs signal for the activation of p53 and, subsequently, p21. This is sufficient to inhibit abnormal centromere duplication and maintain the euploid status of Lig4\(^{-/-}\) p53\(^{-/-}\) lymphoid cells, thereby preventing further genomic instability required for tumorigenesis.

Cellular senescence is a state in which cells withdraw from the cell cycle, and it has been proposed to be a tumor suppression mechanism (26). In human cells, telomere shortening is the primary event that causes cells to undergo senescence. Telomere shortening is a result of excessive cellular proliferation and DNA replication, culminating in a critical state in which the chromosome ends lack the usual protection. It has been proposed that a shortened telomere can be recognized as a broken chromosome, which sends a cellular signal evoking the activation of p53. This makes our model useful for studying the pathway that leads to cellular senescence and its role in suppressing tumorigenesis, as telomere shortening does not frequently occur in murine cells because of the extra length of their telomeres. Our study further indicates a critical role of p21 in inducing cellular senescence to block further genomic instability and tumorigenesis in response to persistent DNA DSBs. Other senescent pathways, such as p16–pRB, are important in response to different stimuli.

In addition, cellular senescence, particularly premature senescence, has been linked to aging. These Lig4\(^{-/-}\) p53\(^{-/-}\) mice could also be an excellent model for studying the connection between senescence and aging. A compelling finding in this regard was that although tumors do not develop in Lig4\(^{-/-}\) p53\(^{-/-}\) mice, they die early of an unknown cause; further pathological analyses are required to explore the cause of death. One possible cause of death in these animals could be premature aging. In support of this, it is well established that nonspecific DNA DSBs occur as a result of normal metabolism and environmental exposure and that DNA ligase IV plays an important role in the repair of DSBs in general. We hypothesize that these nonspecific breaks could accumulate in the Lig4\(^{-/-}\) background and that the mutant p53 inhibits tumorigenesis by inducing senescence, which might lead to premature aging and some aging-related diseases.

**MATERIALS AND METHODS**

**Mouse colony and maintenance.** Mutant mouse strains (mixed genetic background of C57BL/6 and 129SV) and their colony maintenance have been previously described (10, 35, 54). Protocols used in this study were approved by the Institutional Animal Care and Use Committee at the University of Texas M.D. Anderson Cancer Center.
Cell senescence assay and immunohistochemistry studies. Acidic β-gal activity, which indicates cell senescence, was detected as previously described (19). In brief, 6-μm-thick frozen thymic sections from newborn mice of different genotypes were processed for the β-gal assay (staining kit was purchased from Cell Signaling Technology). Bone marrow cell suspension was obtained from 4–6-week-old mice, cytopsin, and fixed with 1:1 acetone/methanol (100% vol/vol). The cells were stained with β-gal and observed under a brightfield microscope.

The cells were also stained for the CD19 B cell marker using a standard protocol. In brief, after the β-gal assay, the cells were processed for antigen retrieval using the proteinase K method, blocked using the streptavidin-biotin system (Vector Laboratories), and incubated with rat anti-CD19 antibody (BD Biosciences) with its corresponding isotype control. The CD19-positive cells were detected using an anti-rat biotinylated antibody and streptavidin–horseradish peroxidase (HRP) (BD). Thymocytes, thymic sections, and bone marrow cells were stained with anti-HP1γ monoclonal antibody (clone 42s2; Millipore), followed by HRP/DAB detection system. Thymocytes or thymic sections were also co-stained with anti-HP1γ and CD25 (BD Biosciences), followed by fluorescence detection.

LMPCR assays. To detect the signal and coding ends in thymocyte DNA, LMPCR assays were performed as previously described (45).

TUNEL assay. A TUNEL assay (DeadEnd Fluorometric TUNEL System; Promega) was performed to identify apoptotic cells in thymic sections of newborn mice, including a DNase-treated positive control. In brief, frozen sections were pretreated with 10 μg/ml proteinase K and equilibrated; DNA breaks were labeled with fluorescein-12-dUTP. The sections were subsequently stained with DAPI (Sigma-Aldrich). The green fluorescence of apoptotic cells against a blue background (DAPI) was detected by fluorescence microscopy.

Western blot. Thymocytes were cultured in Dulbecco’s modified Eagle medium supplemented with 10% fetal calf serum and 10 mM Hepes at a density of 105 cells/ml. The cells were subsequently exposed to 5 Gy of γ-irradiation and cultured for 4 h. Whole-cell protein extracts were prepared (11) and quantified by the Bradford method (Bio-Rad Laboratories). Protein (50–150 μg/lane) was electrophoretically separated on SDS-PAGE and transferred to a PVDF membrane. The membranes were blocked with antibodies specific for p53, which recognizes p53R172P (CM5; Vector Laboratories), p21 (C19; Santa Cruz Biotechnology), PUMA (Cell Signaling Technology), and β-actin (Sigma-Aldrich). An anti-rabbit or –mouse antibody conjugated to HRP was used, and the signal was detected using a chemiluminescence kit (PerkinElmer).

Fluorescence in situ hybridization (FISH). For FISH, fetal liver cells were obtened from newborn mice of different genotypes. Metaphase preparations were prepared as previously described (35). Telomeric FISH was used to detect chromosomal breaks using a Cy3-labeled protein nuclear acid probe (Applied Biosystems).

Online supplemental material. Fig. S1 shows that Lig4+/− p53+/− mice are smaller. Fig. S2 shows a TUNEL assay on thymic sections of newborn mice. Fig. S3 shows HE staining of thymic sections of newborn mice. Fig. S4 shows the SCID phenotype of Lig4−/− p53+/− mice. Fig. S5 shows that HP1γ-positive cells are CD25+ thymocytes. Fig. S6 shows that HP1γ-positive cells are CD19+ bone marrow cells. Fig. S7 shows sequencing of coding ends at the TCR, D82 locus. Fig. S8 shows immunohistochemical detection of p53 protein on thymic sections from WT and Lig4+/− p53+/− mice. Fig. S9 shows immunohistochemical detection of p21 protein on thymic sections from WT and Lig4+/− p53+/− mice. Fig. S10 shows p16INK4a and β-actin protein expression in WT, Lig4+/− p53+/−, and Lig4−/− p53+/− thymocytes. Fig. S11 shows phosphorylated retinoblastoma protein expression in WT, Lig4+/− p53+/−, and Lig4−/− p53+/− thymocytes. Table S1 shows that p53R172P rescues embryonic lethality of Lig4−/− mice. The online version of this article is available at http://www.jem.org/cgi/content/full/jem.20062453/DC1.

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