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An African-specific polymorphism in the TP53 gene impairs p53 tumor suppressor function in a mouse model

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A nonsynonymous single-nucleotide polymorphism at codon 47 in TP53 exists in African-descent populations (P47S, rs1800371; referred to here as S47). Here we report that, in human cell lines and a mouse model, the S47 variant exhibits a modest decrease in apoptosis in response to most genotoxic stresses compared with wild-type p53 but exhibits a significant defect in cell death induced by cisplatin. We show that, compared with wild-type p53, S47 has nearly indistinguishable transcriptional function but shows impaired ability to transactivate a subset of p53 target genes, including two involved in metabolism: Gls2 (glutaminase 2) and Sco2. We also show that human and mouse cells expressing the S47 variant are markedly resistant to cell death by agents that induce ferroptosis (iron-mediated nonapoptotic cell death). We show that mice expressing S47 in homozygous or heterozygous form are susceptible to spontaneous cancers of diverse histological types. Our data suggest that the S47 variant may contribute to increased cancer risk in individuals of African descent, and our findings highlight the need to assess the contribution of this variant to cancer risk in these populations. These data also confirm the potential relevance of metabolism and ferroptosis to tumor suppression by p53.

[Keywords: p53; tumor suppression; metabolism; ferroptosis; polymorphism; Ser46 phosphorylation]

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The p53 tumor suppressor (TP53) holds the distinction of being the most frequently mutated gene in human cancer. Germline mutations in the TP53 gene exist in individuals with Li-Fraumeni syndrome, who suffer from multiple tumors before the third decade of life (Malkin et al. 1992). An additional 50% of sporadic human tumors contain somatic mutations in the TP53 gene (Hollstein et al. 1991). The majority of these are missense mutations that occur in the DNA-binding domain, which inhibit the ability of this protein to bind to p53 response elements in the promoters of p53 target genes and subsequently transactivate gene expression (Vogelstein et al. 2000). In addition to these changes, there are several functionally significant polymorphisms in the TP53 gene as well as in genes encoding proteins that regulate the p53 pathway (such as MDM2 and MDM4); these variants can decrease p53 pathway activation and contribute to increased cancer risk (Pietsch et al. 2006; Grochola et al. 2010).

p53 is believed to possess at least three subsets of target genes through which it suppresses tumor development: It induces senescence through target proteins like CDKN1A (p21), induces apoptosis through target proteins like PUMA and NOXA (which encode “BH3-only” proteins), and controls metabolism/redox state through target proteins like SCO2, TIGAR, GLS2 (glutaminase 2), and

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get genes to induce cell death following cisplatin or 

impaired for the ability to transactivate a subset of p53 tar-

However, it is 

in ferroptosis [Gao et al. 2015].

p53 is heavily post-translationally modified, and, in 
some cases, these modifications have a considerable im-

on the ability of p53 to perform its transcriptional, ap-

optotic, and tumor suppressor functions [Kruse and Gu 

2008; Vousten and Prives 2009]. Most pertinent to this 

study, Ser46 phosphorylation is required for efficient 

p53-mediated cell death in several cell line systems and 
in mice [Bulavin et al. 1999; Oda et al. 2000; D’Orazi 
et al. 2002; Feng et al. 2006]. Over two decades ago, a 
naturally occurring polymorphism in TP53 was reported 
in Africans and African Americans [rs1800371, G/A]. This 
polyorphism converts the proline residue proximal to 
Ser46 in human p53 to a serine [Fellcy-Bosco et al. 1993]; 
we noticed that this eliminates the proline required for 
phosphorylation of Ser46 by the proline-directed kinases 
that phosphorylate this residue, which include 
p38MAPK, HIPK2, and DYRK [Fellcy-Bosco et al. 1993; 
Bulavin et al. 1999; Hofmann et al. 2002; Taia et al. 2007]. We showed that the Ser47 variant (referred to here 
as S47) is markedly impaired for phosphorylation on 
Ser46 and also has significantly impaired ability to induce 
cell death in multiple human cell lines engineered to 
contain inducible forms of human wild-type p53 and S47 [Li 
et al. 2005]. However, the impact of this variant on the 
p53 signaling pathway and cancer risk in an intact animal 
has never been assessed.

The S47 polymorphism appears to be restricted to 
African-descent populations, with a frequency of ~1.5% in Af-

ican Americans and between 6% and 8% in certain 
African populations; in contrast, this variant has not 
been detected in Caucasian Americans (see http://evs.gs. 
washington.edu/EVS). Given the very low allele frequen-
cy for S47, population analyses designed to assess the im-
pact of this polymorphism on cancer risk in African-
descent populations have lacked sufficient power. We rea-
soned that the S47 allele may explain part of the increased 
cancer risk disparities in African Americans relative to 
Caucasians and other ethnic groups. Therefore, in this 
study, we sought to determine the impact of the S47 vari-
ant on p53 function and cancer risk in a mouse model so 
as to better inform the rationale that human studies 
should be done. We found that the S47 variant is modestly 
or not at all impaired for most p53 functions; however, it is 
impaired for the ability to transactivate a subset of p53 tar-
gent genes to induce cell death following cisplatin or ferrop-
tosis inducers. Notably, the S47 variant is also impaired 
tumor suppression, and S47 heterozygous and homo-
ygous mice are markedly predisposed to hepatocellular 
carcinoma and other cancers.

Results

Generation of a mouse model for wild-type p53 and the 
S47 variant

In order to address the influence of the S47 polymorphism 
on p53 function within an organism, we generated a 
knock-in mouse for the S47 allele. For this, we chose the 
humanized p53 knock-in (Hupki) targeting allele, which 
replaces mouse exons 4–9 with the corresponding human 
exons [codons 32–332]. Hupki p53 has been shown by sev-
eral groups to be fully tumor-suppressive and transcription-
ally active and to accurately recapitulate the activity of 
human p53 in mice [Luo et al. 2001; Reinbold et al. 
2008; Frank et al. 2011]. We previously modeled the codon 
72 variants of p53 using the Hupki platform and derived 
considerable information from these Hupki mice that sub-
sequently held true for human p53 codon 72 variants 
[Frank et al. 2011]. Additionally, a knock-in mouse for 
p53 substituting Ser46 with alanine [S46A] was created 
using the Hupki platform, and cells from these mice recap-
itulate the apoptotic defect evident in inducible human 
cell line models [Feng et al. 2006].

We previously showed that the S47 variant appears to 
occur exclusively in cis with the Pro72 variant of p53 [Li 
et al. 2005]. Therefore, we generated S47 embryonic stem 
cell lines using the P72 Hupki targeting construct. Embryonic stem cell lines with successfully targeted al-
leles were confirmed by Southern analysis [Supplemental 
Fig. S1A]. Males with germline transmission of the target-
ed allele were crossed to EIIA-Cre females, and Cre-mediat-
ed excision of the neomycin resistance cassette was monitored by Southern analysis [Supplemental Fig. S1B]. 
RNA was isolated from mouse embryonic fibroblasts 
[MEFs] containing either the wild-type Hupki or S47 
Hupki alleles and used to sequence the full-length p53 
cDNA; the only difference observed was at codon 47, 
which encoded proline [CCG] in wild-type p53 and serine 
[TCC] in the S47 allele [data not shown]. To ensure genetic 
homogeneity, wild-type and S47 Hupki mice were back-
crossed to C57Bl/6 mice for over 10 generations and then 
crossed to each other, for the majority of studies, we ana-
lyzed sibling littermate mice derived from heterozygote 
S47/wild-type crosses.

We generated several independent batches of MEFs 
from wild-type and S47 mice. We exposed these MEFs to 
etoposide, which led to significant phosphorylation of 
p53 on Ser15 [an activating marker] in both wild-type 
and S47 MEFs, along with clear induction of apoptosis. 
The induction of apoptosis was modestly reduced in S47 
cells, as assessed by Western blots for cleaved lamin A 
and cleaved caspase-3 [Fig. 1A,B]. Similar results were ob-
tained following doxorubicin treatment [Supplemental 
Fig. S2A]. Although we noted occasional decreases in 
the level of S47 protein induced by DNA damage

The S47 polymorphism impairs tumor suppression


genes & development
compared with wild-type p53 (for example, see Supplementary Fig. S2A), these differences were not always seen, and we could find no evidence for a difference in the half-life between wild-type and S47 protein in cells treated with DNA-damaging agents (Supplemental Fig. S2B).

We next assessed p53 induction and apoptosis in response to γ radiation in wild-type and S47 mice, focusing on tissues that show p53-dependent radio sensitivity (thymus, small intestine, and colon). Treatment of wild-type and S47 mice with 5 Gy of γ radiation led to an equal number of cells staining positively for p53 in the small intestine, thymus, and colon in wild-type and S47 mice (Fig. 1C,D, Supplemental Fig. S2C,D). In the small intestine and colon, there were reduced numbers of apoptotic cells in S47 mice following γ radiation compared with wild-type (Fig. 1E,F). In contrast, the levels of apoptotic cells in the thymus were nearly identical (Supplemental Fig. S2C). These combined data indicate that there appears to be a modest but consistent reduction in the apoptotic potential of the S47 protein in response to genotoxic stress in some but not all cell types.

Markedly impaired cell death by cisplatin in human and mouse S47 cells

Phosphorylation of Ser46 occurs in response to many genotoxic stresses, but phosphorylation of this residue by p38MAPK is particularly required for p53-mediated cell death following cisplatin treatment [Hernandez Losa et al. 2003; Zhu et al. 2013]. Therefore, we next analyzed the response of wild-type and S47 MEFs and mice to cisplatin [Cis-dichlorodiammineplatinum (CDDP)]. We noted significantly reduced cell death by cisplatin in S47 MEFs compared with wild type (Fig. 2A). Cisplatin-mediated cell death at this dose and time point was clearly p53-dependent, as noted by the absence of cleaved caspase-3 in MEFs from the p53 knockout mice (Fig. 2B). These results were corroborated using two independent assays to assess cell death and viability: Annexin V staining for apoptosis (Fig. 2C) and Alamand blue assays to assess cell viability; the latter cell viability assays indicated a 15-fold difference in cisplatin IC50 between wild-type and S47 MEFs (Fig. 2D). To confirm these results in human cells, we analyzed human lymphoblastoid cell lines (LCLs) that we
obtained from the Coriell Institute, which had been geno-
typed as part of the 1000 Genomes Project (http://www.
1000genomes.org) and identified and confirmed by us to
be homozygous S47 or wild type (see the Materials and
Methods). Treatment of homozygous wild-type and S47
LCLs with cisplatin for 24 h resulted in roughly equiva-
lent p53 induction but greatly impaired apoptosis in S47
cells, as assessed by cleaved lamin A and cleaved cas-
pase-3 protein (Fig. 2E). This impaired apoptosis in S47
LCLs was also evident following Annexin V staining
(Fig. 2F). Even greater differences between wild-type and
S47 LCLs were noted following cisplatin treatment using
cell viability assays, and we found a 10-fold difference in
the IC50 between wild-type and S47 human LCLs for cis-
platin (Fig. 2G). Similar differences in IC50 were noted
for adriamycin as well (Fig. 2H).

We next extended our findings by assessing cisplatin-
mediated cell death in wild-type and S47 mice. Here we fo-
cused on the kidney, which is a key site of p53-mediated
cell death in response to cisplatin (Sprowl et al. 2014).
We noted a marked decrease in apoptotic cells in the
kidneys of S47 mice relative to wild-type following cis-
platin treatment; also evident were decreased regions of
cell clearing (evidence of cell death) in the S47 kidney
(Fig. 2I). We next examined the long-term effect of cisplat-
in on the viability of wild-type and S47 MEFs. To do this,
we first immortalized several lines of wild-type and S47 MEFs by stably infecting them with a short hairpin for p19ARF, this short hairpin [shARF] is specific for ARF and not p16INK4a and immortalizes MEFs, thereby effectively eliminating the selection for p53 mutation that occurs during long-term culture [Humbey et al. 2008]. Treatment of multiple independent clones of wild-type-shARF and S47-shARF MEFs with increasing doses of cisplatin for 24 h, followed by plating of equal numbers of cells, revealed a dramatically enhanced ability of S47-shARF MEFs to survive following cisplatin [Fig. 2],[K]. Similar findings were made following treatment with carboplatin [Supplemental Fig. S3A,C]. In contrast, the clonogenic survival of wild-type and S47 cells following etoposide was not markedly different [Supplemental Fig. S3B,D].

We next extended these studies to analyze cells that were heterozygous for the S47 variant/wild type. Surprisingly, heterozygous S47/wild-type MEFs more closely resembled homozygous S47 MEFs and were markedly impaired for cell death by cisplatin [Fig. 3A,B]. Likewise, the IC50 for cisplatin in S47/wild-type MEFs was markedly increased compared with wild-type MEFs and was more similar to the IC50 in S47 homozygous MEFs [Fig. 3C]. Similar decreases in cisplatin-mediated cell death were also evident in human heterozygous S47/wild-type LCLs [Fig. 3D]. It is of note that these heterozygous S47/wild-type LCLs were from the child of the homozygous wild-type and S47 LCL donors, so genetic heterogeneity is reduced [see the Materials and Methods].

**Figure 3.** Marked impairment of cisplatin-mediated apoptosis in S47/wild-type heterozygous cells. (A) Primary MEFs from the wild-type (Wt) or S47 Hupki mouse or S47/wild-type heterozygous mice were treated with 10 μM cisplatin (CDDP) for 24 h, and protein lysates were analyzed by Western blot analysis for the proteins indicated. The data depicted are representative of three independent experiments in a minimum of three independent batches of MEFs. (B) Quantification of the relative intensity of cleaved caspase-3 and cleaved lamin A blots from three independent experiments (as depicted in A) in primary MEFs from the wild-type (WT), S47, and S47/wild-type heterozygous mice untreated or treated with 10 μM cisplatin (CDDP) for 24 h. The level of signal in wild-type cells treated with CDDP was set to 100. Error bars mark standard deviation. (C) IC50 analysis for cisplatin (CDDP) in primary wild-type, S47, and S47/wild-type MEFs treated with the indicated concentrations of cisplatin for 72 h and analyzed for viability by the Alamar blue assay. The depicted data represent an average of three independent experiments. Error bars represent standard deviation. (D) Quantification of the relative intensity of cleaved lamin A [black box] and cleaved caspase-3 [gray box] signal from three independent experiments in LCLs that are wild type, S47, or heterozygous (S47/wild type). Cells were untreated or treated with 10 μM cisplatin (CDDP) for 24 h. The level of cleaved lamin A in untreated S47 cells was set to 1, and the fold change is depicted relative to that. The averaged results from three independent experiments with standard deviation are depicted.

**Decreased transactivation of GLS2, PMAIP1 (NOXA), and SCO2 in S47 cells**

In order to compare the transcriptional potential of wild-type and S47 forms of p53, we performed quantitative RT–PCR (qRT–PCR) of over two dozen known p53 target genes in wild-type and S47 MEFs following treatment with cisplatin. This analysis revealed that the majority of these p53 target genes is induced similarly in wild-type and S47 MEFs following cisplatin; this includes targets responsible for growth arrest [Cdkn1a/p21, Gadd45, and Ccn1], autophagy [Dram1 and Ulk1], and metabolism [Tigar, Sesn1, Sesn2, and Pparc1a] [Fig. 4A]. This also included p53 target genes that are regulated by transactivation domain II of p53 (amino acids 41–83), where the S47 polymorphism resides: Abhd4, Mgmt, Sidt2, and Pflda3 [Brady et al. 2011]. Of the over two dozen p53 target genes tested, only three showed significantly impaired transactivation by the S47 variant: These were Gls2, Noxa (Pmaip1), and Sco2 [cytochrome c oxidase assembly protein] [Fig. 4B]. The differences in Noxa prompted us to also analyze Bbc3 (Puma), but we saw no difference in Bbc3 induction in S47 and wild-type cells [Supplemental Fig. S4A]. Importantly, S47 LCLs treated with cisplatin also showed significantly reduced levels of GLS2 and NOXA mRNA, while the levels of CDKN1A and MDM2 mRNA were comparable in both genotypes [Fig. 4C]; SCO2 expression was not detectable in this cell type. To assess the impact of GLS2 and NOXA on the impaired apoptosis in S47 cells, we silenced these genes in wild-type MEFs using either of two different short hairpins. This led to consistent abrogation of cisplatin-mediated cell death in these wild-type MEFs compared with a short hairpin control [Supplemental Fig. S4B,C]. These data indicate that the impaired transactivation of Gls2 and Noxa explains at least in part the defect in cisplatin-mediated cell death in S47 cells. The identification of a subset of p53 target genes exhibiting impaired transactivation in S47 MEFs and LCLs provided us with an opportunity to address a fundamental
issue regarding this variant; that is, whether the S47 variant is impaired for apoptosis and transactivation because of lack of phosphorylation on Ser46 or due to a separate, possibly structural, issue. To shed light on this question, we analyzed the transactivation of these three target genes (Sco2, Noxa, and Gls2) by wild-type p53 following cisplatin treatment in the presence and absence of the p38MAPK inhibitor SB203580, which inhibits Ser46 phosphorylation. We were able to confirm the findings of others that SB203580 inhibits Ser46 phosphorylation of wild-type p53 as well as cell death (Fig. 4D). Notably, qRT–PCR of RNA from these MEFs revealed that treatment with SB203580 had no effect on the transactivation of Cdkn1a but led to a significantly decreased ability of p53 to transactivate Sco2 and Noxa (Fig. 4E). Gls2 was decreased as well, but this did not reach statistical significance (Fig. 4E). These data were recapitulated when we silenced p38MAPK using siRNA (Supplemental Fig. S4D). The combined data support the premise that the failure of phosphorylation on Ser46 explains at least part

Figure 4. The S47 variant is impaired for transactivation of a subset of p53 target genes, including Gls2, Noxa [Pmaip1], and Sco2. (A) qRT–PCR analysis of p53 target genes in primary wild-type [Wt] and S47 MEFs treated with 10 μM cisplatin [CDDP] for 24 h. All values were normalized to a control gene [cyclophilin A]. Data are averaged from three independent biological replicates. Error bars indicate standard deviation. (*) P < 0.05. (B) qRT–PCR analysis of the p53 target genes indicated in independent batches of primary MEFs from wild-type and S47 mice treated with 10 μM CDDP for 24 h. All values were normalized to a control gene [cyclophilin A]. Data are averaged from three independent biological replicates. Error bars indicate standard deviation. (*) P < 0.05. (C) qRT–PCR analysis of the p53 target genes indicated in human LCLs that are homozygous for wild-type p53 or S47 treated with 10 μM CDDP for 24 h. All values were normalized to a control gene [cyclophilin A]. Data are averaged from three independent biological replicates. Error bars indicate standard deviation. (*) P ≤0.05. SCO2 was not expressed in LCL cells, so these data are not depicted. (D) Western analysis for the proteins indicated in wild-type and S47 MEFs pretreated with 10 μM p38MAPK inhibitor SB203580 for 2 h followed by 10 μM cisplatin [CDDP] for 24 h. GAPDH served as the loading control. (E) qRT–PCR analysis of the cells in D for the p53 target genes indicated, normalized to control [cyclophilin A]. The depicted data represent the average of three independent experiments. Error bars represent standard deviation. (*) P < 0.05.
of the decreased ability of the S47 variant to transactivate this subset of p53 target genes.

**Decreased binding of S47 to the p53-binding sites in GLS2 and SCO2**

We next sought to delineate the mechanism for impaired transactivation of Gls2, Sco2, and Noxa by S47. We first analyzed the ability of LCL lysates from cells containing wild-type and S47 proteins to bind to oligonucleotides containing the p53-binding site in the human Cdkn1a promoter using a microsphere protein-DNA-binding assay for p53 (Noureddine et al. 2009). In this in vitro binding assay, we saw a consistently reduced ability of S47 lysates to bind to oligonucleotides containing this p53-binding site compared with wild-type lysates, suggesting that an altered DNA-binding ability might underlie part of the transcriptional defect (Supplemental Fig. S5A–C). These data prompted us to perform chromatin immunoprecipitation (ChIP) in primary MEFs containing wild-type p53 and S47 treated with cisplatin. For GLS2, we identified two consensus p53-binding sites in the murine gene—one in the promoter that overlapped the transcription start site and another that was nearly 75 kb upstream of the promoter; both of these sites had significant p53 binding site as well as the previously identified Sco2-binding site; there was also a decreased ability to bind to the Noxa site, but this was not statistically significant [Fig. 5A]. In contrast, there was no significant difference in the ability of S47 and wild-type p53 to chromatin-immunoprecipitate the upstream GLS2 site as well as the previously identified Sco2-binding site; there was also a decreased ability to bind to the Noxa site, but this was not statistically significant [Fig. 5A].

Increased spontaneous cancer in S47 mice

At the beginning of this study, we set aside a cohort of 20 S47 and wild-type mice in order to analyze life expectancy and lecithin; we were surprised to find a significant percentage of our S47 mice developing spontaneous cancer. In all, 16 out of 20 (80%) of the homozygous S47 mice that were analyzed developed cancer between 12 and 18 mo of age. These cancers were of diverse histological types but predominantly included hepatocellular carcinoma, B-cell lymphoma, and histiocytic sarcoma, along with other tumor types [Fig. 6A–C]. The presence of such a high fraction of hepatocellular carcinoma was interesting in light of the fact that high levels of GLS2 protein are normally expressed in this cell type and the data indicating that GLS2 is a tumor suppressor gene in human hepatocellular carcinoma [Liu et al. 2014]. We also noted the presence of metastatic lesions in a small fraction of these mice [Fig. 6B,C]. In a small cohort of S47/wild-type heterozygote mice, we also noted increased cancer incidence, again with a predisposition for hepatocellular carcinoma [Fig. 6C]. Log rank analysis revealed a statistically significant difference in survival between wild-type and S47 mice ($P < 0.0001$) [Fig. 6D].

Decreased ferroptosis in S47 cells

Although we noted a significant defect in cisplatin-mediated apoptosis in S47 cells, some studies have questioned the relevance of the apoptotic pathway of p53 to tumor suppression [Li et al. 2012b]. Moreover, we noted disparities in the amount of cell death induced by cisplatin when we performed assays for apoptosis [Annexin V] versus other cell viability assays (Alamar blue and Trypan blue), suggesting that another, nonapoptotic cell death pathway might be induced by cisplatin. Recent studies have implicated ferroptosis as important for p53-mediated tumor suppression [Jiang et al. 2015]. Moreover, recently, the p53 target gene GLS2 was shown to be essential for ferroptosis [Gao et al. 2015]. Therefore, we next sought to determine whether S47 cells are impaired for ferroptosis. We first treated S47, wild-type, and S47/wild-type MEFs with erastin, a compound that induces ferroptosis [Dixon et al. 2012]. Incubation with 4 µM erastin for 8 h led to profound cell death in wild-type MEFs, consistent with data in the literature [Jiang et al. 2015]; in contrast, there was no effect on either S47 or heterozygote S47/wild-type MEFs [Fig. 7A]. Cell viability assays to assess the IC$_{50}$ for erastin indicated that S47 MEFs were 27-fold resistant to this compound, and heterozygote S47/wild-type MEFs were fourfold resistant compared with wild-type MEFs [Fig. 7B]. Interestingly, we found that the level of GLS2 was markedly up-regulated by erastin treatment in wild-type MEFs but not in S47 cells and that silencing GLS2 in wild-type MEFs phenocopied the cell death defect in S47 cells treated with erastin [Fig. 7C].

p53 is required for erastin-mediated ferroptosis, in part due to the ability of this protein to bind and negatively regulate the promoter for the cystine transporter SLC7A11 [Jiang et al. 2015]. Therefore, we next analyzed the ability of S47 to negatively regulate this gene and found that the S47 variant is impaired for the ability to negatively regulate SLC7A11 ($P = 0.006$) [Fig. 7D]. Consistent with this, ChIP indicated that the S47 protein had reduced ability to chromatin-immunoprecipitate the p53-binding site identified in the SLC7A11 promoter but not the Cdkn1a promoter [Supplemental Fig. S6A,B]. Cisplatin treatment also led to differences in two other markers for ferroptosis between wild-type and S47 cells: Ptgs2 transactivation...
and GPX4 degradation, both of which were impaired in S47 cells treated with cisplatin (Fig. 7E,F).

We next sought to assess the sensitivity of wild-type and S47 LCLs to ferroptosis. In this case, we found that these human LCLs were considerably resistant to cell death by erastin; however, they were sensitive to cell death by another ferroptosis-inducing agent, RSL3 (Yang et al. 2014). We found that S47 LCLs were markedly resistant to ferroptosis induced by RSL3 (>19-fold) compared with wild-type LCLs (Fig. 7G). Finally, we sought to tie together some of our findings with ferroptosis and cisplatin by testing the possibility that some of the cell death induced by cisplatin might be due to ferroptosis; it is of note that both of these cell death pathways require reactive oxygen species (Zhu et al. 2013; Dixon and Stockwell 2014). Toward this end, we assessed the ability of zVAD-fmk, which inhibits apoptosis, and the compound Fer-1, which inhibits ferroptosis, to inhibit cisplatin-mediated cell death. We found that Fer-1 could partially but significantly rescue a percentage of cisplatin-mediated cell death and that zVAD-fmk was likewise only partially able to rescue cell death by cisplatin (Fig. 7H). Our combined findings suggest that S47 cells are resistant to both cisplatin-mediated cell death and ferroptosis and that cisplatin appears to induce some level of ferroptosis.

Discussion

In this study, we show that the S47 polymorphism in TP53 impairs the ability of p53 protein to induce cell death
following cisplatin treatment and to transcribe a subset of target genes due in part to the decreased ability of S47 to bind to the response elements in these promoters. We show that this variant confers increased cancer risk in a mouse model and that it shows a defect in ferroptosis induction. In 2012, the Gu group (Li et al. 2012b) generated a knock-in mouse in which three p53 acetylation sites in the p53 DNA-binding domain were mutated to arginine; this knock-in version of murine p53 failed to transactivate the majority of p53 target genes or induce growth arrest or programmed cell death. Surprisingly, the “3KR” mouse failed to develop cancer, suggesting that tumor suppression by p53 might occur independently of growth arrest or apoptosis (Li et al. 2012b). More recently, this group identified the ability to down-regulate SLC7A11 and induce ferroptosis as one mechanism by which the 3KR mutant may function to suppress tumor development (Jiang et al. 2015). Specifically, in tamoxifen-inducible versions of the S47 form of p53, the investigators reported that interaction of S47 with Pin1 was reduced compared with wild-type p53 (Follis et al. 2015). We analyzed our wild-type and S47 LCLs for a Pin1–p53 interaction in the absence and presence of cisplatin but did not see an impaired interaction of S47 with Pin1; in fact, the interaction between Pin1 and S47 was increased in both S47 and S47/wild-type cells compared with cells containing wild-type p53 following cisplatin treatment (M Jennis, unpubl.). We cannot explain the differences in our findings from those noted above except that these differences may exist between endogenous and exogenous (inducible) p53 or be subject to genotoxic stress or cell type specificity. Additionally, whereas our data indicate that the S47 variant has enhanced interaction with Pin1, the possibility remains that Pin1 binds to the S47 protein but cannot catalyze cis–trans isomerization and instead interferes with p53 function.

The cancer phenotype of S47 mice is unusual. p53 knockout mice typically develop T-cell lymphoma and sarcoma and almost never develop epithelial cancers

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Tumor Type</th>
<th>Lesion</th>
<th>Age (Months)</th>
<th>Gender</th>
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Figure 6. Spontaneous tumorigenesis in S47 but not wild-type mice. (A) Hematoxylin and eosin staining of tumors from the S47 mouse. [Left] Normal liver and liver hepatocellular carcinoma (dotted outline). [Right] Infiltrating B-cell lymphoma in the kidney (arrows). Bar, 100 μm. (B) Hematoxylin and eosin staining of tumors from the S47 mouse. [Top left] Hepatocellular carcinoma. [Top right] Pancreatic ductal adenocarcinoma metastasized to the lung (dotted outline). [Middle left] Pancreatic ductal adenocarcinoma metastasized to a lymph node (asterisk). [Middle right] Pancreatic ductal adenocarcinoma metastasized to liver (asterisk). [Bottom left] Intestinal adenoma. [Bottom right] Stomach adenoma. Bar, 100 μm. (C) Cancer incidence in wild-type and S47 mice and in heterozygous wild-type/S47 mice. The data are representative of a total of 20 S47 and wild-type mice and 12 wild-type/S47 mice; for S47, 16 of these developed cancer. (BCL) B-cell lymphoma; (HCC) hepatocellular carcinoma; (HS) histiocytic sarcoma; (CC) colorectal carcinoma; (PA) pancreatic ductal adenocarcinoma. (D) Kaplan-Meier analysis of survival between wild-type (WT) and S47 mice. n = 20 each. The asterisk represents a single wild-type mouse that died from a noncancerous cause.
Mouse models for Li-Fraumeni syndrome, which contain DNA-binding domain mutants of p53, frequently develop lymphoma and sarcoma but also develop cancers of epithelial origin (Lang et al. 2004). However, hepatocellular carcinoma does not occur in either of these mice. Because of the known role of GLS2 in ferroptosis and the fact that the GLS2 gene is a tumor suppressor in human hepatocellular carcinoma (Liu et al. 2014), we speculate that the impaired ability of S47 to transactivate GLS2 may explain some of the tumor-prone phenotype of the S47 mice. Somewhat surprisingly, we found that S47/wild-type heterozygous cells more closely mirror the cisplatin and ferroptosis defect in homozygous S47 cells; we also found that heterozygous S47/wild-type mice are susceptible to cancer. Presently, there are >50 million African Americans in the United States, and we estimate that up to 1 million of these individuals may be heterozygous for the S47 variant. Furthermore, up to 20,000 individuals may be homozygous for S47. Our data in mice suggest that both of these groups of individuals may be at markedly increased cancer risk. It will be important to perform case control studies on these individuals in order to assess their cancer risk. The studies presented here are powerful rationale for performing genotyping on large African American sample sets for the impact of this variant on cancer risk.

Materials and methods

Cell culture, reagents, and plasmids

Human LCL cultures GM18870 [G/G, wild-type p53], GM18871 [A/A, homozygous S47], and GM18872 [A/G, heterozygous child from GM18870 and GM18871 parents] were identified for genotyping at rs1800371 using the 1000 Genomes Web site and were obtained from the Coriell Institute. These were grown in RPMI supplemented with 15% fetal bovine serum (FBS) and 1% 100 IU/mL penicillin/100 µg/mL streptomycin (pen/strep). The genotype of these lines was confirmed by DNA sequencing. H1299 p53-null human non-small-cell lung carcinoma cells containing a tetracycline regulatory element (H1299 T-Reg) were provided by Steven McMahon (Thomas Jefferson University). The tetracycline-inducible p53 plasmid (Plenti4/TO/V5-DEST) was subject to site-directed mutagenesis to generate the S47 variant. H1299 T-Reg wild-type or S47 p53 cells were maintained at
37°C in Dulbecco’s modified Eagle’s medium [DMEM; Cellgro], 1% pen/strep [Cellgro, 30-002-CL], and 10% tetracycline approved FBS [Clontech, 631106]. MEFs were obtained from 12.5-d-old Hupki mice and were cultured at 37°C in DMEM with 1% pen/strep (Cellgro, 30-002-CI), and 10% tetracycline approved FBS. Endoposide (Sigma, E1383), CDDP (Acros Organics, 193760010), and carboplatin (Sigma, C2538) were used at the indicated concentrations. Doxycycline (BD Biosciences, 631311) was used at a concentration of 100 ng/mL. RSL3 (Aobious, Inc., AO1514), erastin (Sigma Aldrich, C2538) were used at the indicated concentrations. Doxycycline (Invitrogen, K4960-00). Lentivirus was added to cells with 6 μg/mL polybrene for maximum viral transduction. Stable cells were selected using 1 μg/mL puromycin, and gene knockdown was confirmed by qRT–PCR. p38MAPK (Mapk14) was silenced by transfection with siControl or SMARTpool Accell Mapk14 siRNA [A-040125-13].

**Generation of S47 Hupki mice**

Wild-type Hupki mice were generated previously. S47 mice were generated with the Hupki targeting construct as described (Luo et al. 2001) following site-directed mutagenesis to create serum at amino acid 47. All mice were backcrossed to C57Bl/6 for >10 generations, and, in the majority of cases, sibling littersmates were used for analyses. All studies were performed in accordance with federal and institutional guidelines according to Institutional Animal Care and Use Committee protocols. Mice were housed in plastic cages with ad libitum diet and maintained with a 12-h light/dark cycle at 22°C. For irradiation experiments, mice were exposed to a cesium-137 γ irradiation source [The Wistar Institute], and tissues were harvested 4 h later. Mice were injected intraperitoneally with cisplatin at 20 mg/kg.

**Western blotting and immunohistochemistry**

Primary antibodies used for Western blotting included p53 (ab6) (Calbiochem, OP43), p53 Ser-46 (Abcam, ab122898), p53 Ser-15 (Cell Signaling, 9284), MDM2 (ab1 and ab2) (Calbiochem, OP46T and OP115), p21 (ab6) (Calbiochem, OP79), cleaved lamin A (Cell Signaling, 2035), cleaved caspase-3 (Cell Signaling, 9061), GAPDH (14C10) (Cell Signaling, 2118), GPX4 (Abcam, 125066), and GLS2 (Abcam, ab113509). Secondary antibodies conjugated to horseradish peroxidase were used at a dilution of 1:10,000 (Jackson Immunoresearch). ECL was from Amaresham (RPN2232). Densitometry quantification of protein signals was performed using ImageJ software (Taira et al. 2007). Immunohistochemistry of formalin-fixed tissues and Western blotting were performed as described (Frank et al. 2011).

**qRT–PCR**

Cells were lysed using QIAshredder columns [Qiagen]. Total RNA was isolated using RNeasy minikits [Qiagen] and on-column DNase digestions [Qiagen] following the manufacturer’s protocol. Equal amounts of RNA from these samples were then used to create cDNA using a high-capacity reverse transcription kit [Applied Biosciences, 4366814]. qPCR was performed using Brilliant III UltraFast SYBR Green qPCR mix kits [Agilent Technologies] on a Stratagene Mx3005P device [Agilent Technologies]. Data analysis of fold changes in gene transcription levels was done using the MxPro program [Stratagene]. RNA expression levels were normalized to the housekeeping gene cyclophilin A.

**Gene silencing of Noxa, GLS2, and p38MAPK**

Cell lines with shRNA knockdown of Noxa and GLS2 were generated by infection with the lentiviral vector pLKO.1-puro carrying a shRNA sequence against mouse Noxa [shRNA1 [CGTGTGTTATTTGTAAGCATTAT; TRCN0000009706] and shRNA2 [GCACCCGACATAACTGTGTTTT; TRCN0000009709]] or GLS2 [shRNA1 [GAACCTGCATTATTCGGCATTAC; TRCN0000177991] and shRNA2 [CTCCCTCAATGAGGAAGGAAT; TRC N0000198612] (Open Biosystems). VSVG-pseudotyped lentivirus was generated by cotransfection of 293-F cells with shRNA constructs and packaging vectors according to the manufacturer’s protocols (Invitrogen, K4960-00). Lentivirus was added to cells with 6 μg/mL polybrene for maximum viral transduction. Stable cells were selected using 1 μg/mL puromycin, and gene knockdown was confirmed by qRT–PCR. p38MAPK [Mapk14] was silenced by transfection with siControl or SMARTpool Accell Mapk14 siRNA [A-040125-13].

**Cell viability assays, Annexin V staining, clonogenic survival**

For cell viability assays, cells were plated at a density of 2000 cells per well on a 96-well plate and left to grow overnight in complete growth medium at 37°C. Cells were then treated with the indicated drugs at the indicated concentrations and left to incubate for 72 h. Cells were then incubated with Alamar blue [Life Technologies, DAL1025] for 2 h at 37°C, and viability was read out according to the manufacturer’s protocol on a SynergyHT plate reader (BioTek), or the number of cells staining with Trypan Blue was counted using a hemacytometer. Data analysis (including logarithmic transformation, graphical analysis, and IC50 calculation) was conducted using Prism software [GraphPad]. Annexin V staining to detect apoptotic cells and cell viability assay were performed using Guava Nexcel reagent (Millipore, 4500-0450) on the Guava EasyCyte HT system according to the manufacturer’s protocols. For clonogenic survival assays, 5000 viable cells were plated on 10-cm plates in complete growth medium and allowed to grow for 1 wk. The medium was then removed, cells were stained using Crystal Violet (Sigma, C3886), and colonies were captured by camera and counted.

**DNA-binding assays**

For ChIP analysis, primary MEFs or H1299 T-Reg wild-type or S47 cells were grown and treated on 150-mm plates at 60%–80% confluency before being harvested. Assays were carried out as described [Frank et al. 2011], and qPCR was performed and analyzed as described above. Primers for ChIP-qPCR were designed based on established literature [the human cells used were p21, GLS2, and SCO2, the mouse cells used were p21, SCO2, and Noxa] or by using a p53 response element-predictive algorithm [Su et al. 2015] for previously unknown p53 response elements in murine GLS2. For the microsphere assay for protein–DNA binding, allele-specific p53 binding was evaluated using the MAPD assay, as previously described [Noureddine et al. 2009; Bandele et al. 2011]. All binding reactions were performed in triplicate.

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References


