



# Modulation of immune responses by the tumor suppressor p53

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## Abstract

The commonly held view of the tumor suppressor p53 as a regulator of cell proliferation, apoptosis and senescence has expanded greatly in recent years to cover many biological processes as well as external and internal stress responses. Since the discovery over 30 years ago of p53 as a cellular protein that co-precipitates with the large T antigen of Simian Virus SV40, there has been an intertwining of p53 activities with immune-related processes, especially as relates to cancer. A variety of interactions between the p53 and the immune stress systems are currently being addressed that suggest opportunities to utilize p53 in modulating immunological activities. Here, we discuss those interactions along with implications for human disease.

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**List of abbreviations:** ChIP, chromatin immunoprecipitation; CPEB, cytoplasmic polyadenylation element binding protein; HSC, hematopoietic stem cell; ISRE, interferon-sensitive response element; miRNAs, microRNAs; NOS, nitrogen species; p53RE, p53 response element; ROS, reactive oxygen species; TLR, Toll-like receptor; TNF $\alpha$ , tumor necrosis factor alpha; wild type, WT

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## p53 in the immune response: the ace up the sleeve

The tumor suppressor p53 is a sequence-specific transcription factor that is activated in response to various cellular stresses such as DNA damage, oncogene over-expression and associated uncontrolled cell proliferation. p53 functions mainly as a transcription factor and is a key component in preventing cancer development through regulation of apoptosis, cell cycle and senescence genes thereby helping to maintain genome stability within an organism. Alterations of p53 function through mutation or misregulation in the p53 network are common features in human cancers with over 80-90% of tumors having an altered p53 pathway [1, 2]. However, in recent years this “guardian of the genome” has been established as central to many additional biological processes including

autophagy, fertility, “stemness,” nutritional responses, development of cell motility/migration and cell-cell communication [3-5]. Recent studies have emphasized the role of p53 in modulating the human immune system, one of the most important defenses against external as well as internal threats including tumorigenesis.

In this review we explore the interactions between p53 and the immune system. The focus is mainly on the role that wild type (WT) p53 plays in immune-related processes such as inflammation, innate and adaptive responses as well as functional interactions of p53 with NF- $\kappa$ B, which is considered a key regulator in immune responses. Emphasis is placed on p53 as a transcription factor in modulating expression of target genes involved

in immunity pathways (see Figure 1).

The immune system is a collection of biological processes whose tasks in preventing disease include identification and destruction of pathogens and tumor cells. Given the broad diversity in p53 controls and functions, it is not surprising that p53 touches multiple aspects of immunity. For example, DNA damage can trigger p53 responses that help orchestrate clearance of damaged cells via the innate immune system [6, 7], which can influence tumor suppression. In addition p53 is up-regulated at sites of inflammation [8, 9], likely due to the appearance of reactive oxygen species (ROS) that might damage DNA and proteins. The seminal work of Xue and colleagues [10] demonstrated the functional relationship between p53 and the immune system in a mouse liver carcinoma model containing a “switchable” p53. In this study they showed that p53 and the immune system can cooperate to promote tumor clearance. They found that p53-dependent tumor regression was related to induction of a tumor cell-senescence program, associated differentiation, up-regulation of pro-inflammatory cytokines and activation of innate immune response.

p53 also appears to be involved during the generation of immune cells. In agreement with its role as a modulator in stem cell appearance, p53 can limit expansion of hematopoietic stem cells (HSC) [11, 12]. The HSC are multipotent, self-renewing progenitor cells for all differentiated blood cells in the lymphoid and myeloid lineages. Some responses during the interplay of p53 with the inflammatory and innate immune response appear also to be evolutionarily conserved across species. Recently, Fuhrman and collaborators [13] found that in the worm *Caenorhabditis elegans* the nucleolar proteins and p53

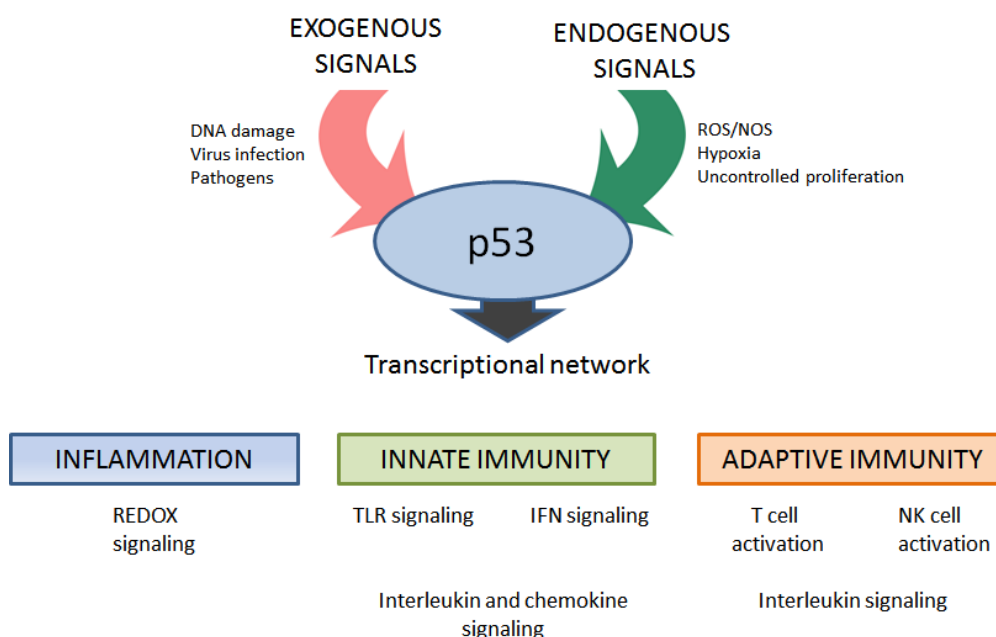
transcriptional activity play a role in defense responses against bacterial infections. They observed that activation of innate immunity through inhibition of nucleolar proteins requires potential immune effectors whose expression in worms in response to stress is regulated by the p53 homologue CEP-1.

## Inflammation and p53: maintaining homeostasis

Inflammation, a common immune response, is a protective first-responder attempt to remove injurious stimuli and to initiate healing. It is a complex signal-mediated reaction by vascular tissues to cellular insults such as pathogens and infectious agents, toxins, physical stress or damaged cells. Acute inflammation is an important mode of immune response, while chronic inflammation can cause tissue destruction or even autoimmunity.

p53 has several roles in inflammation including modifying cell growth and cellular behavior in response to DNA and inflammatory stressors. p53 is activated by DNA damage that is induced by both ROS and reactive nitrogen species (NOS) that are produced during inflammation [5, 14]. Also, the regulation of cellular ROS levels has been suggested to involve interaction of WT p53 with its  $\Delta 40$ -p53 and  $\Delta 133$ -p53 isoforms [14]. Mice that constitutively express an analogue of human  $\Delta 133$ -p53 ( $\Delta 122$ -p53) develop an autoimmune phenotype characterized by increased production of autoantibodies and pro-inflammatory cytokines [15]. p53 is also responsive to other inflammatory stressors such as TNF $\alpha$  [16].

As a transcription factor, p53 can modulate expression



**Figure 1.** Interactions of p53 with the immune system.

of several genes encoding enzymes involved in both production or elimination of reactive species contributing to inflammation including, for example, up-regulation of the antioxidant glutathione peroxidase (*GPXI*) [17], aldehyde dehydrogenase 4 (*ALDH1*) [18] and cyclooxygenase 2 (*COX2*) [19]. p53 also transactivates genes encoding pro-oxidant or redox active proteins, including the ROS generating enzyme proline oxidase (*POX*) [20] and *NCF2/p67hox* [21]. NCF2 is the cytosolic subunit of the NADPH oxidase enzyme complex involved in production of NADP<sup>+</sup> and superoxide from molecular oxygen. Also, p53 can mediate repression of genes affecting ROS repression including the inducible nitric oxide synthase *NOS2* genes and the mitochondrial superoxide dismutase *SOD2* [22].

Thus, p53 can play a significant role in modulating intracellular ROS/NOS levels to aid in appropriate balance of the inflammatory responses. In addition, since p53 is subject to modifications in the presence of reactive compounds, it can be considered a cellular sensor of redox changes [23]. Modulations of the p53 redox state can affect cell signaling as well as influence cell and tissue integrity [24].

The relationship between p53 and pathogenesis of inflammation-associated cancer and other immune related diseases extends beyond induction/restriction of inflammatory responses, all of which can be affected by p53 expression, mutation or alterations in its regulatory pathway. For example, there is greater invasion of inflammatory and fibroblast cells into IR damaged tissues in p53-null compared to WT mice [25]. Several autoimmune disorders characterized by increased or deregulated inflammation including rheumatoid arthritis, ulcerative colitis and lupus (systemic lupus erythematosus-SLE) exhibit elevated p53 protein or defective p53 functions [26-31], tying p53 dysfunction to autoimmunity. Furthermore, increased p53 protein expression within inflamed tissues has been associated with the appearance of somatic dominant-negative p53 mutations [29, 32, 33].

Innate and adaptive immune responses in p53 null mice can be skewed toward pro-inflammation, suggesting p53 may act as a negative regulator of inflammation (34-40). Additionally, p53 null mice are susceptible to autoimmune diseases including collagen-induced arthritis [31] and experimentally induced autoimmune encephalitis [34]. Also, p53 can directly repress *IL-4* [35], *IL-6* [36] and *IL-12* [37] promoter activities in murine cells, consistent with the view that p53 may inhibit autoimmune inflammation by suppressing the expression of inflammatory cytokine encoding genes. Moreover, as discussed below, p53 may inhibit inflammation through suppressing the mostly pro-inflammatory NF-kappa B transcription factor [38, 39].

## p53, viral infections and immune responses

Up-regulation of p53 in response to viral infections is a part of host cell defenses. For example, increased p53-dependent apoptosis can reduce viral replication [40]. Furthermore, “super p53 mice” that carry an extra p53 gene have slightly increased immune response over that in mice with 2 copies, and they are more resistant to viral infections than p53 null mice, which is due in part to the absence of a p53 apoptotic response in null mice [41].

Since the discovery over 30 years ago of p53 as a binding partner of SV40 LTag [42], its interaction with viral proteins provided early insights into p53 function [43-47]. Over the years, infections by several viruses, including Epstein-Barr, adenovirus, influenza A and HIV-1, were shown to activate the p53 pathway. The induction of p53 can lead to cell cycle arrest and apoptosis of the infected cells, which can result in control or elimination of the infection in human cells [48-50]. (Also, see recent reviews by Lazo and Santos [51] and Sato [52] for extensive descriptions of p53-virus interactions as well as mechanisms of inactivation.)

The ability of viruses to alter p53 functions and pathways is an important step in their establishment and pathogenesis in animal hosts. Described in Table 1 are examples of viral proteins that interact with p53. Viruses can disrupt p53 functions either directly or through cellular factors involved in downstream activities so as to override cell-cycle checkpoints or protect cells from p53-dependent apoptosis. p53 can be sequestered and/or inactivated by posttranslational modifications (phosphorylation, ubiquitination) induced by viral proteins or by modulation of host enzymes such as Mdm2 that promote proteasome degradation of p53 (see review by Lazo and Santos [51]). Soria and colleagues [53] recently reported that in addition to degradation of p53, which can be induced by adenovirus E1B-55k protein, another adenoviral protein E4-ORF3 promotes *de novo* H3K9me3 heterochromatin silencing at p53 target promoters, blocking p53–DNA binding. p53 can also positively regulate viral replication as found for HIV-1 viral infectivity factor (VIF) that interacts with p53 and promotes cell cycle arrest to facilitate HIV-1 replication [54].

In response to viral infections, one of the most efficient and rapid responses triggered by the immune system is induction of type I interferon mediated signaling. This response involves activation of the STAT (signal transducer and activator of transcription) signaling pathway and subsequent expression of antiviral genes. Several years ago, the seminal discovery of Takaoka *et al.* [40] revealed the existence of crosstalk between p53 and the IFN pathway when an interferon-sensitive response

Table 1. Examples of viral proteins that interact with p53.

Virus	Viral protein	Reference
<b>DNA viruses</b>		
Simian Virus 40	T large antigen	[137]
Adenovirus	E1B55K, E4-ORF3	[53, 138]
Epstein -Barr virus	EBNA-3C, BZLF1	[139, 140]
Human Papillovirus	E6	[141]
Kaposi's Sarcoma -Associated Herpes Virus	LANA	[142]
Hepatitis B	HBV-X	[143]
<b>RNA viruses</b>		
Hepatitis C virus	NS5A, NS3	[144, 145]
Human immunodeficiency virus 1	Tat	[146]
Influenza A	NS1	[147]
Human T-lymphotropic virus Type I	Tax	[148]
Parainfluenza virus 5	V protein	[149]

element (ISRE) was found in the promoter of the *p53* gene. *p53* was identified as one of the transcriptional targets of a type I IFN response following stimulation of cells with interferon-alpha/beta. Later, other studies revealed that *p53* can also be activated indirectly by other IFN-inducible proteins such as STAT-1 or promyelocytic leukemia protein [55, 56]. In addition, IFN- $\beta$  can activate *p53* in a dose-dependent manner in human peripheral blood mononuclear cells. This activation leads to altered expression of several genes involved in the *p53* signal pathway, including *p53* itself, which regulate cell proliferation and cell death following stimulation with IFN- $\beta$  [57].

Alternatively, *p53* can influence both IFN production and signaling, enhancing the antiviral response through direct transcriptional up-regulation of several IFN-inducible genes. Included are transcriptional activators such as interferon regulatory factor 9 (*IRF9*) [58] and *IRF5* [59], the toll-like receptor 3 (*TLR3*) whose gene product is involved in recognition of virus infection through sensing of double-stranded RNA [60] and activated protein kinase R (*PKR*) [61]. Interestingly, *PKR* is able to phosphorylate *p53 in vitro* [61-62], suggesting a possible functional loop. *p53* also induces expression of IFN-stimulated gene 15 (*ISG15*) that encodes a ubiquitin homologue capable of modifying several antiviral proteins, protecting them from degradation [63, 64]. The ubiquitin E3 ligase TRIM22 is another IFN inducible protein that is also a *p53* target gene [65]. It co-localizes with the centrosome in primary human mononuclear cells where it appears that both viral replication and protein degradation may occur [66].

Overall, these findings have established important roles for *p53* transcriptional activities in host defense against viral infection and support the relevance of *p53* in antiviral innate immunity.

### **p53 general influence on immune response pathways**

While there is substantial evidence that *p53* protects against inflammation (mostly under chronic conditions), recent studies in mouse and human cells reveal that *p53* may promote acute inflammation and immune responses ([67]; Lowe, Menendez and Resnick, unpublished), suggesting a delicate balance in the influence of *p53* on immunity pathways. Nearly 25% of *p53* null mice die before tumor development due to unresolved infections [68], suggesting a defective innate immune system. *p53* knockout mice are also more severely affected by influenza A virus due in part to reduction in cytokine and interferon production [69]. Below, we provide an overview of *p53* modulation and enhancement of innate and adaptive immune responses.

*p53* can influence several innate and adaptive immune pathways through regulation of genes involved in signaling (chemokines, interleukins), pathogen recognition (TLRs) and activation of specific subsets of immune cells such as T and B lymphocytes, NK cells and macrophages. Interleukins and chemokines are signaling molecules that affect a variety of cellular functions and are stimulated when tissue homeostasis is altered. Both are mediators of inflammation and play critical roles in host defense

by attracting and activating specific subsets of effector leukocytes, cells from the monocyte/macrophage lineage as well as natural killer (NK) cells.

Expression of chemokines and cytokines are subject to p53, depending on stimulus and cell type. p53 can increase transcription of several cytokines involved in innate immunity including colony-stimulating factor 1 (*CSF1*) and monocyte chemotactic protein (*MCP1*), chemokine CXC motif ligand (*CXCL1*) and interleukin 15 (*IL-15*) that attract macrophages, neutrophils, and natural killer cells, contributing to immune elimination of senescent cells [10, 70]. Activation of p53 also results in expression of *fractalkine*, a CX3C chemotactic factor for monocytes, NK cells, and T lymphocytes [71]. p53 is also able to repress directly or indirectly the expression of chemokines since loss of p53 has been found to result in overexpression of proinflammatory chemokines such as *CXCL2*, *-3*, *-5* and *-8*, *CCL20*, *CCL28* and *CXR4* in breast, ovarian and lung human cancer cells [72-75].

Chemokines also can influence p53 activities. For example, the macrophage migration inhibitory factor (MIF), a product of activated macrophages, sustains macrophage survival and pro-inflammatory function by inhibiting p53 [76], while MCP-1 can induce endothelial cell apoptosis *in vitro* through a p53-dependent mitochondrial pathway [77]. In addition, ROS production and subsequent premature senescence in response to CXCR2 activation is partially dependent on p53 [78]. Expression of the RANTES chemokine receptor CCR5 increases p53 transcriptional activity in breast cancer cells through activated protein kinase-dependent mechanisms by pertussis toxin, JAK2, and p38 mitogen. Importantly, this signaling circuit between p53 and CCR5 is involved in regulating proliferation of breast tumor cells *in vivo* [79].

The expression of several surface markers on cells involved in immune responses is subject to p53 regulation. Genotoxic activation of p53 leads to up-regulation of intracellular-adhesion molecule-1 (*ICAM-1*) mRNA and protein [80]. ICAM-1 (also known as CD54) is a member of the immunoglobulin gene superfamily and binds to several surface molecules that participate in cell-cell interactions. It can contribute to initiation of immune responses and is a co-stimulatory molecule for T-cell activation. The p53/ICAM-1 relationship may be important for immune surveillance since activation of ICAM-1 by p53 has been implicated in leukocyte infiltration during tumor-targeted inflammation, suggesting intercellular as well as intracellular guardian roles for p53 [81]. Other genes encoding surface cell markers targeted by p53 include *CD200* that is regulated during apoptosis and provides immune tolerance in murine dendritic cells (DCs) [82] and *CD59* (or *MIRL*, membrane inhibitor of reactive lysis) involved in complement signaling regulation [83].

Another surface marker CD43/leukosialin is repressed by p53. CD43 is an important contributor to immune homeostasis and is expressed on most hematopoietic cells. It regulates immune cell adhesion and proliferation [84]. Also, overexpression of CD43 activates the ARF-p53 tumor-suppressor pathway, which can lead to cell death [85].

## Boosting innate and adaptive immune responses with p53

Recently, employing a genome-wide *in silico* search we found that most members of the human Toll Like Receptor (TLR) gene family contain potential p53 targets [86]. The *TLR* genes (10 in humans) mediate innate immunity, providing front-line protection against pathogens through recognition of common features referred to as PAMPs (pathogen-associated molecular patterns). Many of the targets did not match the consensus sequence that contains two decamers of RRRCWWGYYY (where R = G,A; Y = C,T; W = A,T). Instead the p53 targets contained only a ½-site (single decamer) or a ¾-site, which we discovered earlier could support p53-mediated transactivation directly or in cooperation with other transcription factors such as estrogen receptor [87-90].

Using primary lymphocytes and alveolar macrophages from healthy subjects [86] as well as various cancer cell lines [91], we established that chromosomal damage can affect the innate immune system by altering expression of most *TLRs*. Furthermore, common anti-tumor agents led to p53-dependent regulation of expression of most *TLR* genes, resulting in modulation of downstream responses to cognate ligands. These results suggest new chemotherapeutic strategies based on agonists or antagonists targeting the TLR pathway [92]. Using an established tumor-bearing human p53 knock-in (Hupki) mouse model, Ishizaki *et al.* [93] demonstrated that treatment with the TLR ligands polyinosinic:polycytidylic acid (TLR3) and CpG-oligodeoxynucleotide (TLR9) in combination with heterologous p53 immunization enhances tumor regression.

p53 also has transcriptional targets in antigen cell-signaling pathways of T and B lymphocytes. The TAP1 protein (transporter associated with antigen processing) is required for the major histocompatibility complex (MHC) class I antigen presentation pathway that plays a key role in host tumor surveillance. In response to DNA damage, *TAP1* expression is induced by p53 in cooperation with its family member protein p73. This up-regulation enhances transport of MHC class I peptides, expression of surface MHC-peptide complexes and activation of the MHC class I pathway [94]. On the other hand, it has been reported that p53 reduces expression of *RGS13* [95], which inhibits G protein-coupled receptor signaling in B cells and mast

cells (MCs).

Regulation of the NK cells activities provides another example of p53 influence on the host immune system. These cells are specialized immune cells that eliminate foreign, stressed, transformed and senescent cells through specialized surface receptors, such as NKG2D [96, 97]. p53 can activate an antitumor immune response via direct transcriptional regulation of NK ligands *ULBP1* and *ULBP2* in cancer cells, which enhances NK cell activation [97, 98].

Innate and adaptive immunity are also connected to p53 through transcriptional regulation of microRNAs (miRNAs), which are small non-coding endogenous RNAs that bind complementary sequences of target mRNAs and regulate translation of specific genes. miRNAs affect inflammation and cancer [99] and are required for differentiation of immune cells [100]. Many miRNAs have been validated as p53 targets in immune cells including miR15a, miR16-1, miR34 a,b,c, let-7 miRNA and several members of the miR-17–92 cluster. Included in the miRNA targets are genes involved in immune related activities such as *Myb*, *BCL2* and *ULBP2* [96, 101]. Furthermore, dysregulation of these miRNAs is generally associated with poor clinical outcomes in several lymphoid malignancies. (See [102] for a description of the functional and clinical importance of microRNAs regulated by p53 in human lymphocytes.)

### p53 as a direct target in cancer immunotherapy

Since the immune system must distinguish between self and non-self antigens, p53 has been considered a target for immunotherapy. First identified in the sera of cancer patients more than 30 years ago [103, 104], the appearance of circulating antibodies against p53 has led to an alternative p53 antigen approach to cancer therapy. In addition to alteration of the p53 regulatory network in most human cancers, the overexpression of mutated p53 protein in several human tumors [105] suggests it could be a potential antigen in cancer immunotherapy since mutated p53 has features of non-self antigen [106]. One strategy is based on the observation that most p53 mutants are due to single amino acid changes that extend protein half-life, leading to accumulation in tumor cells [105, 107, 108]. Degradation of overexpressed mutant p53 in tumor cells might result in generation of peptide fragments specific for tumor cells. However, the large number of hotspot mutations in the DNA binding domain could limit development of vaccines against mutant p53 for use in “personalized medicine” [109]. In addition, the p53-specific T-cell repertoire may be restricted due to the ubiquitous expression of WT p53 in normal somatic tissues [110]. A variety of p53-based vaccines have proved

effective in animal models and have led to several clinical trials using immunization with p53 derived peptides [111–115]. Overall, immune responses to both WT and mutant p53 have provided opportunities in treating cancer patients including diagnosis, prognosis and immunotherapy [116, 117].

### p53 and NF-κB cross-talk in immune responses

As described above, roles for p53 in immunity are continually emerging. However, these must be considered in light of the other well-established modulators of immunity and inflammation especially NF-κB, a master regulator of immune responses .

Most discussions of p53 and NF-κB interactions have focused on their roles in cancer. While p53 and NF-κB are generally considered to be opposing factors where p53 promotes apoptosis while NF-κB enhances survival (reviewed in [118, 119]). They are capable of directly inhibiting each other resulting in opposing functional consequences. However, there are also positive interactions between these two transcription factors in a manner that is often context dependent (see below).

The complicated relationship between p53 and NF-κB is also seen in the context of immune responses. p53 can play an inhibitory role in NF-κB signaling and consequently the inflammatory response. For example, p53 inhibits IKK β and NF-κB mediated transactivation in IgE-mediated degranulation of mast cells and anaphylaxis [120]. Additionally, glucocorticoid inhibition of NF-κB activation and inflammation is dependent on p53 since p53 loss enhances NF-κB activation and impairs glucocorticoid rescue of death in an LPS shock mouse model [121]. Recently, Madenspacher and colleagues [122] showed up-regulation of several pro-inflammatory genes in the lungs of naïve p53 deficient mice compared to the WT counterparts, which appeared to be through enhanced NF-κB activation since the promoter region of nearly all of these genes contained a NF-κB DNA binding motif sequence.

Positive p53/NF-κB relationships in the immune response have also been described. p53 stabilization by treatment of cells with Nutlin-3 was able to enhance retrovirus-induced apoptosis of host cells in part through augmented activation of NF-κB [123]. p53 is also important in *Helicobacter pylori* infection; however, truncated p53 isoforms rather than WT p53 are implicated. Although *H. pylori* infection results in p53 degradation [124], the Δ133p53 and Δ160p53 isoforms are transcriptionally up-regulated through enhanced alternative P2 promoter activity within the p53 gene in a manner dependent on the *H. pylori* type IV secretion system (the syringe-like pilus structure whereby bacterial components are transferred

to host cells). The isoforms then enhance NF- $\kappa$ B transcriptional activity, but inhibit WT p53- and p73- pro-apoptotic and cell cycle arrest effects, which may provide a mechanism of adaptation of *H. pylori* in host gastric cells [125]. In another example of a p53/ NF- $\kappa$ B positive relationship in the immune response, p53 containing the P72 codon 72 polymorphism, but not the R72 variant, was able to bind to the p65 NF- $\kappa$ B subunit in the mouse thymus and cooperatively induced caspase 4/11 as well as some inflammatory-related genes including *Gdf-15* in response to DNA damage [67]. Thus, although signaling interactions between p53 and NF- $\kappa$ B in the immune response are generally negative, there are clear examples of positive interactions.

### p53 and NF- $\kappa$ B in senescence

In recent years, both p53 and NF- $\kappa$ B have been shown to play a role in senescence (irreversible cell cycle arrest) based on a strong link with inflammation [126]. After a limited number of divisions in somatic cells, senescence can be triggered by excessive DNA damage and by oncogenic stress to prevent transformation to a cancerous phenotype. The senescence process involves cell cycle arrest, which requires p53. On the other hand the senescence-associated secretory phenotype (SASP), and the production and secretion of cytokines and chemokines, require NF- $\kappa$ B [126-128]. All these factors appear to be linked through IL-6 signaling [128, 129]. In murine fibroblasts, activation of NF- $\kappa$ B by ATM in the DDR pathway directly induces the expression of the senescence regulator *IL-6*, which then causes further p53

and CPEB (cytoplasmic polyadenylation element binding protein) dependent signal transduction, ultimately leading to senescence (Figure 2) [128, 129]. In addition to the SASP requirement for senescence, an opposing SASP function can trigger immune system responses including recruitment of immune cells that destroy senescent cells. Interestingly, reactivation of p53 in tumor cells led to tumor regression in a mouse model through triggering senescence, expression of inflammatory genes and infiltration of immune cells that destroyed the senescent tumor cells [10]. While there is no evidence yet that p53 and NF- $\kappa$ B directly regulate each other during senescence, both factors have independent but positive roles in regulating senescence and the associated inflammatory phenotype, as summarized in Figure 2.

### The connection between p53 and immunity: concluding remarks

p53 has an important role in innate and adaptive immune responses where activation of p53 can be both beneficial and detrimental. In addition to cancer, there are many infectious disease implications, as we had proposed for a loop between pathogen detection by TLRs, inflammation and p53 induction [4, 86, 92]. Typical of p53 functions, the overall picture of interactions between the tumor suppressor p53 and immune system is complex and subject to specific scenarios including activating stimuli, cell type and even species.

The p53/immune interaction is especially relevant to cancer as indicated in a recent review of “hallmarks of cancer” by Hanahan and Weinberg [130], revisiting a

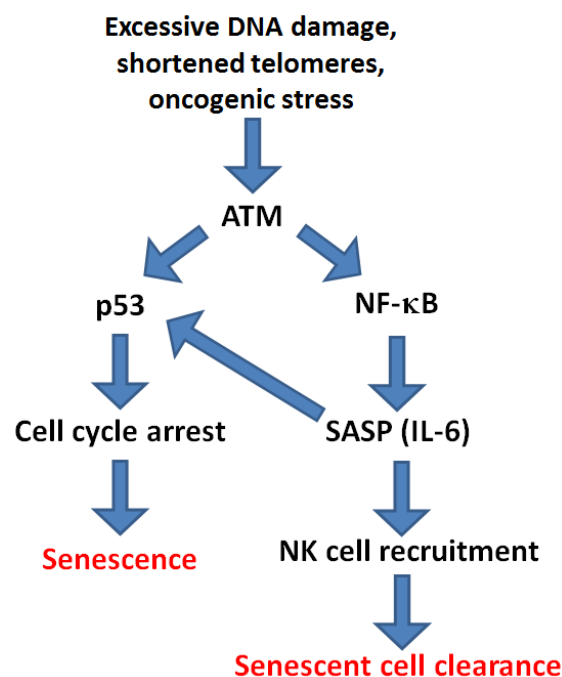


Figure 2. p53 and NF- $\kappa$ B signaling in senescence and SASP.

concept they developed a decade earlier [131]. Included in the hallmarks were avoidance of the immune response and tumor inflammation, highlighting the importance of the immune system. p53 is intimately related with these as well as other hallmarks [132]. Alteration of p53 expression can affect growth and death of cells that are directly responsible for tumors, modify immune surveillance and enhance inflammation. Thus, new opportunities in cancer/disease diagnosis and in chemotherapeutic strategies are expected to develop with further understanding of the interactions between p53 and the immune system.

Although there are nearly 30 immune-related genes (including miRNAs) targeted by p53, many new targets are expected to be identified in the near future through genome-wide methods. The combination of chromatin immunoprecipitation (ChIP) with high throughput sequencing (ChIP-seq) and expression analysis has already

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