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Interplay between Mdm2 and HIPK2 in the DNA damage response

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The tumour suppressor p53 is activated to induce cell-cycle arrest or apoptosis in the DNA damage response (DDR). p53 phosphorylation at Ser46 by HIPK2 (homeodomain-interacting protein kinase 2) is a critical event in apoptosis induction. Interestingly, HIPK2 is degraded by Mdm2 (a negative regulator of p53), whereas Mdm2 is downregulated by HIPK2 through several mechanisms. Here, we develop a four-module network model for the p53 pathway to clarify the role of interplay between Mdm2 and HIPK2 in the DDR evoked by ultraviolet radiation. By numerical simulations, we reveal that Mdm2-dependent HIPK2 degradation promotes cell survival after mild DNA damage and that inhibition of HIPK2 degradation is sufficient to trigger apoptosis. In response to severe damage, p53 phosphorylation at Ser46 is promoted by the accumulation of HIPK2 due to downregulation of nuclear Mdm2 in the later phase of the response. Meanwhile, the concentration of p53 switches from moderate to high levels, contributing to apoptosis induction. We show that the presence of three mechanisms for Mdm2 downregulation, i.e. repression of mdm2 expression, inhibition of its nuclear entry and HIPK2-induced degradation, guarantees the apoptosis of irreparably damaged cells. Our results agree well with multiple experimental observations, and testable predictions are also made. This work advances our understanding of the regulation of p53 activity in the DDR and suggests that HIPK2 should be a significant target for cancer therapy.

1. Introduction

Upon DNA damage, the tumour suppressor p53 is stabilized and activated to induce cell-cycle arrest or apoptosis by regulating expression of target genes [1]. Apoptosis can also be induced by p53 through transcription-independent mechanisms [2–4]. How p53 guides the cell-fate decision after DNA damage is still incompletely understood although it has been investigated extensively. The posttranslational modifications of p53 markedly influence the cellular outcome [5]. For example, the phosphorylation of p53 at Ser46 is induced only in response to severe damage, promoting cell death [6]. In human cells, HIPK2 (homeodomain-interacting protein kinase 2) specifically phosphorylates p53 at Ser46 after lethal damage caused by ultraviolet (UV) radiation or chemotherapeutic agents such as adriamycin (ADR) and cisplatin [7]. p53DINP1 (p53-dependent damage inducible nuclear protein 1) acts as a cofactor for HIPK2-mediated p53 phosphorylation [8,9]. However, such phosphorylation can be prevented due to Mdm2-dependent degradation of HIPK2 [10]. This raises the issue of how HIPK2 accumulates to promote apoptosis following severe damage.

On the other hand, HIPK2 can modulate Mdm2 activity through several mechanisms. Once p53 is phosphorylated by HIPK2 at Ser46, transcription of the mdm2 gene is reduced [11,12]. HIPK2 also interacts with Mdm2, promoting its nuclear export and proteasomal degradation [11,13]. Moreover, phosphatase and tensin homologue (PTEN), which is induced by p53 phosphorylated at Ser46 [12], represses the nuclear entry of Mdm2 by inhibiting the phosphorylation of Akt [14]. Therefore, HIPK2 and Mdm2 regulate each other in a complicated manner. It is intriguing to explore the significance of their interplay during the p53-mediated DNA damage response (DDR).
A series of experimental and theoretical studies have recently probed the dynamics and function of p53 in the DDR [15–17]. Although the phosphorylation of p53 at Ser6 is considered a critical event in apoptosis induction, how it is modulated by the interplay between Mdm2 and HIPK2 is largely unknown. Moreover, the p53 dynamics depend heavily on cellular context and stress type, exhibiting pulsatile or switch-like behaviours [18]. For example, a series of fixed pulses was observed in p53 levels upon ionizing radiation (IR) [19]. By contrast, p53 shows a graded behaviour with its concentration in proportion to the dose of UV radiation [20]. How the UV-irradiated cells make a decision between life and death remains unclear.

In this study, we aim to clarify the mechanism for cell-fate decision in response to UV radiation, focusing on the interplay between Mdm2 and HIPK2. We proposed an integrated model for the p53 signalling network, characterizing DNA repair, ATR (ataxia telangiectasia mutated (ATM) and Rad3-related) activation, p53 activation and determination of cellular output. We found that p53 undergoes one- or two-phase dynamics, depending on the severity of DNA damage. Upon mild damage, the concentration of p53 reaches a moderate level, and a transient cell-cycle arrest is induced; the cell resumes proliferation after the damage is fixed. Following severe damage, the concentration of p53 rises from a moderate to high level, and apoptosis is evoked. The interplay between Mdm2 and HIPK2 is crucial to a reliable cell-fate decision. The degradation of HIPK2 is important for survival of repairably damaged cells, whereas the HIPK2-dependent downregulation of nuclear Mdm2 promotes apoptosis of severely damaged cells. Our findings suggest a critical role for Mdm2 downregulation in p53-dependent tumour suppression.

2. Model and method
The p53 signalling network responding to DNA damage is rather complicated and can be considered as an information processing network [21]. We develop an integrated model of the p53 network, composed of four modules: the DNA repair module, the ATR sensor, the p53-centred feedback control module and the cell-fate decision module (figure 1). A large difference from our previous models [16,17] is that the current model characterizes the cellular response to UV radiation as well as the interplay between HIPK2 and Mdm2. To this end, we consider several new aspects including the detection of UV-induced DNA damage by ATR, repression of mdm2 transcription in apoptosis induction, degradation of Mdm2 by HIPK2, Mdm2-dependent HIPK2 degradation and regulation of p53Ser46 phosphorylation by HIPK2 and p38MAPK. The key points of the model are addressed as follows.

2.1. Detection and repair of DNA damage
When cells are exposed to UV radiation, DNA single-strand breaks (SSBs) are produced [22]. The level of DNA damage is denoted by \( L_4 \). For simplicity, the damage is assumed to be repaired at a constant rate (electronic supplementary material, equations (1) and (2)). SSBs are mainly detected by the ATR kinase, which is activated by phosphorylation [22]. Phosphorylated ATR (ATRp) indirectly promotes the further activation of ATR [23], thereby enclosing a positive-feedback loop.

The total level of ATR is assumed to be constant, because ATR is mainly regulated posttranslationally [24]. The dynamics of ATR are characterized by equations (3) and (4) of the electronic supplementary material. The phosphorylation and dephosphorylation of ATR are taken as enzyme-catalysed reactions and assumed to follow the Michaelis–Menten kinetics [25]. The activation rate of ATR is positively associated with the ATRp level and the extent of DNA damage [23]. In simulations, we set \( k_{\text{cat}} > k_{\text{cat}} \gg k_{\text{cat}} \) to ensure that ATR is inactive in unirradiated cells but is activated strongly upon DNA damage.

2.2. Regulation of p53 activity and cell-fate decision
Upon UV-induced DNA damage, p53 is activated by ATRp and regulated by several feedback loops. ATRp activates p53 in two manners, blocking the interaction between p53 and Mdm2 via phosphorylating p53 and inhibiting the ubiquitin-ligase activity of Mdm2 via phosphorylating Mdm2 in the nucleus [26,27]. Note that the c-Abl kinase is activated by ATM in response to IR and some DNA-damaging agents [28,29]. Active c-Abl activates p53 by phosphorylating Mdm2 [30]. However, c-Abl cannot be activated following UV irradiation [31]. Thus, we do not include c-Abl in the model.

Four forms of Mdm2 are included here: Mdm2c (dephosphorylated cytoplasmic Mdm2), Mdm2cp (phosphorylated cytoplasmic Mdm2), Mdm2n (nuclear Mdm2 with ubiquitin-ligase activity) and Mdm2np (phosphorylated nuclear Mdm2 without ubiquitin-ligase activity). The \( \text{mdm2} \) mRNA, \( \text{mdm2m} \), is also included in the model. Only nuclear p53 is considered, comprising non-phosphorylated p53 (p53, inactive form), primarily phosphorylated p53 (p53-arrester, primarily active form) and further phosphorylated p53 (p53-killer, fully activated form). Here, p53-arrester refers to p53 primarily phosphorylated at Ser15, whereas p53-killer is p53 further phosphorylated at Ser46, i.e. the doubly phosphorylated form; they promote cell-cycle arrest and apoptosis, respectively [6]. Phosphorylated p53 is collectively symbolized by p53p.

The production rate of p53 is assumed to be constant (electronic supplementary material, equation (6)), because p53 is mainly regulated by posttranslational modifications [32]. The conversion between inactive p53 and p53-arrester is controlled by its reversible phosphorylation [33]. It is assumed that the rate constants of p53 activation and inactivation, \( k_{\text{acp53}} \) and \( k_{\text{dcp53}} \), depend on the levels of ATRp and Wip1 (wild-type p53-induced phosphatase 1), respectively (electronic supplementary material, equations (9) and (10)) [27,34]. As the E3-ligase activity of Mdm2, is inhibited after it is phosphorylated by ATR [26], p53 is targeted for proteasomal degradation by Mdm2, rather than Mdm2np, which is characterized by the Michaelis–Menten kinetics [25]. We set \( k_{\text{dcp53}} \ll k_{\text{dcp53}} \) because the weak binding affinity of Mdm2n for p53-arrester and p53-killer prevents their degradation [33]. We consider only the degradation of p53 in the nucleus, whereas the Mdm2-dependent nuclear export and cytoplasmic degradation of p53 are ignored.

p53-arrester transactivates Wip1, p21 and p53DINP1, whereas p53-killer transactivates p53DINP1, p53AIP1 (p53-regulated apoptosis-inducing protein 1) and PTEN [6,12]. p53-killer is more efficient in inducing p53DINP1 [8], i.e. \( k_{\text{dcp53}} \gg k_{\text{dcp53}} \) in equation (31) of the electronic supplementary material. p53DINP1 promotes the accumulation of
p53-killer by acting as a partner of HIPK2 [8]. Wip1 promotes the reversion from p53-killer to p53-arrester by inhibiting p38MAPK, which is another kinase for p53 phosphorylation at Ser46 [35]. Following UV-induced DNA damage, p38MAPK is activated through the ATR–MAP3K–MAP2K–MAPK phosphorylation cascade [36]. Here, MAP3K mainly refers to TAO kinases [37], and MAP2K could be MKK3/6 [38]. The characterization of MAPK activation is derived from a recent modelling study on MAPK cascade [39]. All p53-mediated expression of genes is characterized by the Hill function, and the Hill coefficient is set to 4 given the cooperativity of the tetrameric form of p53 as a transcription factor [40].

The mdm2 gene is transactivated by both p53-arrester and p53-killer. Because mdm2 transcription is repressed after p53 phosphorylation at Ser46 [11,12], the rate constant of mdm2 transcription by p53-killer is much smaller than that by p53-arrester, i.e. $k_{s2mdm2} \ll k_{s1mdm2}$ in equation (11) of the electronic supplementary material. Such a reduction in mdm2 transcription is termed transcriptional suppression in the following text. After the synthesis of mdm2 transcripts, Mdm2 proteins are produced. Mdm2, can be phosphorylated by Akt, promoting its nuclear entry [41]. For simplicity, we assume that only Mdm2$_{tp}$ can enter the nucleus. Akt is activated by phosphatidylinositol-3,4,5-trisphosphate (PIP3) through phosphorylation [42], whereas it is deactivated indirectly by PTEN dephosphorylating PIP3 into phosphatidylinositol-4,5-bisphosphate [43]. Thus, there exists a double-negative feedback loop among p53, PTEN, Akt and Mdm2. Mdm2n also targets HIPK2 for proteasomal degradation [10], whereas HIPK2 promotes the degradation of Mdm2 [11]. Taken together, our model includes the double-negative feedback loops between Mdm2 and HIPK2 at both the transcriptional and posttranslational levels.

As downstream effectors of p53, p21 and p53AIP1 induce cell-cycle arrest and apoptosis, respectively [6]. p53AIP1 promotes the release of cytochrome c (CytoC) from mitochondria [44]. Subsequently, CytoC activates the caspase cascade in the cytoplasm [45]. Finally, caspase-3 (Casp3) is activated and apoptosis ensues. We consider the positive feedback between CytoC release and Casp3 activation, where Casp3 cleaves the inhibitors of CytoC release [46]. The enhancement of CytoC release by Casp3 and that of Casp3 activation by CytoC release are characterized by Hill functions. To ensure the irreversibility of apoptosis induction, the Hill functions should have high cooperativity [47], and thus the Hill coefficients are set to 4 (electronic supplementary material, equations (35) and (36)).

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**Figure 1.** Schematic diagram of the integrated model. The model is composed of four modules, separately characterizing the repair of DNA damage caused by UV, ATR activation, regulation of p53 activity and cell-fate decision. Based on its phosphorylation status, active p53 is further divided into p53-arrester and p53-killer. We focus on the interplay between Mdm2 and HIPK2: Mdm2 targets HIPK2 for proteasomal degradation, whereas HIPK2 promotes the accumulation of p53-killer followed by the repression of mdm2 transcription and sequestration of Mdm2 in the cytoplasm by PTEN. Dashed lines denote gene expression, while arrow-headed solid lines signify the transitions between different states. The promotion and inhibition of state transition are denoted by circle- and bar-headed lines, respectively. The implications of acronyms in the figure are listed in the electronic supplementary material, table S1.
2.3. Remarks on the model

Although we include various proteins related to regulation of p53-dependent apoptosis in the model, some others that influence p53Ser46 phosphorylation are still ignored for simplicity. It was suggested that HIPK2-mediated p53 phosphorylation at Ser46 facilitates p53 acetylation at K382 [7,48]. Li et al. [49] showed that p53 with mutations at three lysine sites in the central DNA-binding domain is deficient in inducing cell-cycle arrest, senescence and apoptosis, but retains its tumour suppressor function. How the phosphorylation and acetylation of p53 influence each other is not well understood and remains to be investigated. Several other kinases (like PKCθ and DYRK2) are also involved in the phosphorylation of p53 at Ser46 [7,50]. It would be intriguing to investigate whether there exists mutual regulation between Mdm2 and those kinases in apoptosis induction. The proteins such as PML, Axin and Daxx act as cofactors of HIPK2 in p53Ser46 phosphorylation [7,51], and their dynamic regulation of HIPK2 is worth considering. We do not explicitly characterize the activation of HIPK2 kinase activity; HIPK2 preferentially interacts with its activator Mdm2 in the cytoplasm. Moreover, PTEN can translocalize into the nucleus and form a complex with p53 after DNA damage, enhancing its transcriptional activity [53]. As how the subcellular localization of PTEN is regulated remains unclear, we do not consider the direct interaction in the nucleus. Overall, it is important to add more factors to the p53 signalling network and evaluate their roles when enough data are available.

2.4. Methods

The concentration of each species is represented by a dimensionless state variable in rate equations ( [...] denotes the concentration of species throughout the paper). These ordinary differential equations are presented in the electronic supplementary material. All the initial values of parameters are their lower steady-state values under unstressed conditions. The standard parameter values together with notes on parameter setting are listed in the electronic supplementary material, table S2. The robustness of the network dynamics to parameter variations is analysed in the electronic supplementary material, Text, and the corresponding data are presented in the electronic supplementary material, table S3. The unit of time is minutes, and the units of parameters are determined such that the concentrations of proteins are dimensionless. The rate equations are numerically solved using Oscill8 (http://oscill8.sourceforge.net). Experimentally, p53Ser46 phosphorylation and apoptosis begin to appear in response to UV radiation of 20–25 J m⁻² [6]. Here, the minimum \( L_D \) capable of inducing apoptosis is around 4.8 with the standard parameter setting, and thus one unit of \( L_D \) roughly corresponds to the damage caused by 5 J m⁻² UV radiation.

3. Results

3.1. Cell-fate determination by the p53 signalling network

DNA SSBs are induced upon UV irradiation [22]. The initial level of DNA damage, \( L_{\text{DO}} \), is taken as the input to the p53 signalling network. Our model can characterize the whole process from the detection and repair of DNA damage to the choice of cell fate. We associate the network dynamics with cellular outcome. To illustrate the typical dynamics of the p53 network, we show the temporal evolution of the output of each module under typical stress conditions (figure 2).

At \( L_{\text{DO}} = 3 \), the concentration of phosphorylated ATR rises quickly to a high level and remains there until the damage is fixed (figure 2a). Accordingly, the concentration of phosphorylated p53 is maintained at a moderate level until [ATRp] drops to a basal level. p21 is induced by p53p to arrest the cell cycle, whereas both [p53AIP1] and [Casp3] are kept at basal levels. Consequently, the cell recovers to normal proliferation, surviving mild DNA damage.

At \( L_{\text{DO}} = 10 \), [ATRp] remains at a high level for a long time (figure 2b). [p53p] exhibits two-phase dynamics: it stays at a moderate level in the first phase and switches to a high level in the second phase. p21 and p53AIP1 are induced in the first and second phases, respectively. Consequently, Casp3 is activated to evoke apoptosis. The timing of Casp3 activation (about 11 h) is consistent with the observation that p53Ser46 phosphorylation becomes marked between 8 and 12 h post-irradiation [6]. Here, the irreversible activation of Casp3 is considered a marker of apoptosis induction, and the events following apoptosis induction are not represented (as we concern only the determination of cell fate). Thus, [p53p] and [p53AIP1] still return to their basal levels after the damage is fixed. In fact, DNA repair proteins will be cleaved by Casp3, and the repair process will stop after Casp3 activation. Together, apoptosis is triggered before the damage can be entirely repaired in response to severe DNA damage.

The irreversibility of Casp3 activation results from the positive feedback between CytoC release and Casp3 activation. The relationship between the steady-state levels of Casp3 and p53AIP1 is shown in the electronic supplementary material, figure S1. The activation of Casp3 behaves like a bistable switch. [Casp3] switches to the 'ON' state when \([\text{p53AIP1}]) > \text{1.41} \) and remains there until \([\text{p53AIP1}]) < \text{0.003} \). The switching is actually irreversible because the basal level of p53AIP1 is 0.1. Therefore, Casp3 activation requires a sufficient amount of p53AIP1, but can be sustained robustly.

3.2. Detecting DNA damage by ATR

Here, we explore the mechanism for ATR activation. As shown above, [ATRp] exhibits a switch-like behaviour upon DNA damage. In the bifurcation diagram of [ATRp] versus \( L_D \) (ignoring DNA repair), there exists a saddle-node bifurcation (figure 3a). [ATRp] remains in the lower state when \( L_D \) is less than the upper threshold (0.139). When \( L_D \) exceeds...
this threshold, [ATRp] switches to the upper state. Reversely, [ATRp] returns to the lower state only when $L_D$ is less than the lower threshold (0.065). Thus, ATR is competent and reliable as a sensor of DNA damage [54].

Figure 3b displays the temporal evolution of [ATRp] at different initial levels of DNA damage. Given the repair of DNA damage, ATR can be activated when $L_{D0}$ ≥ 0.7. Notably, the duration of the activation state extends with increasing $L_{D0}$, and ATRp is deactivated only after the damage is effectively fixed. Collectively, ATR is sensitive to DNA damage, and the activation of ATR signifies the presence of DNA damage.

3.3. Dynamics of p53 and Mdm2

ATRp transmits the stress signal by activating p53. Upon sublethal damage (e.g. $L_{D0} = 3$), [p53p] accumulates to a moderate level (figure 4a). Although [p53-killer] is greater than [p53-arrester] after a transient, it is too low to induce apoptosis before the damage is fixed. On the other hand, [Mdm2m] evidently rises following p53 activation (figure 4b). As most Mdm2 molecules enter the nucleus, [Mdm2n] is close to zero. The majority of nuclear Mdm2 is phosphorylated by ATRp, and loses its E3-ligase activity [26]. Thus, [Mdm2n] rises mildly. Together, ATRp activates p53 and inhibits Mdm2 by phosphorylating them.

Following lethal damage (e.g. $L_{D0} = 10$), [p53p] first reaches a moderate level and then rises to a high level in the second phase, where p53-killer is absolutely dominant over p53-arrester (figure 4c). In contrast to p53p, [mdm2m] drops evidently in the second phase (figure 4d), consistent with the experimental observations that mdm2 transcription is repressed in the later phase of the cellular response to lethal damage [6,11]. As most of Mdm2 is sequestered in the cytoplasm, [Mdm2m] is much higher than [Mdm2n] in the second phase. These results indicate the connection between marked downregulation of nuclear Mdm2 and higher levels of p53p.

3.4. Dynamics of Wip1 and the p38MAPK cascade

In addition to HIPK2, p38MAPK is another kinase for p53Ser46 phosphorylation, and its activity can be inhibited by Wip1 via dephosphorylation. We show the temporal evolution of the levels of MAP3Kp, MAP2Kpp, p38MAPKpp, Wip1 and p53-killer in the electronic supplementary material, figure S2. Upon DNA damage, [MAP3Kp] and [MAP2Kpp] quickly rise to high platforms and remain there until the damage is fixed, whereas the dynamics of [p38MAPKpp] depend on the extent of DNA damage.

3.5. Repression of p53 phosphorylation at Ser46 by Mdm2-regulated HIPK2 degradation

It was reported that HIPK2 is degraded by Mdm2 to promote cell survival after sublethal DNA damage [10]. In our model, the drop in HIPK2 levels originates from its degradation by nuclear Mdm2. Upon mild damage, [HIPK2] falls slightly because [Mdm2n] rises mildly (figure 5a, upper). When the damage is severe, [HIPK2] remains lower than its basal level in the first phase but rises to a high level in the second phase, where [Mdm2n] drops to a rather low level (figure 5a, lower). These results agree with the observation that HIPK2 is differently expressed following distinct levels of DNA damage [10].

We further probe the influence of the rate constant of HIPK2 degradation by Mdm2, $k_{dHIPK2}$, on cellular outcome. With the standard parameter setting ($k_{dHIPK2} = 0.2$), p53-killer accumulates slowly and becomes remarkable after about 11 h poststimulus at $L_{D0} = 10$, whereas p21 is induced only in the first phase (cf. figures 2b and 4c). At $k_{dHIPK2} = 0$, [HIPK2] rises quickly towards a high level even at $L_{D0} = 3$ because of weakened degradation (figure 5b); the duration of p21-induced cell-cycle arrest is shortened significantly, and Casp3 is activated around 6.5 h poststimulation. These results agree with the experimental observation that the
HIPP2K\textsuperscript{1182R} mutant, which is resistant to Mdm2-regulated degradation, is more competent than the wild-type one in apoptosis induction [10]. At $k_{\text{HIPK2}} = 0.4$, [HIPK2] drops very fast to a low level even at $L_{\text{D0}} = 20$ (figure 5c); p21 is induced persistently throughout the response, whereas Casp3 is inactivated. Consequently, the severely damaged cell may undergo senescence when apoptosis is inhibited [55]. Together, the degradation rate of HIPK2 markedly affects the cell fate.

The minimum level of initial DNA damage required for apoptosis induction, $L_{\text{D0},n}$, reflects the sensitivity of the p53 pathway to DNA damage. $L_{\text{D0},n}$ becomes larger with increasing $k_{\text{HIPK2}}$ (figure 5d). When $k_{\text{HIPK2}}$ is less than 0.15, $L_{\text{D0}}$ is lower than 3.5. This means that the damaged cell becomes more sensitive to DNA damage when the degradation of HIPK2 by Mdm2 is inefficient. Differently, $L_{\text{D0}}$ rises quickly with increasing $k_{\text{HIPK2}}$ when it is greater than 0.15. At $k_{\text{HIPK2}} = 0.24$, for example, apoptosis is triggered only after very severe damage with $L_{\text{D0}} \geq 12$ (compared with 4.8 under the standard parameter setting). Together, the degradation rate of HIPK2 can markedly influence the sensitivity of the cell to DNA damage. These results suggest that inhibition of HIPK2 degradation is an efficient way to convert a cytostatic stimulus into a pro-apoptotic one [10].

Following severe DNA damage, the degradation of HIPK2 mainly occurs in the first phase and is affected markedly by the level of Mdm2$_{\text{on}}$ which depends on the rate constant $k_{1\text{mdm2}}$. Thus, $L_{\text{D0}}$ also varies as a function of $k_{1\text{mdm2}}$. $L_{\text{D0}}$ is rather low if $k_{1\text{mdm2}} < 0.008$ (figure 5e), in agreement with the finding that Mdm2 depletion results in apoptosis even in response to sublethal damage [10]. On the other hand, it becomes very difficult to induce apoptosis when Mdm2 is overexpressed. With further increasing $k_{1\text{mdm2}}$, $L_{\text{D0}}$ rises quickly and equals 21.2 at $k_{1\text{mdm2}} = 0.0117$. At $k_{1\text{mdm2}} = 0.015$, [p53$_{\text{S46}}$] remains at a moderate level and cannot be fully activated even at $L_{\text{DO}} = 20$ (figure 5f). p21 is induced persistently, whereas Casp3 remains inactive. Thus, the cell may become senescent, consistent with the observation that Mdm2 overexpression markedly inhibits p53-mediated apoptosis by enhancing HIPK2 degradation [10]. This provides another explanation for the carcinogenic role of Mdm2 in many tumours [56].

The ATR-induced Mdm2 phosphorylation only inhibits its E3-ligase activity rather than leads to its degradation [26]. The dephosphorylation of Mdm2$_{\text{np}}$ contributes to Mdm2 reactivation and HIPK2 degradation. To explore the effect of Mdm2$_{\text{np}}$ dephosphorylation on cell-fate decision, the rate constant $k_{\text{dphm2n}}$ is set to different values in the electronic supplementary material, figure S2. At $k_{\text{dphm2n}} = 0$ and $L_{\text{D0}} = 10$, [Mdm2$_{\text{on}}$] drops to a low level after a transient (electronic supplementary material, figure S3a). With increasing $k_{\text{dphm2n}}$, the downregulation of Mdm2$_{\text{on}}$ occurs later. When $k_{\text{dphm2n}}$ is large enough, [Mdm2$_{\text{on}}$] instead remains relatively high. Thus, it takes a longer time for [HIPK2] to reach its peak with increasing $k_{\text{dphm2n}}$ or [HIPK2] stays at low levels when $k_{\text{dphm2n}}$ is sufficiently large (electronic supplementary material, figure S3b). Consequently, Casp3 is activated later with increasing $k_{\text{dphm2n}}$ or it cannot be activated at all (electronic supplementary material, figure S3c). These results reveal that the reactivation of nuclear Mdm2 via dephosphorylation promotes the cellular resistance to apoptosis. This is also manifested in the electronic supplementary material, figure S3d, where $L_{\text{D0}}$ rises markedly with increasing $k_{\text{dphm2n}}$. Only when the extent of DNA damage exceeds some threshold can the anti-apoptotic effect of Mdm2 reactivation be overcome by downregulation of Mdm2, leading to apoptosis.

### 3.6. Mdm2 downregulation promotes p53 phosphorylation at Ser46

We have shown that the Mdm2-dependent HIPK2 degradation prevents phosphorylation of p53 at Ser46 and contributes to cell survival. Thus, downregulation of Mdm2 is essential for HIPK2-mediated p53Ser46 phosphorylation and apoptosis after severe DNA damage. Indeed, nuclear Mdm2 can be downregulated at both the transcriptional and posttranslational levels: repressed expression of mmd2 by p53-killer, sequestration of Mdm2 in the cytoplasm by p53-killer-induced PTEN, and HIPK2-dependent degradation of Mdm2 [11–13]. In this sense, there exists a positive-feedback mechanism in the induction of p53-killer, i.e. p53-killer promotes its own accumulation by downregulating Mdm2. The feedback strength is related to the rate constants of mmd2 and PTEN expression by p53-killer and HIPK2-dependent degradation of nuclear Mdm2, i.e. $k_{2\text{mdm2}}, k_{\text{dPTEN}}$ and $k_{1\text{mdm2}}$. In the following, we investigate how the mechanisms for Mdm2 downregulation affect p53Ser46 phosphorylation, whose extent is represented by the accumulation of p53-killer.

Figure 6a shows the bifurcation diagrams of the steady-state level of p53-killer versus $k_{\text{dPTEN}}$ under different conditions of Mdm2 downregulation at fixed $L_{\text{D0}} = 10$ (without DNA repair). With suppression of mmd2 expression and
HIPK2-dependent Mdm2 degradation, [p53-killer] rises monotonically with increasing $k_{\text{PTEN}}$; it remains relatively high even at $k_{\text{PTEN}} = 0$. Without transcriptional repression (i.e. $k_{s2mdm2} = k_{s1mdm2} = 0.007$), [p53-killer] shows bistability over some range and switches to the upper state only when $k_{\text{PTEN}} > 0.093$. This is, a sufficient amount of PTEN is required for the induction of p53-killer to trigger apoptosis in the absence of repression of mdm2 expression in the second phase. Without both transcriptional repression and HIPK2-dependent degradation ($k_{s2mdm2} = 0.007$ and $k_{s2mdm2n} = 0$), [p53-killer] is always at low levels. Thus, PTEN induction alone cannot ensure marked accumulation of p53-killer.

With $k_{\text{PTEN}} = 0$ and $k_{s2mdm2} = 0.001$, [Mdm2n] drops in the second phase due to a marked reduction in [mdm2m] at $L_{\text{D0}} = 10$ despite PTEN deficiency (figure 6b). Consequently, [p53-killer], [p53API1] and [Casp3] reach high levels in the late phase. Therefore, the marked downregulation of nuclear Mdm2 by transcriptional repression and HIPK2-dependent degradation is sufficient to induce p53-killer and apoptosis. On the other hand, with $k_{\text{PTEN}} = 0.2$ and $k_{s2mdm2} = 0.007$, enough PTEN is induced at $L_{\text{D0}} = 10$, and most of Mdm2 is sequestered in the cytoplasm despite abundant Mdm2 produced in the second phase (electronic supplementary material, figure S4a). Whereas [mdm2m] rises mildly in the second phase, [Mdm2n] falls markedly. Casp3 is still activated to trigger apoptosis (electronic supplementary material, figure S4b). Thus, suppression of mdm2 transcription and PTEN-induced sequestration of Mdm2 in the cytoplasm can complement each other in downregulating nuclear Mdm2.

In the absence of both transcriptional repression and PTEN induction (e.g. $k_{s2mdm2} = 0.007$ and $k_{\text{PTEN}} = 0$), the amount of mdm2 mRNA in the second phase is comparable to that in the first phase at $L_{\text{D0}} = 10$, and most of Mdm2 enters the nucleus to degrade p53 and HIPK2 (figure 6c). Accordingly, the levels of p53-killer and p53API1 in the second phase are much lower than those in figure 6b, and Casp3 cannot be activated to induce apoptosis. This may account for both the PTEN deficiency and Mdm2 overexpression in tumour cells [57].

We also show the diagrams of the steady-state level of p53-killer versus $k_{s2mdm2}$ for three cases in figure 6d. With both PTEN induction and HIPK2-dependent degradation of Mdm2, the change of $k_{s2mdm2}$ almost has no influence on [p53-killer]. Without PTEN induction ($k_{\text{PTEN}} = 0$), [p53-killer] drops monotonically with increasing $k_{s2mdm2}$. The repression of mdm2 transcription becomes critical for the induction of p53-killer in PTEN-deficient cells. When both the two mechanisms are impaired (i.e. $k_{\text{PTEN}} = 0$ and $k_{s2mdm2} = 0$), [p53-killer] settles at basal levels even at $k_{s2mdm2} = 0$. That is, suppression of mdm2 transcription alone cannot drive [p53-killer] to high levels. These results suggest that both transcriptional repression and HIPK2-dependent degradation of Mdm2 are required for remarkable p53Ser46 phosphorylation in PTEN-deficient cells.

We display how the minimum extent of DNA damage required for apoptosis induction varies with $k_{\text{PTEN}}$ in figure 6e. Generally, $L_{\text{Dm}}$ falls with increasing $k_{\text{PTEN}}$ because enhancing the expression of PTEN facilitates apoptosis induction. At $k_{s2mdm2} = 0.001$, only a small amount of Mdm2 could be induced in the second phase, and apoptosis can be triggered in response to DNA damage with intermediate intensities even at $k_{\text{PTEN}} = 0$. At $k_{s2mdm2} = 0.007$, a sufficient amount of cytoplasmic Mdm2 could be induced in the second phase; to induce apoptosis, abundant PTEN is required to sequester Mdm2 in the cytoplasm. Here, apoptosis cannot be induced when $k_{\text{PTEN}} \leq 0.07$, and $L_{\text{Dm}}$ drops markedly with increasing $k_{\text{PTEN}}$. Therefore, a sufficient amount of PTEN is required for apoptosis induction in the absence of marked repression of mdm2 transcription following p53Ser46 phosphorylation.

We also present the curves of $L_{\text{Dm}}$ versus $k_{s2mdm2}$ for different values of $k_{\text{PTEN}}$ in figure 6f. At $k_{\text{PTEN}} = 0.2$, $L_{\text{Dm}}$ rises moderately from 4.6 to 6.3 when $k_{s2mdm2}$ is increased from 0 to 0.007. Clearly, the presence of PTEN induction compensates for a deficiency in transcriptional repression. At $k_{\text{PTEN}} = 0$, apoptosis can be triggered only when $k_{s2mdm2}$ is below 0.002, and $L_{\text{Dm}}$ rises quickly from 5.6 to 12.1 as $k_{s2mdm2}$ is increased from 0 to 0.002. Thus, marked transcriptional repression is required for apoptosis induction in the absence of PTEN induction. Together, these two mechanisms can cooperate to downregulate Mdm2, and the malfunction in one mechanism can be compensated for by the other when the latter is strong enough. The significance of HIPK2-dependent Mdm2 degradation in apoptosis induction is further analysed in the electronic supplementary material, Text (see also the electronic supplementary material, figure S5).

**Figure 6.** Effects of downregulation of nuclear Mdm2 on the phosphorylation of p53 at Ser46. (a) Bifurcation diagrams of the steady-state level of p53-killer versus $k_{\text{PTEN}}$ at fixed $L_{\text{D0}} = 10$. Different lines correspond to different conditions of Mdm2 downregulation: normal case (black), without repression of mdm2 transcription (red), without both transcriptional repression and HIPK2-dependent Mdm2 degradation (green). (b,c) Time courses of the levels of mdm2m (black), Mdm2n (blue), p53-killer (magenta), p53API1 (green) and Casp3 (red) at $L_{\text{D0}} = 10$ with $k_{\text{PTEN}} = 0$ and $k_{s2mdm2} = 0.001$ (b) or $k_{s2mdm2} = 0.007$ (c). The steady-state level of p53-killer versus $k_{s2mdm2}$ at fixed $L_{\text{D0}} = 10$ under different conditions of Mdm2 downregulation: normal case (black), without PTEN induction (red) and without both PTEN induction and HIPK2-dependent Mdm2 degradation (blue). (e) Minimum extent of DNA damage required for apoptosis induction as a function of $k_{\text{PTEN}}$ under the same conditions corresponding to the red and black lines in (a). (f) Minimum of $L_{\text{D0}}$ required for apoptosis induction as a function of $k_{s2mdm2}$ under the same conditions corresponding to the red and black lines in (d).
4. Discussion and conclusion

It is assumed here that p53-arrester and p53-killer induce pro-arrest and pro-apoptotic genes, respectively. This assumption is based on several facts: p53 phosphorylation at Ser46 is closely related to the induction of pro-apoptotic genes including PTEN and p53AIP1 [6,12]; p21 is induced transiently, and its level significantly drops later in response to lethal damage [6]. The downregulation of p21 may result from either transcriptional inhibition or degradation [58,59]. Most recently, Kacikova et al. [60] reported that p53 transactivates both pro-apoptotic and pro-apoptotic genes proportionally to its levels and apoptosis is induced after p53 levels reach some threshold. These phenomena were observed in B5/589 cells, whereas the selective expression of p53-targeted genes was observed in MCF-7 and several other cell lines. Notably, p53 levels should also exceed some threshold to induce apoptosis in our work. It would be intriguing to clarify how to make a decision between cell-cycle arrest and apoptosis when p53 induces pro-arrest and pro-apoptotic genes simultaneously.

The degradation of HIPK2 by Mdm2 promotes cell survival. Upon sublethal damage, Mdm2 degrades HIPK2 to inhibit p53Ser46 phosphorylation, while the cell cycle is arrested by p21 to allow for DNA repair. HIPK2 can also be degraded by other E3-ligases such as p53-inducible Siah-1 [61]. However, Siah-1 becomes unstable after it is phosphorylated by ATM or ATR, leading to accumulation of HIPK2. It still remains unclear how the degradation of HIPK2 by Siah-1 is differently modulated based on the severity of DNA damage. Moreover, the E3- ligase for HIPK2 degradation may depend on cellular context and stress type.

The downregulation of nuclear Mdm2 in three manners represents a robust mechanism for p53 activation and apoptosis induction. Specifically, when one mechanism is impaired, apoptosis can still be triggered provided that the others function normally. Their action modes may be cell- and stress-type dependent. In U2OS cells, for example, PTEN induction and repression of mdm2 transcription promote the full activation of p53 in the DDR [12]. In PTEN-deficient MCF-7 cells, suppression of mdm2 transcription may play a major role in p53Ser46 phosphorylation; a remarkable reduction in mdm2 transcription was observed following lethal DNA damage caused by UV radiation [6]. By contrast, mdm2 transcription is repressed mildly in human embryonic kidney 293 cells after ADR treatment, and HIPK2-dependent Mdm2 degradation may contribute to apoptosis induction [11]. Collectively, downregulation of nuclear Mdm2 provides an effective manner to induce apoptosis.

In this study, we mainly explored how the interplay between Mdm2 and HIPK2 affects the p53-mediated cellular response to UV-induced DNA damage. We found that p53 is activated progressively: upon repairable damage, it reaches a moderate level and becomes primarily activated to induce cell-cycle arrest; it further rises to a high level and gets fully activated to trigger apoptosis when the damage is irreparable. HIPK2 can be degraded by nuclear Mdm2 to prevent apoptosis induction after sublethal damage. Following lethal damage, nuclear Mdm2 can be downregulated via three manners: suppression of gene transcription by p53-killer, inhibition of its nuclear entry by PTEN and degradation by HIPK2. As a result, HIPK2 accumulates and promotes p53 phosphorylation at Ser6. Our results suggest that inhibition of the E3-ligase activity of Mdm2 may make cells more sensitive to cancer treatment such that cancer cells can be killed more easily through p53-dependent apoptosis. Moreover, reactivation of PTEN in some tumours may improve the efficacy of cancer therapy.

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References


Supporting Material

Interplay between Mdm2 and HIPK2 in the DNA damage response

Xiao-Peng Zhang, Feng Liu and Wei Wang

Supplemental Method: Equations of the model

\[
\frac{dL_D}{dt} = -k_{\text{repair}} H(L_D)
\]  

\[
H(x) = \begin{cases} 
1 & x \geq 0 \\
0 & x < 0 
\end{cases}
\]  

\[
\frac{d[\text{ATR}]_p}{dt} = \left( k_{\text{cat}0} + k_{\text{catr}} \frac{L_D}{L_D + J_D} [\text{ATR}]_p \right) \frac{[\text{ATR}]}{[\text{ATR}]+[\text{catr}]} - k_{\text{deatr}} \frac{[\text{ATR}]_p}{[\text{ATR}]_p+J_{\text{deatr}}}
\]  

\[
[\text{ATR}] = [\text{ATR}]_{\text{tot}} - [\text{ATR}]_p
\]  

\[
[p53_\text{p}] = [p53-\text{arrester}] + [p53-\text{killer}]
\]  

\[
\frac{d[p53]}{dt} = k_{\text{sp}53} - k_{d\text{p}53_0}[p53] - k_{d\text{p}53}[Mdm2_n] \frac{[p53]}{[p53]+J_{\text{p}53n}} - k_{\text{acp}53}[p53] + k_{\text{dep}53}[p53-\text{arrester}]
\]  

\[
\frac{d[p53-\text{arrester}]}{dt} = k_{d\text{p}46}[p53-\text{killer}] + k_{\text{acp}53}[p53] - k_{\text{dep}53}[p53-\text{arrester}] - k_{d\text{p}53_0}[p53-\text{arrester}] - k_{d\text{p}53}[Mdm2_n] \frac{[p53-\text{arrester}]}{[p53-\text{arrester}]+J_{\text{p}53n}} - (k_{p46_1}[p53\text{DINP1}][\text{HIPK2}] + k_{p46_2}[p38\text{MAPK}pp]) \frac{[p53-\text{arrester}]}{[p53-\text{arrester}]+J_{\text{p}46}}
\]  

\[
\frac{d[p53-\text{killer}]}{dt} = (k_{p46_1}[p53\text{DINP1}][\text{HIPK2}] + k_{p46_2}[p38\text{MAPK}pp]) \frac{[p53-\text{arrester}]}{[p53-\text{killer}]+J_{\text{p}46}} - k_{d\text{p}46}[p53-\text{killer}] - k_{d\text{p}53_0}[p53-\text{killer}] - k_{d\text{p}53}[Mdm2_n] \frac{[p53-\text{killer}]}{[p53-\text{killer}]+J_{\text{p}53n}}
\]  

\[
k_{\text{acp}53} = k_{\text{acp}53_0} + k_{\text{acp}53_1} \frac{[\text{ATR}]_p}{[\text{ATR}]_p+J_{\text{at}}}
\]  

\[
k_{\text{dep}53} = k_{\text{dep}53_0} + k_{\text{dep}53_1}[\text{Wip1}]
\]  

\[
\frac{d[Mdm2m]}{dt} = k_s0\text{Mdm2} + k_s1\text{Mdm2} \frac{[p53-\text{arrester}]}{[p53-\text{killer}]+J_{\text{p}46}} + k_s2\text{Mdm2} \frac{[p53-\text{killer}]}{[p53-\text{killer}]+J_{\text{p}46}} - k_{d\text{Mdm2m}}[\text{Mdm2m}]
\]  

\[
\frac{d[Mdm2_c]}{dt} = k_t\text{Mdm2}[Mdm2m] - k_d\text{Mdm2}[Mdm2_c] + k_{d\text{Mdm2}} \frac{[\text{Mdm2}_c]}{[\text{Mdm2}_c]+J_{\text{p}dm}} - k_{p\text{Mdm2}}[\text{Akt}_p] \frac{[\text{Mdm2}_c]}{[\text{Mdm2}_c]+J_{\text{p}dm}}
\]
\begin{equation}
\frac{d[Mdm2_{cp}]}{dt} = k_{pmdm2} [Akt]_p \frac{[Mdm2_c]}{[Mdm2_c] + J_{pmdm2}} - k_{dpm2} [Mdm2_{cp}] + \frac{Mdm2_{cp}}{J_{dpm2}} + k_{omd2} ([Mdm2_n] + [Mdm2_{np}]) - k_{dmd2} [Mdm2_{cp}]
\end{equation}

\begin{equation}
\frac{d[Mdm2_{n}]}{dt} = k_{imd2} [Mdm2_{cp}] - k_{omd2} [Mdm2_n] + k_{dphm2} [Mdm2_{np}] - k_{phm2} [Mdm2_n]
- \left(k_{dmd2} + k'_{dmd2n} \frac{[HIPK2]}{[HIPK2] + J_{m2HIPK2}}\right) [Mdm2_n]
\end{equation}

\begin{equation}
\frac{d[Mdm2_{np}]}{dt} = k_{phm2} [Mdm2_n] - k_{omd2} [Mdm2_{np}] - k_{dphm2} [Mdm2_{np}]
- \left(k_{dmd2} + k'_{dmd2n} \frac{[HIPK2]}{[HIPK2] + J_{m2HIPK2}}\right) [Mdm2_{np}]
\end{equation}

\begin{equation}
\frac{d[Akt]}{dt} = k_{pakt} [PIP3] \frac{[Akt]}{[Akt] + J_{pakt}} - k_{dakt} [Akt]_p + J_{dakt}
\end{equation}

\begin{equation}
\frac{d[PIP3]}{dt} = k_p^2 [PIP2] + J_{p2} - k_p^3 [PTEN] \frac{[PIP3]}{[PIP3] + J_{p3}}
\end{equation}

\begin{equation}
[PTEN] = [Akt]_{tot} - [Akt]_p
\end{equation}

\begin{equation}
\frac{d[MAP3K]}{dt} = k_{cat1} [ATR_p] \frac{[MAP3K]}{J_{m1} + [MAP3K]} - k_{max2} \frac{[MAP3Kp]}{J_{m2} + [MAP3Kp]}
\end{equation}

\begin{equation}
\frac{d[MAP2K]}{dt} = k_{cat4} [MAP3K] \frac{[MAP2K]}{J_{m3} + [MAP2K]} - k_{max5} \frac{[MAP2Kp]}{J_{m4} + [MAP2Kp]}
\end{equation}

\begin{equation}
\frac{d[p38MAPK]}{dt} = k_{cat7} [MAP2K] \frac{[p38MAPK]}{J_{m7} + [p38MAPK]} - k_{cat8} [MAP2K] \frac{[p38MAPK]}{J_{m8} + [p38MAPK]}
\end{equation}
\[
\frac{dp38MAPK_{pp}}{dt} = k_{cat8} \left[ MAP2K_{pp} \right] \frac{[p38MAPK_p]}{[p38MAPK_p] + [p38MAPK_p]} - k_{max9} \left[ Wip1 \right] \frac{[p38MAPK_{pp}]}{[p38MAPK_{pp}] + [p38MAPK_{pp}]} + \frac{k_{max10} \left[ p38MAPK_{pp} \right]}{[p38MAPK_{pp}] + [p38MAPK_{pp}]} - k_{max10} \left[ p38MAPK_{pp} \right] \frac{[p38MAPK_{pp}]}{[p38MAPK_{pp}] + [p38MAPK_{pp}]}
\]

\[
\frac{dp53DINP1}{dt} = k_{sdinp10} + k_{sdinp11} \frac{[p53-killer]^4}{[p53-killer]^4 + [f_{sdinp11}]} + k_{sdinp12} \frac{[p53-killer]^4}{[p53-killer]^4 + [f_{sdinp12}]} - k_{ddinp1} \left[ p53DINP1 \right]
\]

\[
\frac{d[Wip1]}{dt} = k_{swip10} + k_{swip1} \frac{[p53-killer]^4}{[p53-killer]^4 + [f_{swip1}]} - k_{dwip1} \left[ Wip1 \right]
\]

\[
\frac{d[HIPK2]}{dt} = k_{sHIPK2} - k_{dHIPK2} \left[ HIPK2 \right] - k_{dHIPK2} \left[ Mdm2_n \right] - \frac{[HIPK2]}{[HIPK2] + [f_{dHIPK2}]} - k_{dHIPK2}
\]

\[
\frac{d[p53AIP1]}{dt} = k_{sAIp10} + k_{sAIp1} \frac{[p53-killer]^4}{[p53-killer]^4 + [f_{sAIp1}]} - k_{dAIp1} \left[ p53AIP1 \right]
\]

\[
\frac{d[CytoC]}{dt} = \left( k_{acytoc0} + k_{acytoc} \left[ p53AIP1 \right] \frac{[Casp3]^4}{[Casp3]^4 + [f_{Casp3}]} \right) \left( [CytoC]_{tot} - [CytoC] \right)
\]

\[
- k_{dCytoC} \left[ CytoC \right]
\]

\[
\frac{d[Casp3]}{dt} = \left( k_{acasp30} + k_{acasp3} \frac{[CytoC]^4}{[CytoC]^4 + [f_{CytoC}]} \right) \left( [Casp3]_{tot} - [Casp3] \right) - k_{dCasp3} \left[ Casp3 \right]
\]

(29) (30) (31) (32) (33) (34) (35) (36)
Supplemental Text:

**Coordination of HIPK2-dependent degradation and PTEN-dependent cytoplasmic sequestration of Mdm2**

Here, we evaluate the significance of HIPK2-dependent Mdm2 degradation in the induction of p53-killer. The rate constant of HIPK2-dependent Mdm2 degradation is denoted by $k_{dMdm2n}$. The bifurcation diagrams of the steady-state level of p53-killer versus $k_{sPTEN}$ are plotted for different values of $k_{dMdm2n}$ in the absence of repression of $mdm2$ transcription (i.e., $k_{s2mdm2}=0.007$) (figure S5a). With $k_{dMdm2n} = 0.008$ or 0.004, [p53-killer] shows bistability. [p53-killer] rises to high levels when $k_{sPTEN}$ exceeds some threshold. With $k_{dMdm2n}=0$, [p53-killer] cannot switch to high levels any more. We further show the temporal evolution of protein levels at $L_{X0}=10$ (figure S5b-d). Consistently, when [$Mdm2_n$] is kept at low levels, [p53-killer] rises to high levels, and Casp3 is activated. In contrast, when [$Mdm2_n$] is relatively high, Casp3 cannot be activated. Therefore, the coordination between HIPK2-dependent Mdm2 degradation and PTEN induction promotes apoptosis induction.

**Robustness analysis of the model**

Finally, we analyze the robustness of p53 dynamics to parameter variations. Although there exist 110 parameters altogether in the model, we only select 26 parameters involved in p53 regulation since we focus on the regulation of p53 activity by Mdm2 and HIPK2. The duration of the first phase, $T_1$, and the steady-state level of p53$_p$ in the second phase, $L_{p53}$, are chosen to describe the properties of p53 dynamics. $T_1$ can be considered as the time required for the marked induction of p53-killer. Each parameter is increased or decreased by 10% with respect to the standard setting, and the relative changes in $T_1$ and $L_{p53}$ are listed in Table S3.

$T_1$ and $L_{p53}$ exhibit different sensitivity to parameter variations. $T_1$ is more sensitive to the following parameters: the parameters related to Mdm2 regulation ($k_{dMdm2}, k_{s1mdm2}, k_{phm2n1}$ and $k_{imdm2}$), those associated with p53 regulation ($k_{sp53}$ and $k_{dp53}$), and those involved in regulation of p53Ser46 phosphorylation ($k_{swip1}, k_{sdinp11}, k_{p46}, k_{d0HIPK2}$ and $k_{dHIPK2}$). This occurs because all the above parameters affect p53Ser46 phosphorylation directly or indirectly. In contrast, $L_{p53}$ is robust to changes in most parameters except $k_{sp53}$, which directly controls the level of p53$_p$. Moreover, the sensitivity of p53 dynamics to other parameters
excluded in Table S3 can be easily deduced from the given ones. For example, both $T_1$ and $L_{p53}$ should be robust to variations in $k_{\text{deat0}}$ or $k_{\text{deat1}}$ since they are robust to changes in $k_{\text{acatr}}$, whereas $T_1$ should be sensitive to fluctuations in the rate constants of $p53\text{DINP1}$ and Wip1 degradation, $k_{\text{dwip1}}$ and $k_{\text{ddinp1}}$. Together, our results are fairly robust to changes in most parameters except those that control the induction of p53-killer and regulation of p53 levels.

**Supplemental Table S1:** Description of acronyms in Figure 1

<table>
<thead>
<tr>
<th>Acronym</th>
<th>Description</th>
<th>Acronym</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ATR</td>
<td>ATM- and Rad3-related</td>
<td>Mdm2</td>
<td>mouse double minute 2</td>
</tr>
<tr>
<td>p53-arrested</td>
<td>primarily phosphorylated p53</td>
<td>p53-killer</td>
<td>fully phosphorylated p53</td>
</tr>
<tr>
<td>PTEN</td>
<td>phosphatase with tensin homology</td>
<td>PIP3</td>
<td>phosphatidylinositol (3,4,5) triphosphate</td>
</tr>
<tr>
<td>PIP2</td>
<td>Phosphatidylinositol 4,5-bisphosphate</td>
<td>p38MAPK</td>
<td>p38 mitogen-activated protein kinase</td>
</tr>
<tr>
<td>MAP2K</td>
<td>MAP kinase kinase</td>
<td>MAP3K</td>
<td>MAP kinase kinase kinase</td>
</tr>
<tr>
<td>p53DINP1</td>
<td>p53-dependent damage-inducible nuclear protein 1</td>
<td>Wip1</td>
<td>wild-type p53-induced phosphatase 1</td>
</tr>
<tr>
<td>HIPK2</td>
<td>homeo-domain interacting protein kinase 2</td>
<td>p53AIP1</td>
<td>p53-regulated apoptosis-inducing protein 1</td>
</tr>
<tr>
<td>CytoC</td>
<td>cytochrome c</td>
<td>Casp3</td>
<td>Caspase-3</td>
</tr>
</tbody>
</table>

Notes: The subscripts “p”, “cp”, “np” refer to the phosphorylated form, cytoplasmic phosphorylated form and nuclear phosphorylated form of proteins, respectively. $\text{MAP3K}_p$, $\text{MAP2K}_{pp}$, $\text{p38MAPK}_{pp}$ are the active forms of the three kinases.
### Supplemental Table S2: Standard parameter values

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
<th>Note</th>
<th>Parameter</th>
<th>Value</th>
<th>Note</th>
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<tr>
<td>$k_{\text{repair}}$</td>
<td>0.008</td>
<td>Estimated</td>
<td>$k_{\text{acatr}}$</td>
<td>0.0003</td>
<td>$k_{\text{acatr}} &lt; k_{\text{acatr}}$</td>
</tr>
<tr>
<td>$k_{\text{acatr}}$</td>
<td>0.56</td>
<td>The fast kinetics of ATR (ref. 1)</td>
<td>$k_{\text{deatr}}$</td>
<td>0.5</td>
<td>Estimated (ref. 1)</td>
</tr>
<tr>
<td>$j_{\text{deatr}}$</td>
<td>2.5</td>
<td>Estimated</td>
<td>$j_{\text{acatr}}$</td>
<td>1.0</td>
<td>Ensuring ATR as a sensitive sensor of DNA damage [1]</td>
</tr>
<tr>
<td>ATR$_{\text{tot}}$</td>
<td>5.0</td>
<td>Estimated (ref. 1)</td>
<td>$j_{\text{D}}$</td>
<td>2.0</td>
<td>Estimated</td>
</tr>
<tr>
<td>$k_{\text{s0mdm2}}$</td>
<td>0.0025</td>
<td>$k_{\text{s0mdm2}} &lt; k_{\text{s1mdm2}}$ (ref. 1)</td>
<td>$j_{\text{atr}}$</td>
<td>1.0</td>
<td>Estimated (ref. 1)</td>
</tr>
<tr>
<td>$j_{\text{s1mdm2}}$</td>
<td>0.5</td>
<td>Estimated</td>
<td>$k_{\text{s1mdm2}}$</td>
<td>0.007</td>
<td>$k_{\text{s0mdm2}} &lt; k_{\text{s1mdm2}}$ (ref. 1)</td>
</tr>
<tr>
<td>$j_{\text{s2mdm2}}$</td>
<td>1.0</td>
<td>Estimated</td>
<td>$k_{\text{s2mdm2}}$</td>
<td>0.001</td>
<td>$k_{\text{s0mdm2}} &lt; k_{\text{s1mdm2}}$ (ref. 2)</td>
</tr>
<tr>
<td>$k_{\text{tmdm2}}$</td>
<td>0.03</td>
<td>Estimated</td>
<td>$k_{\text{dmmdm2m}}$</td>
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<td>Estimated</td>
</tr>
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<td>$j_{\text{dpmddm2}}$</td>
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<td>0.1 in ref. 3</td>
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<td>Ensuring the induction of p53-killer only upon lethal damage (ref. 5)</td>
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| $k_{cat1}$ | 0.17 | Estimated | $j_{dp46}$ | 0.2 | Ensuring the induction of p53-killer only upon lethal damage (ref. 5) |
| $k_{max2}$ | 0.17 | Estimated | $j_{m1}$ | 0.5 | Estimated |
| $k_{cat3}$ | 0.35 | Estimated | $j_{m2}$ | 0.5 | Estimated |
| $k_{cat4}$ | 1.6 | Estimated | $j_{m3}$ | 1.3 | Estimated |
| $k_{max5}$ | 0.83 | Estimated | $j_{m4}$ | 0.5 | Estimated |
| $k_{max6}$ | 0.83 | Estimated | $j_{m5}$ | 1.0 | Estimated |
| $k_{cat7}$ | 0.035 | Estimated | $j_{m6}$ | 1.0 | Estimated |
| $k_{cat8}$ | 0.5 | Estimated | $j_{m7}$ | 0.5 | Estimated |
| $k_{max9}$ | 1.5 | Estimated | $j_{m8}$ | 0.5 | Estimated |
| $k_{max10}$ | 0.017 | Estimated | $j_{m9}$ | 0.1 | Estimated |
| $[\text{MAP3K}]_{\text{tot}}$ | 2.0 | Estimated | $j_{m10}$ | 0.18 | Estimated |
| $[\text{p38MAPK}]_{\text{tot}}$ | 3.6 | Estimated | $[\text{MAP2K}]_{\text{tot}}$ | 2.0 | Estimated |
| $k_{swip1}$ | 0.035 | 0.042 in ref. 6 | $k_{swip10}$ | 0.001 | $k_{swip10} \ll k_{swip1}$ |
| $k_{dswip1}$ | 0.02 | Estimated | $j_{swip1}$ | 0.2 | Lower threshold for p53-induced Wip1 expression (ref. 4) |
| $k_{sdinp11}$ | 0.005 | $k_{sdinp11} \ll k_{sdinp12}$ (refs. 7 and 8) | $k_{sdinp10}$ | 0.0005 | $k_{sdinp10} \ll k_{sdinp11}$ (ref. 7) |
| $k_{sdinp12}$ | 0.015 | $k_{sdinp11} \ll k_{sdinp12}$ (refs. 7 and 8) | $j_{sdinp11}$ | 0.8 | Estimated |
| $k_{ddinp1}$ | 0.005 | Estimated | $j_{ddinp12}$ | 1.0 | Estimated |
| $k_{dHIPK2}$ | 0.2 | Estimated | $k_{dHIPK2}$ | 0.035 | Estimated |
| $k_{d0HIPK2}$ | 0.008 | $k_{d0HIPK2} \ll k_{dHIPK2}$ | $j_{dHIPK2}$ | 0.5 | Estimated |
| $k_{saip1}$ | 0.15 | $k_{saip10} \ll k_{saip1}$ | $k_{saip10}$ | 0.005 | $k_{saip10} \ll k_{saip1}$ |
| $k_{daip1}$ | 0.05 | Estimated | $j_{daip1}$ | 3.0 | Higher threshold for p53-induced p33AIP1 expression (ref. 4) |
| $k_{acccytoc0}$ | 0.001 | $k_{acccytoc0} \ll k_{acccytoc}$ | $k_{acccasp30}$ | 0.001 | $k_{acccasp30} \ll k_{acccasp3}$ |
| $k_{acccytoc}$ | 0.9 | Ensuring quick activation of caspases after cytochrome c release (ref. 9) | $k_{acccasp3}$ | 0.9 | Ensuring quick activation of caspases after cytochrome c release (ref. 9) |
| $k_{decasp3}$ | 0.07 | Ensuring quick activation of caspases after cytochrome c release (ref. 9) | $k_{decytoc}$ | 0.05 | Ensuring quick activation of caspases after cytochrome c release (ref. 9) |
| $j_{cytoc}$ | 0.5 | Estimated | CytoCtot | 3.0 | Estimated |
| Casp3$_{\text{tot}}$ | 3.0 | Estimated | $j_{casp3}$ | 0.5 | Estimated |

Notes: The unit of the parameters starting with “$k$” is “min$^{-1}$”, and all the other parameters are dimensionless.
**Supplemental Table S3: Parameter robustness analysis**

<table>
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<th>Parameter</th>
<th>+10%</th>
<th>-10%</th>
<th>Parameter</th>
<th>+10%</th>
<th>-10%</th>
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<td></td>
<td>$T_1%$</td>
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<td>$T_1%$</td>
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Notes: Each parameter is increased or decreased by 10% with respect to the default setting. “$T_1\%$” and “$L_{p53}\%$” denote the percentage of change in the duration of the first phase and the steady-state level of p53 in the second phase, respectively. Each bold number indicates that $T_1$ or $L_{p53}$ is more sensitive to variation in this parameter. In simulations, we obtained the two measures by computing the time required for [Casp3] to exceed 2.7 and the steady-state level of [p53] at $L_{Dam}=10$ without DNA repair.
Supplemental Figures

**Supplemental Figure S1**: Relationship between the steady-state levels of Casp3 and p53AIP1. The stable and unstable steady states are represented by solid and dashed lines, respectively.

**Supplemental Figure S2**: Temporal evolution of $[\text{MAP3K}]$ (black), $[\text{MAP2K}]$ (red), $[\text{p38MAPK}]$ (blue), $[\text{Wip1}]$ (magenta) and $[\text{p53-killer}]$ (green) at $L_{120}=3$ (a) or 10 (b).
**Supplemental Figure S3**: Effect of Mdm2ₚₚ dephosphorylation on HIPK2 degradation and cellular outcomes.

The rate constant of Mdm2ₚₚ dephosphorylation is denoted by \( k_{\text{dphm2n}} \). Time courses of the levels of Mdm2 (a), HIPK2 (b), and Casp3 (c) at \( L_{D0} = 10 \) with \( k_{\text{dphm2n}} = 0 \) (black), 0.005 (red), 0.01 (blue), 0.015 (magenta), or 0.02 (green). (d) Minimum of \( L_{D0} \) required for apoptosis induction as a function of \( k_{\text{dphm2n}} \).
**Supplemental Figure S4:** Temporal evolution of [mdm2m] (black) and [Mdm2n] (red) (a), and [p53-killer] (black), [p53AIP1] (blue), and [Casp3] (red) (b) with $k_{2mdm2}=0.007$ and $k_{PTEN}=0.2$ at $L_{D0}=10$.

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**Supplemental Figure S5:** Effect of HIPK2-dependent Mdm2 degradation on the cellular response to DNA damage. (a) Bifurcation diagram of the steady-state level of p53-killer versus $k_{PTEN}$ in the absence of repression of $mdm2$ transcription at fixed $L_{D0}=10$. The rate constant of HIPK2-dependent Mdm2 degradation is denoted by $k'_{dmdm2n}$. Different lines correspond to different values of $k'_{dmdm2n}$: 0 (blue), 0.004 (red), and 0.008 (black). Time courses of the levels of Mdm2n (b), HIPK2 (c), and Capsp3 (d) at $L_{D0}=10$ with $k_{PTEN}=0.2$ and $k'_{dmdm2n}=0$ (blue), 0.004 (red), or 0.008 (black).
References


