

## Novel Insights into Chk1 Regulation by Phosphorylation

Hidemasa Goto<sup>1,2</sup>, Kousuke Kasahara<sup>1,3</sup>, and Masaki Inagaki<sup>1,2\*</sup>

<sup>1</sup>Division of Biochemistry, Aichi Cancer Center Research Institute, Nagoya, Aichi 464-8681, Japan,

<sup>2</sup>Department of Cellular Oncology, Nagoya University Graduate School of Medicine, Nagoya, Aichi 466-8550, Japan, <sup>3</sup>Department of Oncology, Graduate School of Pharmaceutical Sciences, Nagoya City University, Nagoya, Aichi, 467-8603, Japan

**ABSTRACT.** Checkpoint kinase 1 (Chk1) is a conserved protein kinase central to the cell-cycle checkpoint during DNA damage response (DDR). Until recently, ATR, a protein kinase activated in response to DNA damage or stalled replication, has been considered as the sole regulator of Chk1. Recent progress, however, has led to the identification of additional protein kinases involved in Chk1 phosphorylation, affecting the subcellular localization and binding partners of Chk1. In fact, spatio-temporal regulation of Chk1 is of critical importance not only in the DDR but also in normal cell-cycle progression. In due course, many potent inhibitors targeted to Chk1 have been developed as anticancer agents and some of these inhibitors are currently in clinical trials. In this review, we summarize the current knowledge of Chk1 regulation by phosphorylation.

**Key words:** Chk1, cell-cycle checkpoint, phosphorylation

### Introduction

DNA damage or stalled replication is sensed by cell-cycle checkpoints, which arrest the cell cycle to allow the time necessary to repair damaged DNA or to relieve the stalled replication fork (Ciccio and Elledge, 2010; Jackson and Bartek, 2009). These checkpoint signals are mediated by two evolutionally conserved protein kinases, ataxia-telangiectasia mutated (ATM) (Cremona and Behrens, 2014; Shiloh and Ziv, 2013)/ATM- and Rad3-related (ATR; Fig. 1) (Cimprich and Cortez, 2008; Flynn and Zou, 2011; Zeman and Cimprich, 2014). ATM and ATR phosphorylate and then activate checkpoint kinase 2 (Chk2) (Antoni *et al.*, 2007) and Chk1 (Lukas *et al.*, 2003; Reinhardt and Yaffe, 2009; Zhang and Hunter, 2014), respectively (Fig. 1). The ATM-Chk2 pathway primarily reacts to DNA double strand

break (DSB; Fig. 1). With regard to cell-cycle arrest, the transcription factor p53 is one of the most important substrates for ATM and Chk2 (Fig. 1) (Appella and Anderson, 2001; McGowan, 2002; Polager and Ginsberg, 2009; Riley *et al.*, 2008). These phosphorylations block p53 degradation by E3 ligase MDM2 (Fig. 1) (Appella and Anderson, 2001; Polager and Ginsberg, 2009; Riley *et al.*, 2008; Wade *et al.*, 2013). The stabilized p53 induces p21, which binds and then inhibits cyclin-dependent kinases (CDKs; Fig. 1) (Polager and Ginsberg, 2009; Riley *et al.*, 2008). Unlike ATM-Chk2, the ATR-Chk1 pathway detects a broader spectrum of DNA abnormalities (e.g. UV light, DNA replication inhibition, interstrand DNA crosslinking, or DSB end resection; Fig. 1). With regard to cell-cycle arrest, Cdc25A phosphatase is an essential target for Chk1 (Fig. 1) (Boutros *et al.*, 2007; Goto *et al.*, 2012; Neely and Piwnicka-Worms, 2003). Chk1-induced phosphorylation triggers Cdc25A polyubiquitination and degradation (Fig. 1) (Boutros *et al.*, 2007; Busino *et al.*, 2004; Jin *et al.*, 2003; Neely and Piwnicka-Worms, 2003). Since Cdc25A is a critical phosphatase for CDK activation (Boutros *et al.*, 2007; Goto *et al.*, 2012), the activation of ATR-Chk1 pathway results in cell-cycle arrest (Fig. 1).

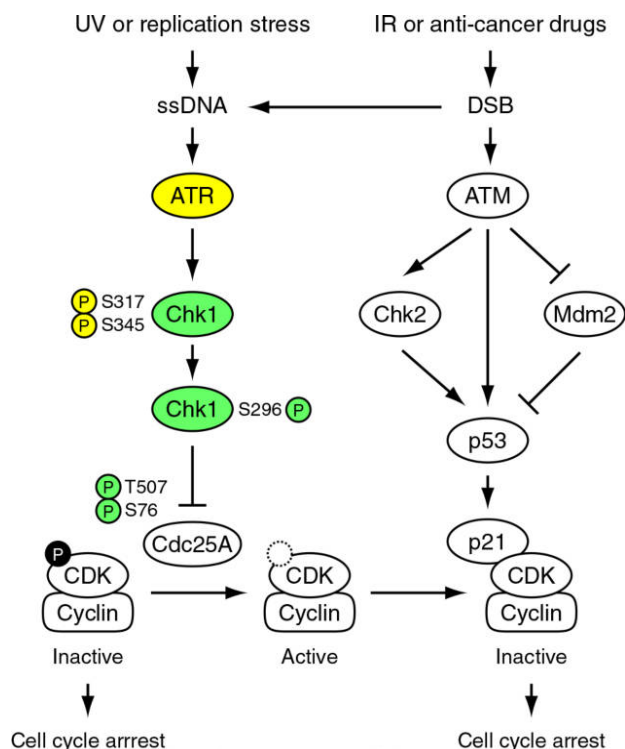
In cancer cells, the ATM-Chk2-p53 pathway is often impaired due to the mutations or deletions of *ATM*, *CHEK2*, and/or *TP53* (Antoni *et al.*, 2007; Cremona and Behrens, 2014; Goto *et al.*, 2012; Riley *et al.*, 2008; Shiloh and Ziv, 2013). These mutations are also identified as can-

\*To whom correspondence should be addressed: Masaki Inagaki, Division of Biochemistry, Aichi Cancer Center Research Institute, Nagoya, Aichi 464-8681, Japan.

Tel: +81-52-762-6111 (ext. 7020), Fax: +81-52-763-5233

E-mail: minagaki@aichi-cc.jp

Abbreviations: ATM, ataxia-telangiectasia mutated; ATR, ATM- and Rad3-related;  $\beta$ -TrCP,  $\beta$ -transducin repeated-containing protein; CDK, cyclin-dependent kinase; Chk, Checkpoint kinase; DDR, DNA damage response; DSB, DNA double strand break; MAPK, mitogen-activated protein kinase; MK2, MAPK-activated protein (MAPKAP) kinase-2; NES, nuclear export signal; NLS, nuclear localization signal; RSK, ribosomal S6 kinase; PKB, protein kinase B; ssDNA, single strand DNA; UV, ultraviolet.



**Fig. 1.** A schema of DNA damage/replication checkpoint responses. The ATM-Chk2-p53 pathway is activated by DNA double strand breaks (DSBs), whereas the activation of ATR-Chk1-Cdc25A pathway is induced by single strand DNA (ssDNA) adjacent to double strand DNA. At the S or G2 phase of the cell cycle, DSBs are processed to ssDNA, which secondly activates the ATR-Chk1-Cdc25A pathway. The activation of these pathways ultimately suppresses cyclin-dependent kinases (CDKs).

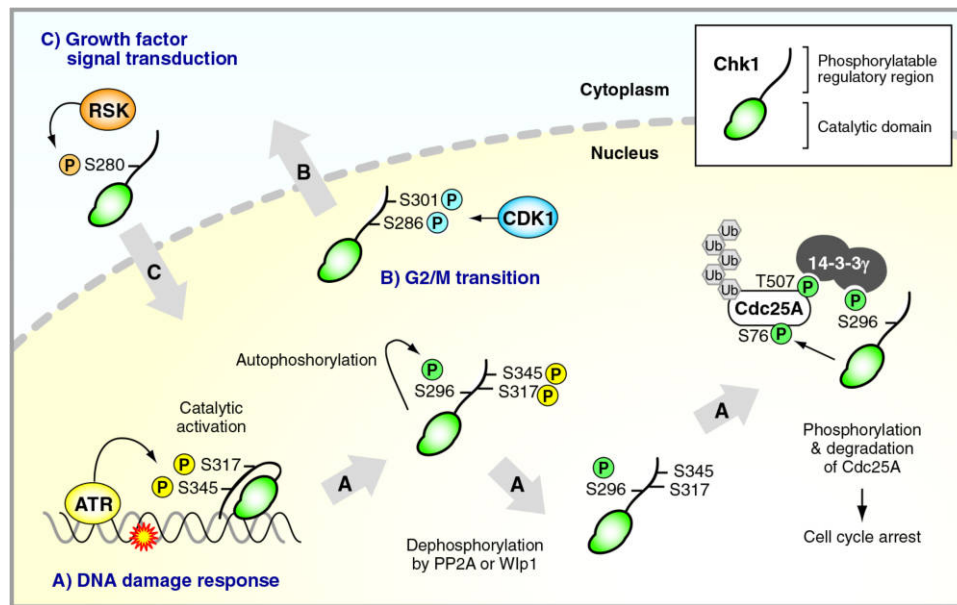
cer driver mutations involved in tumor initiation and progression (Kandoth *et al.*, 2013; Lawrence *et al.*, 2014; Vandin *et al.*, 2012). Due to this defect, cancer cells rely much more heavily on the ATR-Chk1-Cdc25A pathway for survival than normal cells (Goto *et al.*, 2012; Zhang and Hunter, 2014). Chk1 inhibitors were originally developed and tested to sensitize tumors to existing cancer therapies, such as radiation therapy and chemotherapy with various DNA-damaging agents and/or anti-metabolites (Carrassa and Damia, 2011; Dai and Grant, 2010; Ma *et al.*, 2011). Since Chk1 also regulates normal (unperturbed) cell-cycle progression (Goto *et al.*, 2012; Zhang and Hunter, 2014), Chk1 inhibitors are also expected to kill cancer cells as single agents (Carrassa and Damia, 2011; Maugeri-Sacca *et al.*, 2013; Thompson and Eastman, 2013). Due to the fact that the mechanism underlying Chk1 function in normal (unperturbed) cell-cycle progression remains poorly understood (Goto *et al.*, 2012; Zhang and Hunter, 2014), little is known about the mechanisms by which Chk1 inhibitors preferentially kill cancer cells without inducing exogenous DNA damages.

Chk1 phosphorylation by ATR is essential for cell-cycle checkpoint (especially at the intra-S phase or at the G2/M transition) (Capasso *et al.*, 2002; Niida *et al.*, 2007; Wilsker *et al.*, 2008) and conserved from yeast to mammals (Rhind and Russell, 2000). Recent studies have also revealed that Chk1 is phosphorylated and regulated by various types of protein kinases other than ATR (Goto *et al.*, 2012; Zhang and Hunter, 2014). In this review, we will summarize functional change of Chk1 by phosphorylation with a particular focus on human Chk1.

### Chk1 Phosphorylation by ATR

ATR activation requires the generation of structures containing single strand DNA (ssDNA) adjacent to double strand DNA (dsDNA; Fig. 1) (Cimprich and Cortez, 2008; Flynn and Zou, 2011; Zeman and Cimprich, 2014). Such ssDNA is coated with replication protein A (RPA) complex and then attracts the complex of ATR and its regulatory protein ATR-interacting protein (ATRIP) (Cimprich and Cortez, 2008; Flynn and Zou, 2011; Zeman and Cimprich, 2014). The accumulation of ATR/ATRIP complex to damage sites results in initial (weak) activation of ATR (Cimprich and Cortez, 2008; Flynn and Zou, 2011; Zeman and Cimprich, 2014). The ssDNA-RPA structure also functions as a platform to recruit a number of checkpoint regulators including Rad17, Rad9-Hus1-Rad1 (9-1-1) complex, DNA topoisomerase II binding protein 1 (TopBP1), Timeless (TIM), TIM-interacting protein (TIPIN), and Claspin to damaged sites (Ciccica and Elledge, 2010; Jackson and Bartek, 2009). ATR phosphorylates some of these recruited proteins (Cimprich and Cortez, 2008; Flynn and Zou, 2011; Zeman and Cimprich, 2014). The accumulation and phosphorylation of these checkpoint regulators further stimulates the catalytic activity of ATR (Ciccica and Elledge, 2010; Cimprich and Cortez, 2008; Flynn and Zou, 2011; Jackson and Bartek, 2009; Zeman and Cimprich, 2014). For the efficient phosphorylation of Chk1 by ATR, Chk1 needs to form a complex with Claspin (Chini and Chen, 2004; Kumagai and Dunphy, 2000; Kumagai *et al.*, 2004). Based on the localization of these proteins, ATR-induced Chk1 phosphorylation likely occurs at the sites of DNA damage on chromatin (Fig. 2) (Kasahara *et al.*, 2010; Smits *et al.*, 2006; Zhang *et al.*, 2005).

The activated ATR phosphorylates Chk1 at Ser317 and Ser345 in its C-terminal regulatory domain (Fig. 2 and Table I) (Zhao and Piwnicka-Worms, 2001). Chk1 phosphorylation at these sites (especially at Ser345) is critical for DNA damage checkpoint activation, replication control, and cell viability (Capasso *et al.*, 2002; Niida *et al.*, 2007; Wilsker *et al.*, 2008). Functionally, ATR-induced phosphorylation elevates Chk1 catalytic activity (Fig. 2 and Table I) (Katsuragi and Sagata, 2004; Walker *et al.*, 2009; Zhao and Piwnicka-Worms, 2001): Ser345 is a more critical phosphor-



**Fig. 2.** Functional change of Chk1 by phosphorylation. A schematic representation of functional change by Chk1 phosphorylations during DNA damage response (DDR; A), at the G2/M transition (B), or in response to growth factor stimulation (C).

**Table I.** FUNCTIONAL CHANGE BY PHOSPHORYLATION AT ITS C-TERMINAL REGULATORY DOMAIN

Site	Stimulus	Kinase	Interactor	Effect on Chk1 function
Ser-280	Growth factor UV irradiation	p90 RSK p90 RSK		Transport from cytoplasm to nucleus Acceleration of activation processes
Ser-286 & Ser-301	G2/M transition	CDK1		Transport from nucleus to cytoplasm
Ser-296	DNA damage response (DDR)	Chk1	14-3-3γ	1) Interaction with Cdc25A via 14-3-3γ 2) Release from DNA damage sites to entire nucleus
Ser-317 & Ser-345	DDR	ATR		Catalytic activation
Ser-345	DDR	ATR	14-3-3β/ζ	Nuclear retention
Ser-345	DDR	ATR		Polyubiquitylation & degradation

ylation site for catalytic activation (Walker *et al.*, 2009). The N-terminal catalytic domain of Chk1 adopts an open kinase conformation (Chen *et al.*, 2000) and the deletion of C-terminal domain increases Chk1 catalytic activity (Chen *et al.*, 2000; Katsuragi and Sagata, 2004). In fission yeast, the C-terminal domain contains a pseudo-substrate motif that facilitates the intra-molecular interaction (Biggins *et al.*, 2008). These observations suggest a model in which the phosphorylation at two residues relieves an auto-inhibitory effect by the C-terminal regulatory domain (Biggins *et al.*, 2008; Chen *et al.*, 2000; Katsuragi and Sagata, 2004; Walker *et al.*, 2009; Zhang *et al.*, 2009). However, the pseudo-substrate motif does not appear to be conserved in Chk1 from other species. In addition, the deletion of the C-terminus abrogates Chk1 function in fission yeast (Caparelli and O'Connell, 2013; Kosoy and O'Connell, 2008), suggesting that the regulatory domain may play diverse roles in Chk1 activity. Therefore, much is still

unknown about molecular mechanism by which Chk1 is structurally activated by phosphorylation.

Chk1-Ser345 phosphorylation regulates Chk1 function in addition to the catalytic activation. This phosphorylation creates a docking site for 14-3-3 β or ζ (Table I) (Jiang *et al.*, 2003). Since putative nuclear export signal (NES) sequence is located near Ser345 on Chk1 (Jiang *et al.*, 2003; Wang *et al.*, 2012), 14-3-3 β or ζ competes with Crm-1 (a protein required for nuclear export; also called exportin 1) to the binding to Chk1 (Jiang *et al.*, 2003), resulting in nuclear retention of Chk1 during DNA damage response (DDR; Table I) (Sanchez *et al.*, 1997). Since nuclear Chk1 activity is critical to establish a checkpoint (Matsuyama *et al.*, 2011; Reinhardt *et al.*, 2010), the checkpoint activation processes are accelerated by nuclear accumulation of Chk1, together with its catalytic activation.

At later stage of DDR, Chk1 binds E3 ligases (such as SCF<sup>Fbx6</sup> in the cytoplasm and Cul4A<sup>CDT2</sup> in the nucleus),

which requires preceding Chk1-Ser345 phosphorylation (Table I) (Huh and Piwnica-Worms, 2013; Leung-Pineda *et al.*, 2009; Zhang *et al.*, 2009, 2005). The interaction with E3 ligases induces proteasome-dependent Chk1 degradation (Table I), resulting in checkpoint termination and cell-cycle resumption (Huh and Piwnica-Worms, 2013; Leung-Pineda *et al.*, 2009; Zhang *et al.*, 2009; Zhang *et al.*, 2005). However, there is ~4-hr difference between Chk1 phosphorylation and the onset of degradation (Zhang *et al.*, 2005). Thus, much is still unknown about a signaling pathway from Chk1 phosphorylation to degradation during DDR.

### ***Chk1 Autophosphorylation (Especially at Ser296)***

During DDR, Chk1 is autophosphorylated at several sites including Ser296 just after Chk1 phosphorylation at Ser317 and Ser345 by ATR (which implies Chk1 catalytic activation; Fig. 2) (Clarke and Clarke, 2005; Kasahara *et al.*, 2010). After Chk1 autophosphorylation, ATR sites are rapidly dephosphorylated by phosphatases such as protein phosphatase 2A (PP2A) (Kasahara *et al.*, 2010; Leung-Pineda *et al.*, 2006) or PPM1D (also called Wip1 or PP2C $\delta$ ; Fig. 2) (Lu *et al.*, 2005). Ser296-phosphorylated Chk1 is diffusely detected in the entire nucleus (nucleoplasm; soluble nuclear fraction), whereas Ser345-phosphorylated Chk1 is predominantly observed at DNA damage foci (Kasahara *et al.*, 2010). These observations lead to a model in which this phosphorylation shift promotes the release of Chk1 from DNA damage foci on the chromatin (Fig. 2 and Table I). Since ATR-mediated phosphorylation induces Chk1 autophosphorylation (the most likely direct trigger to spread Chk1 signals over nucleus) (Kasahara *et al.*, 2010), this model fits with the observation that Ser345 phosphorylation triggers Chk1 release from the chromatin (Shimada *et al.*, 2008; Smits *et al.*, 2006; Zhang *et al.*, 2005). Since important downstream effectors such as Cdc25A are distributed diffusely in the nucleus (Bekker-Jensen *et al.*, 2006), the redistribution to the entire nucleus is essential for Chk1 to deliver checkpoint signals (Smits *et al.*, 2006).

Among Chk1 autophosphorylation sites, Ser296 is the most critical phosphorylation site for the checkpoint function (Kasahara *et al.*, 2010). Ser296 phosphorylation creates a docking site for 14-3-3 $\gamma$  (Fig. 2 and Table I) (Kasahara *et al.*, 2010). Since Chk1 also generates 14-3-3-binding sites on Cdc25A (Chen *et al.*, 2003), dimerization of 14-3-3 proteins (Mohammad and Yaffe, 2009) facilitates the formation of ternary complex among Chk1, Cdc25A, and 14-3-3 $\gamma$  (Fig. 2) (Kasahara *et al.*, 2010). This complex formation is essential for Chk1 to phosphorylate Ser76 on Cdc25A (Fig. 2), whereas it is dispensable for Cdc25 phosphorylation at Thr507 (a phosphorylation site required for 14-3-3 binding) (Chen *et al.*, 2003) by Chk1 (Kasahara *et*

*al.*, 2010). Ser76 is known as a rate-limiting phosphorylation site for Cdc25A degradation (Boutros *et al.*, 2007; Busino *et al.*, 2004; Jin *et al.*, 2003; Neely and Piwnica-Worms, 2003). Ser76 phosphorylation triggers additional Cdc25A phosphorylations by NEK11 (Melixietian *et al.*, 2009) and casein kinase 1 (CK1) (Honaker and Piwnica-Worms, 2010), which generate a  $\beta$ -TrCP (E3 ligase) recognition motif (phosphodegron) on Cdc25A. This proteasome-dependent Cdc25A degradation prevents premature activation of CDKs, resulting in cell-cycle arrest. Thus, Chk1-Ser296 autophosphorylation is one of critical steps for checkpoint signaling during DDR.

### ***Chk1 Phosphorylation by CDKs***

Chk1 also plays critical roles in normal (unperturbed) cell-cycle progression. Essential functions of Chk1 during development are well documented by the early embryonic lethality of Chk1-knockout mice (Liu *et al.*, 2000; Takai *et al.*, 2000). It is conceivable that Chk1 monitors replication forks in S phase (Maya-Mendoza *et al.*, 2007; Syljuasen *et al.*, 2005; Takai *et al.*, 2000). Chk1 activity is necessary to prevent late-origin firing and then irreversible replication fork collapse (Maya-Mendoza *et al.*, 2007). At the G2 phase, Chk1 inhibits premature mitotic entry (Enomoto *et al.*, 2009; Kramer *et al.*, 2004; Matsuyama *et al.*, 2011). Thus, Chk1 has an activity to negatively regulate cell-cycle progression even without exogenously introducing DNA damage. However, there is a debate as to whether or not ATR participates in Chk1 activity during normal (unperturbed) cell-cycle progression (Brown and Baltimore, 2000; de Klein *et al.*, 2000; Shimada *et al.*, 2008).

At the G2/M transition, Chk1 is phosphorylated at Ser286 and Ser301 by CDK1 (Shiromizu *et al.*, 2006), a mitotic inducer kinase (Fig. 2 and Table I). This phosphorylation stimulates Chk1 transport from the nucleus to the cytoplasm in a Crm-1-dependent manner (Fig. 2 and Table I) (Enomoto *et al.*, 2009; Matsuyama *et al.*, 2011). This transport relieves Chk1 inhibitory activity against CDK1 in the nucleus, leading to mitotic progression (Table I) (Enomoto *et al.*, 2009; Matsuyama *et al.*, 2011). This nuclear model appears to conflict with reports that a small fraction of Chk1 localizes to the centrosome to block premature mitotic entry (Kramer *et al.*, 2004; Tibelius *et al.*, 2009). However, an anti-Chk1 antibody used for immunostaining in these studies (Kramer *et al.*, 2004; Tibelius *et al.*, 2009) clearly cross-reacts with a centrosomal protein other than Chk1 (Matsuyama *et al.*, 2011). In addition, forced immobilization of Chk1 to the centrosome has little impact on the timing of mitotic entry, whereas Chk1-NLS (a mutant localized predominantly in the nucleus) clearly delays mitotic entry in the same experimental condition (Matsuyama *et al.*, 2011). Therefore, nuclear but not centrosomal Chk1 prevents CDK1 from unscheduled activa-

tion before mitosis. CDK1 relieves the inhibitory effect though nuclear exclusion of Chk1 by phosphorylation. In other words, there is a positive feedback loop between CDK1 and Chk1 at the G2/M transition.

As described above, accumulating data support the view that Chk1 functions as a negative cell-cycle regulator mainly in the nucleus. However, CDK1 is first activated at the centrosome during the G2/M transition (Jackman *et al.*, 2003), raising the question as to which factor(s) transduce checkpoint signals to the cytoplasm and the centrosome. Several groups pointed out a novel checkpoint pathway mediated by p38 and MK2 that operates parallel to Chk1 and is activated downstream of ATM and ATR (Bulavin *et al.*, 2001; Manke *et al.*, 2005; Raman *et al.*, 2007; Reinhardt *et al.*, 2007; Reinhardt and Yaffe, 2009). Chk1 controls nuclear events but p38-MK2 pathway regulates cytoplasmic events in the checkpoint responses (Reinhardt *et al.*, 2010). Since p38 phosphorylates and then inhibits Cdc25B (a centrosomal subtype of Cdc25) (Bulavin *et al.*, 2001), the p38-MK2 pathway may be one of likely candidates to transmit checkpoint signals to the cytoplasm and the centrosome.

Ser286 and Ser301 are also phosphorylated during DDR (Ikegami *et al.*, 2008). CDK2 or CDK1 is responsible for Chk1 phosphorylation at Ser286 and Ser301 during DDR (Ikegami *et al.*, 2008; Xu *et al.*, 2012, 2011). Unlike in mitosis, CDK-induced phosphorylation occurs simultaneously with the phosphorylation at Ser317 and Ser345 by ATR during DDR (Ikegami *et al.*, 2008). The co-existence of Ser345 phosphorylation likely turns off Crm-1-mediated nuclear export by CDK-induced phosphorylation, because Ser345 phosphorylation promotes Chk1 binding to 14-3-3  $\beta$  or  $\zeta$ , which competes with Crm-1 (Jiang *et al.*, 2003). Although CDK-mediated Chk1 phosphorylation was reported to reinforce checkpoint signaling (Xu *et al.*, 2012, 2011), less is known about the significance of this phosphorylation during DDR than at the G2/M transition.

### Chk1 Phosphorylation at Ser280

In quiescent cells (G0 phase cells), Chk1 is localized diffusely both in the nucleus and the cytoplasm (Li *et al.*, 2012). At the G0/G1 transition, Chk1 is phosphorylated predominantly at Ser280 by p90 RSK downstream of the Ras-MAPK cascade (Fig. 2 and Table I) (Li *et al.*, 2012). Ser280 phosphorylation promotes Chk1 translocation from the cytoplasm to the nucleus (Fig. 2 and Table I) (Li *et al.*, 2012). Since Chk1 is activated in the nucleus during DDR (Jiang *et al.*, 2003; Sanchez *et al.*, 1997), such nuclear accumulation is likely to be of great use to maintain genomic integrity during cell-cycle progression. In support of this hypothesis, Ser280 phosphorylation accelerates Chk1 activation processes after UV irradiation (Table I) (Li *et al.*, 2012).

In response to DNA damage during the G2 phase, Akt/PKB was also reported to induce Chk1 phosphorylation at Ser280 (King *et al.*, 2004; Shtivelman *et al.*, 2002) and to reduce nuclear localization of Chk1 (Puc *et al.*, 2005). However, the *in vitro* analysis reveals that Akt/PKB phosphorylates Chk1 at several sites, among which Ser280 is only a minor phosphorylation site (Li *et al.*, 2012). In addition, Chk1-Ser280 mutants behaved like Chk1 wild type in the G2/M checkpoint (Tonic *et al.*, 2010; Xu *et al.*, 2010). Although Akt/PKB negatively regulates the G2/M checkpoint (Henry *et al.*, 2001; Nimbalkar and Quelle, 2008; Shtivelman *et al.*, 2002; Xu *et al.*, 2010), there is a debate as to whether G2/M checkpoint is negatively regulated by Chk1-Ser280 phosphorylation.

### Conclusion

Remarkable progress has been made in understanding Chk1 regulation. Chk1 is phosphorylated by a variety of protein kinases. The resulting phosphorylations change catalytic activity, binding partners and/or localization of Chk1. The functional change(s) by phosphorylation(s) enable Chk1 to control not only DDR but also normal cell-cycle progression. The development of Chk1-targeted molecular therapies calls for a more advanced molecular understanding of Chk1 especially in normal cell-cycle progression in the absence of exogenous DNA damages.

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