Checkpoint kinase 2 regulates prostate cancer cell growth through physical interactions

with the androgen receptor

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Running title: CHK2 and AR interact to regulate PCa

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ABSTRACT

We have previously demonstrated that CHK2 is a critical negative regulator of AR

transcriptional activity, PCa cell growth, and androgen sensitivity. We have now

uncovered that the AR directly interacts with CHK2, and ionizing radiation (IR) increases

this interaction, which crests one hour after IR-induced DNA damage. This IR-induced

increase in CHK2–AR interactions requires AR phosphorylation on both serine81 and

serine308 and CHK2 kinase activity. Kinase-impaired CHK2 variants, including the

K373E variant associated with 4.2% of PCa, blocked IR-induced CHK2–AR interactions.

The destabilization of CHK2-AR interactions induced by the CHK2 variants impairs CHK2

function as a negative regulator of cell growth. CHK2 depletion in LNCaP cells increases

transcription of DNAPK and RAD54 and increases clonogenic survival. The data support

a model where CHK2 sequesters the AR through direct binding which in turn decreases

AR transcription and leads to suppression of PCa cell growth.

INTRODUCTION

Mammalian cells are continuously being bombarded by endogenous and exogenous forces that jeopardize the integrity of DNA. In response to DNA damage, a conserved network of signaling pathways known as the DNA damage response (DDR) is activated to maintain cell viability and genome stability [1]. Prostate cancer (PCa) remains one of the leading causes of death among men of all races (cdc.gov), as castration-resistant prostate cancer (CRPC) is currently incurable. Recently, the DDR has been a focus of PCa research since the androgen receptor (AR), a major driver of PCa, modulates the transcription of DDR genes [2] and DNA repair [3]. We have previously shown that checkpoint kinase 2 (CHK2) negatively regulates androgen sensitivity and PCa cell growth [4].

CHK2 is a serine/threonine protein kinase that plays a crucial role in sensing DNA damage and initiating the DDR, comprising of cell cycle arrest, DNA repair, and apoptosis [5]. CHK2 consists of an amino-terminal SQ/TQ cluster domain (SCD) where threonine 68 serves as a substrate for phosphorylation by ataxia-telangectasia mutated (ATM) kinase [6]; a carboxy-terminal kinase domain (KD) and nuclear localization sequence [7]; and a central forkhead-associated domain (FHA) that provides an interface for interactions with phosphorylated proteins [8]. Currently, there are approximately 24 CHK2 substrates in human cells that have been experimentally validated, including polo-like kinase 1 (PLK1), promyelocytic leukemia protein (PML), E2F1, p53, and cell division cycle 25C (CDC25C) [9]. These studies show that one mechanism CHK2 utilizes to affect cellular function is through direct protein-protein interactions.

For example, the association of CHK2 with PLK1 leads to its localization at

centrosomes where it regulates mitotic entry [10]. CHK2 autophosphorylation and

activation are regulated by the tumor suppressor PML within PML-nuclear bodies, which

are nuclear matrix-associated structures [11]. Binding to PML keeps CHK2 in an inactive

state within these PML-nuclear bodies. In return, activated CHK2 can phosphorylate PML

on S117 and induce PML-mediated apoptosis. CHK2 can also modify the transcription of

apoptotic genes through binding and S364 phosphorylation of the E2F1 transcription

factor in response to DNA damage, which stabilizes E2F1 and activates gene

transcription [12]. Another way that CHK2 regulates apoptosis is through p53

phosphorylation, resulting in the promotion of p53-mediated cell death [13]. The

interaction with the core domain of p53 induces an allosteric change in CHK2 which

permits p53 S20 phosphorylation [14]. Moreover, CHK2 modulates CDC25C localization

by associating with and phosphorylating CDC25 on S216, which creates a binding site

for 14-3-3 proteins [15]. 14-3-3 proteins in turn sequester CDC25C in the cytoplasm and

block the G2/M transition since cyclin dependent kinase 1 (CDK1) cannot be activated.

Finally, our group has shown that CHK2 co-immunoprecipitated with AR in PCa cells and

regulated growth, suggesting that AR may be a novel substrate of CHK2 [4]. Thus, given

the importance of CHK2 and AR to the DDR and prostate cancer, a full understanding of

the functional consequences of the CHK2–AR interaction is required, with the hope of

possible clinical applications towards CRPC.

Here, we uncovered novel molecular interactions between CHK2 and AR that

provide mechanistic insight into our observation that CHK2 negatively regulates prostate

cancer growth. We demonstrate that AR directly binds CHK2, and that this interaction

increases with ionizing radiation (IR) peaking one hour following exposure. The IR-

induced increase in CHK2–AR interaction requires AR phosphorylation on both serine 81

and serine 308. The binding of CHK2 with AR is disrupted with CHK2 kinase inhibitors,

suggesting that the kinase activity of CHK2 is required for the IR-induced CHK2–AR

interaction. This was verified using kinase-impaired CHK2 variants, including the K373E

variant associated with 4.2% of PCa. Furthermore, these CHK2 variants exhibit

diminished effect on prostate cancer cell growth. Interestingly, CHK2 depletion in LNCaP

cells increase transcription of DNAPK and RAD54, as well as clonogenic survival,

following IR while decreasing radiation-induced DNA damage repair.

RESULTS

CHK2 directly binds AR

We previously showed that AR coimmunoprecipitated with CHK2 immune

complexes in several prostate cancer cell lines [4]. To determine whether this co-

association was through direct protein-protein interaction, we performed far western

blotting. To generate purified protein for the far westerns, 293T cells were transfected

with mammalian plasmids expressing Flag-wtAR, Flag-ERK2, or V5-wtCHK2 (Fig. 1A).

We used Flag-ERK2 as a positive control since it has been reported that CHK2 physically

associated with ERK1/2 in cancer cells [16]. Flag-ERK and Flag-wtAR targets were

immunoaffinity purified and resolved by SDS-PAGE. The target proteins (AR and ERK)

on the membrane were probed with purified V5-wtCHK2 protein, crosslinked, and stained

with V5 antibodies to detect bound V5-wtCHK2. Membranes were also immunoblotted

with AR and ERK1/2 antibodies to confirm that the molecular weight of AR and ERK1/2

corresponded with the CHK2 signal, which then indicates direct protein-protein

interaction. We found that V5-wtCHK2 bound to Flag-wtAR, as well as the control Flag-

ERK2. Moreover, we observed similar results when we performed the converse

experiment and observed that the HA-wtAR probe directly associated with the target

protein Flag-wtCHK2 (Fig. 1B). These data indicate that the interaction of AR with CHK2

is authentic and direct.

Radiation increases CHK2-AR association

Since IR is a standard of care for patients with localized advanced prostate cancer

and CHK2 is a known mediator of the DDR, we wanted to assess the impact of IR on

CHK2–AR interactions. To examine the effect of radiation on the binding of AR to CHK2,

hormone-sensitive LNCaP and castration-resistant Rv1 cells were exposed to 6Gy IR,

which is representative of the fractionated dose of IR prostate cancer patients receive

[17]. CHK2 immune complexes were generated one hour following radiation. The AR

signal was quantified and normalized to total CHK2 protein (Fig. 2). IR significantly

increased endogenous CHK2-AR immune complexes by 2-fold and 1.8-fold in LNCaP

(Fig. 2A) and Rv1 (Fig. 2B) cells, respectively. Rv1 cells also express AR variant 7 (AR^{V7}),

which is a truncated isoform of AR that lacks the ligand binding domain (LBD) [18].

Interestingly, endogenous AR^{V7} also bound endogenous CHK2, and IR induced a similar

increase in CHK2 – AR^{V7} complexes as that observed with full length AR. Thus, these

results suggest that IR drives CHK2 to bind both full length and variant AR.

To further characterize the effect of radiation on CHK2-AR associations, we

evaluated the kinetics of the increase in CHK2–AR protein complexes in response to IR.

CHK2 was immunoprecipitated from irradiated LNCaP and C4-2 cells 1, 4, and 24 hours

following IR exposure (Fig. 2C). We found that AR was maximally bound to CHK2 one

hour after radiation treatment in both cell lines. This interaction was dramatically reduced

to near baseline levels by 4hrs, and returned to baseline levels 24hrs after IR.

Interestingly, we noticed that the temporal protein binding of CHK2 to AR paralleled the

activation state of CHK2, as represented by CHK2 phosphorylation on threonine 68 (Fig.

2C) [Matsuoka, 1998]. Thus, these data show that the CHK2–AR protein complexes are

transient, cresting one hour following IR. Furthermore, these observations suggest that

the interaction between CHK2 and AR may be regulated by the activation state of CHK2.

AR phosphorylation regulates CHK2–AR interaction

The phosphorylation of AR on serine 81 (S81) by CDK1 and CDK9 stimulates AR

transcriptional activity and growth of PCa cells [19]–[21]. Whereas, AR phosphorylation

on serine 308 (S308) represses transcription and proliferation and alters AR localization

during mitosis [22], [23]. To address whether S81 or S308 phosphorylation influences

CHK2–AR complexes, LNCaP cells were transduced with lentiviral particles containing

wtAR or AR mutants S81A or S308A (Fig. 3A). The association of AR was analyzed from

endogenous CHK2 immune complexes generated one hour after irradiation. There was

a 4-fold increase in AR co-immunoprecipitating with CHK2 after IR treatment of cells

expressing wtAR. However, neither S81A nor S308A increased in association with CHK2

upon IR treatment indicating that phosphorylation of AR on S81 and S308 are required

for the IR-induced increase in the interaction between CHK2 and AR.

The requirement for irradiation of AR expressing target cells and AR

phosphorylation for the IR-induced increase in CHK2–AR association led us to test if AR

phosphorylation on S81 and S308 were increased in response to IR. AR was

immunoprecipitated from irradiated cells, and phospho-S81 and phospho-S308 were

measured by western blotting using phospho-specific antibodies to those sites [20], [24]

(Supplemental Figure 1). There were no significant consistent changes in S81 or S308

phosphorylation in response to radiation in either cell line. Thus, these findings indicate

that while the intensity of S81 and S308 phosphorylation does not markedly change with

IR, S81 and S308 phosphorylation is required for CHK2–AR interactions.

CHK2 kinase activity is required for CHK2–AR interaction

To determine if CHK2 kinase activity was necessary for the CHK2–AR association,

we tested if CHK2 mutants that are found in PCa and have impaired kinase activity could

interact with the AR, and if that interaction increased with IR. We expressed Flag-

wtCHK2, Flag-K373E, or Flag-T387N in combination with HA-wtAR in LNCaP cells. The

K373E CHK2 mutation impairs CHK2 function suppressing cell growth and promoting

survival in response to IR, as a result of reduced kinase activity due to the disruption of

CHK2 autophosphorylation [25]. Less is known about the heterozygous missense

mutation T387N, but it is reported to diminish kinase activity, and thus, CHK2 function

[26]. Flag-CHK2 immunoprecipitations were performed and HA-AR association was

evaluated (Fig. 3B). In response to IR there was a striking increase in CHK2–AR co-

association in cells expressing Flag-wtCHK2 and HA-wtAR. However, the amount of IR-

induced increase in CHK2–AR association in cells expressing either K373E or T387N

was dramatically reduced. Therefore, these data indicate that the kinase activity of CHK2

is required for the interactions of CHK2 and AR, and that the CHK2 mutant associated

with PCa, T387N, has a diminished ability to interact with the AR.

IR increases direct CHK2–AR binding

To both confirm that IR induces the increase of CHK2–AR protein complexes and

determine if the increase is due to direct protein-protein interaction, we carried out far

western blotting where target (Flag-wtAR and Flag-ERK2) or probe proteins (V5-wtCHK2)

were isolated from cells either irradiated with 6Gy 48hrs following transient transfection,

and purified one hour after radiation exposure, or kept untreated prior to immunoaffinity

purification of target and probe proteins. When the cells expressing the V5-wtCHK2 probe

and Flag-wtAR target were irradiated there was a 2-fold increase in V5-wtCHK2 binding

to the target Flag-wtAR in response to IR (Fig. 4A). However, when the V5-wtCHK2 probe

was not treated with IR, no increase in probe binding to target was observed (Fig. 4B).

Together, these data indicate that radiation of cells expressing the V5-wtCHK2 probe is

required for the increased CHK2–AR interaction that occurs in response to IR. Since IR

increases the activity state of CHK2 as measured by phosphorylation of CHK2, this result

supports the above data indicating that CHK2 kinase activity is required for the IR induced

CHK2–AR association.

AR and CHK2 activity required for direct CHK2-AR binding

To determine whether AR activity is required for the increase in CHK2–AR direct

binding in response to IR, far westerns were again performed by treating 293T cells

expressing Flag-wtAR, Flag-ERK2, or V5-wtCHK2 with 6Gy ionizing radiation in the

presence or absence of the anti-androgen Enzalutamide (Fig. 5A). As expected, far

western blots revealed that radiation increased purified CHK2 binding to purified AR by

2-fold. The presence of enzalutamide blocked the IR induced increase in CHK2–AR

interaction, suggesting that transcriptionally activated AR is required for the IR-induced

increase in association of CHK2 and AR. This is consistent with the loss of AR

phosphorylation on S81 decreasing the CHK2–AR association.

CHK2 activity is also required for the direct CHK2–AR binding in response to IR.

In parallel to the far western in Fig 5A, we performed far westerns with the cells expressing

the V5-CHK2 probe pre-treated with the CHK2 inhibitor BML-277 one hour prior to IR.

(Fig. 5B). Remarkably, inhibition of CHK2 kinase activity completely blocked the increase

in CHK2–AR interactions that we observed when the probe was irradiated in the absence

of BML-277 (Fig. 5A). We also did not detect increased binding to the control target Flag-

ERK2. These data confirm the lack of increased CHK2–AR binding when cells the V5-

CHK2 probe was isolated from were not irradiated (Fig. 4B). These results, along with the

data in Figure 3B, indicate that the direct CHK2–AR protein binding requires CHK2 kinase

activity.

PCa CHK2 mutants limit suppression of PCa growth

Since CHK2 regulates the cell cycle and PCa cell growth [4], [14], we investigated

the effect of CHK2 PCa mutations, which disrupt the CHK2–AR interaction, on CHK2

regulation of PCa cell growth (Fig. 6). PCa cells were transduced with vector or CHK2

shRNA lentivirus to deplete endogenous CHK2, and then CHK2 expression was rescued

with wtCHK2, K373E, or T387N. Cell growth was quantitated in the presence and

absence of 0.05nM synthetic androgen R1881 seven days following transduction using

CyQUANT, which assesses cell proliferation as a function of DNA content. In agreement

with previous reports [4], hormone stimulated growth of vector-expressing cells and

knockdown of CHK2 significantly augmented growth in all PCa cell lines tested. Re-

expression of wtCHK2, K373E, and T387N in CHK2-depleted cells markedly suppressed

the increase in growth induced by CHK2 knockdown in all PCa cell lines tested.

Interestingly, in LNCaP cells the extent of growth inhibition induced by K373E and T387N

was significantly less than that generated by wtCHK2 (Fig. 6A). The effect of CHK2 re-

expression on cell growth in castration-resistant C4-2 (Fig. 6B) and Rv1 (Fig. 6C) cells

was not significantly different between wtCHK2 and the kinase deficient K373E and

T387N mutants, although the magnitude of inhibition caused by the mutants was

consistently less than that produced by wtCHK2. Expression levels of wtCHK2, K373E,

and T387N do not account for the difference observed between LNCaP and C4-2 or Rv1

(Fig. 6) since the relative expression of wtCHK2, K373E, and T387N were similar across

the cell lines. These observations suggest that CHK2 kinase activity, which is reduced in

the PCa mutant K373E, limits the ability of CHK2 to negatively regulate PCa cell growth,

especially in androgen dependent PCa. This then raises the possibly that the PCa CHK2

K373E mutant with diminished AR binding is selected for decreasing CHK2 suppression

of AR activity and PCa cell growth.

CHK2 suppresses IR induction of DNAPK and RAD54

Reports in the literature suggest that the AR is a critical regulator of genes in the

DDR [2], [3]. Therefore we evaluated the impact of CHK2 knockdown on IR induced

transcription of DDR genes in LNCaP cells (Fig. 7). In our experiments, androgen and IR

only affected DNAPK and RAD54 transcript levels; we did not observe androgen or IR

induction of XRCC2, XRCC3, XRCC4, XRCC5, MRE11, RAD51, FANC1 and BRCA1

transcripts as reported by others (data not shown) [2], [3]. This discrepancy is consistent

with the observation that androgen regulation of DDR genes is specific to the model

system and disease state examined [27]. Knockdown of CHK2 in LNCaP cells grown in

CSS and stimulated with 1nM DHT led to an increase in transcription of DNAPK and

RAD54. This increase was further augmented by IR suggesting that CHK2 may suppress

AR transcription of DDR genes in response to IR.

CHK2 effect on IR sensitivity and DNA repair

We next examined the impact of CHK2 interactions on cell survival and sensitivity

to IR (Fig. 8A). Increasing doses of IR were delivered to LNCaP cells expressing CHK2

(pLKO) or depleted of CHK2 (CHK2 KD). Cells were seeded and allowed to grow for 14

days. Clonogenic assays revealed that CHK2 knockdown promoted cell survival following

ionizing radiation. This data, along with the data above indicating that CHK2 suppresses

AR transcription of DNA repair genes suggested the hypothesis that loss of CHK2 could

facilitate DNA repair.

To assess the effect of IR-induced DNA damage in the presence or absence of

CHK2 knockdown we performed comet assays, which measures DNA breaks [28], and

immunofluorescence staining of phospho-γH2AX, a marker for DNA double-strand breaks

[29], [30]. Since the majority of IR induced DSBs are repaired rapidly [29], [31] we focused

on early timepoints following DNA damage. Neither LNCaP or Rv1 cells showed a change

in IR induced comet tail moment following 1 hour of IR (Supplemental Figure 2). In order

to quantify phospho-γH2AX foci in an unbiased manner we developed an approach that

utilizes automated quantitation of immunofluorescence that enables us to rapidly

determine the signal intensity (Supplemental Figure 3). LNCaP cells were transduced

with vector or CHK2 shRNA 48hrs before delivery of IR. Radiation induced similar levels

of DNA damage 15min after exposure regardless of CHK2 expression (Fig.8B,C).

However, CHK2 knockdown exhibited a significant increase in phospho-γH2AX signal

compared to vector control cells 45min after IR. γH2AX is phosphorylated in response to

inputs in addition to IR induced DNA double strand breaks including RNA polymerase II

dependent transcription [32]–[34]. Thus, the apparent discrepancy in the comet and

γH2AX foci assay may be explained by the increase in AR transcription when CHK2 is

knocked down as in Figure 7 and in our previous study [4].

Since superphysiological doses of androgen has been associated with

transcription dependent double strand breaks [35], [36], we tested if CHK2 knockdown

would augment superphysiological androgen dependent phospho-γH2AX foci. LNCaP

and Rv1 cells were transduced with vector or CHK2 shRNA 48hrs before treatment with

a range of the synthetic androgen R1881 up to 100nM for 6 hours (Supplemental Figure

4). We saw modest hormone induced phospho-γH2AX foci and no change with CHK2

knockdown. The superphysiologic dose of androgen likely maximally activates AR

dependent transcription negating the increase in AR transcriptional activity typically

observed with CHK2 knockdown.

DISCUSSION

PCa is the most frequently diagnosed cancer and the second leading cause of cancer death among American men, with approximately 88 men dying from PCa every day (pcf.org). While androgen deprivation therapy (ADT) is effective initially, most patients will relapse and develop incurable CRPC. Recently, there has been an emphasis on understanding the link between the DDR and AR, since radiation is a standard of care for locally advanced PCa where the AR is a major driver, and PARP inhibitors may be efficacious in CRPC patients with mutations in DDR genes [2]–[4], [37]–[39].

Our study identifies AR as a direct interacting protein with CHK2 in PCa cells. Several studies elucidated the role of DDR protein-AR interactions in modulating AR transcriptional activity. PARP-1 was recruited to AR binding sites, enhancing AR occupancy and transcriptional function [40]. Tandem mass spectroscopy analysis identified Ku70 and Ku80 as direct AR-interacting proteins that positively regulate AR transactivation [41]. Furthermore, BRCA1 physically interacted with the DNA-binding domain (DBD) of AR to enhance AR transactivation and induce androgen-mediated cell death through p21 expression [42]. In contrast, the association of the LBD of AR with hRad9, a crucial member of the checkpoint Rad family, suppressed AR transactivation by preventing the androgen-induced interaction between the n-terminus and c-terminus of AR [43]. Other groups reported non-genomic effects as a result of DDR protein-AR interactions. Mediator of DNA damage checkpoint protein 1 (MDC1), an essential player in the Intra-S phase and G2/M checkpoints, physically associated with FL-AR and AR^{V7} to negatively regulate PCa cell growth and migration [44]. Yin and colleagues, on the other hand, showed that increased clonogenic survival following IR was a consequence

of DNA-PKc directly complexing with both FL-AR and AR^{V5-7}, with radiation increasing

these interactions and enzalutamide blocking the association with FL-AR but not AR^{V5-7}

[45]. These data support a model where AR is integrated in the DDR, interfacing at

multiple points in the DDR.

We show that the association of CHK2 and AR requires phosphorylation of AR on

S81 and S308. Since proteins containing FHA domains bind phosphoproteins [8], we

hypothesize that AR interacts with CHK2 through the CHK2 FHA domain. In support of

this, the Zhao lab determined that AR physically associated with the FHA domain of

another critical DDR member, MDC1 [44]. Expression of truncation mutants of different

MDC1 domains in LNCaP cells led to the discovery that AR only co-immunoprecipitated

with MDC1 mutants containing the FHA domain in the absence and presence of

dihydrotestosterone. Their results indicated that the FHA domain of MDC1 mediated the

interaction with AR. Here we report that AR phosphorylation on S81 and S308 is required

for CHK2–AR binding. Interestingly neither of these phosphorylation sites were altered by

IR. AR S81 and S308 can both be phosphorylated by CDK1, which is downstream of

canonical CHK2 signaling [21], [24], and was the motivation for us examining these sites

in response to IR. The prediction is that IR would lead to a decrease in S81 and S308

phosphorylation. However, our previous studies demonstrated that S81 is predominantly

phosphorylated by CDK9, and thus is more indicative of AR transcriptional activity [20].

We also found that S308 phosphorylation was restricted to late G2 and M phase of the

cell cycle [24]. CDK9 phosphorylation of S81 and the restriction of S308 phosphorylation

to G2/M likely accounts for not observing significant changes in these phosphorylation

sites in response to IR. The disconnect between these sites being required for the IR

induced increase in CHK2–AR association but not being regulated by IR suggests that

the hormone induced activation state of the AR is a critical determinant in the IR induced

increase in CHK2–AR association.

In our experiments examining CHK2–AR binding, we used ERK as a positive

control for a protein that interacts with CHK2 [16]. Interestingly, we observed a significant

increase in CHK2–ERK association with IR. This is consistent with IR increasing CHK2

T68 phosphorylation, which is required for the CHK2–ERK interaction. These data point

to a potential larger role for CHK2 beyond canonical DDR and cell cycle checkpoint

signaling; consistent with this notion CHK2 has been implicated in diverse cellular

processes [46]–[48]. MEK inhibition is effective in lung tumors with ATM mutations where

CHK2 is inactive [49] providing further support that CHK2 negatively regulates ERK.

CHK2 negatively regulating both the AR and ERK suggests the hypothesis that CHK2

may serve as a general negative regulator of mitogenic signals in response to IR.

We found that CHK2 variants with diminished kinase activity impaired the IR-

induced increase in CHK2–AR interaction but did not completely block the CHK2–AR

interaction. This correlated with a reduced inhibition of cell growth by the CHK2 variants.

CHK2-depleted cells re-expressing CHK2 variants exhibited an approximate 2-3-fold

reduction in growth inhibition in response to hormone when compared to cells re-

expressing wtCHK2. Moreover, the fold change in suppression of growth between

wtCHK2 and CHK2 variants was greater in androgen-dependent LNCaP cells than in

castration-resistant C4-2 and Rv1 cells, suggesting that in hormone sensitive PCa CHK2

variants may play a larger role in regulating growth. Berge and colleagues discovered

numerous CHK2 splice variants in breast cancer tissue, where all variants were co-

expressed with wtCHK2 [50]. Furthermore, several of these variants reduced kinase

activity when simultaneously expressed with wtCHK2 and displayed a dominant negative

effect on wtCHK2. The impact of the CHK2 variants found in PCa on wtCHK2 function

has not yet been fully explored.

Multiple studies indicate that the AR is a critical regulator of genes in the DDR [2],

[3]. Reports by others demonstrate that androgen and IR increased DNAPK, XRCC2, and

XRCC3 [3]. This concept was supported by more global analysis of transcripts

demonstrating androgen regulation of DDR genes [2]. Our data indicating that CHK2

knockdown increases DNAPK and RAD54 transcript levels leads to the hypothesis that

CHK2 binding to the AR suppresses AR transcription of DDR genes enabling cells to turn

off the DDR following DNA repair. This is consistent with our earlier observation that

CHK2 knockdown led to the increase in the transcripts of canonical AR target genes [4].

We observed radiation resistance in CHK2 knockdown cells, consistent with CHK2

suppression of AR transcription of DDR genes. We also observed an increase in

phospho-γH2AX signal when CHK2 was knocked down, but no change in DNA breaks as

measured by the comet assay under similar conditions. These paradoxical results may

be explained by phosphorylation of γH2AX in response to transcription induced DNA

breaks [32]–[34]. These incongruous results may also be due to competing effects of

CHK2 as both a regulator of the cell cycle and apoptosis [46].

The data reported herein along with our previous work [4] indicate that CHK2 acts

as a tumor suppressor in PCa, either through loss of expression or mutation. This raises

the concern that CHK2 antagonists in clinical development may paradoxically lead to

enhanced PCa growth and resistance to IR. However, it is important to note that we have

predominately used a RNAi/overexpression approach. Our RNAi approach is more similar

to the CHK2 variants in PCa that have reduced kinase activity. It is important to consider

that pharmacologic inhibition is different than inhibition by RNAi [51]. A pharmacologic

approach that provides a sudden and complete inhibition of CHK2 kinase activity may

impact PCa differently than our RNAi approach, especially when combined with IR or AR

antagonists. Our work and that in the literature also suggests that approaches

downstream of CHK2 may be more straightforward than targeting CHK2.

In this study, we presented data that provides mechanistic insight into our

observation that CHK2 negatively regulates PCa growth. We demonstrated that AR

directly bound CHK2, and that IR elevated the CHK2–AR interaction, which peaked one

hour following exposure. Not only did these CHK2–AR protein complexes require AR

phosphorylation on both serine 81 and serine 308, but CHK2 kinase activity was also

necessary, as CHK2 kinase inhibitors disrupted CHK2–AR binding. This was verified

using kinase-impaired CHK2 variants, including the K373E variant associated with 4.2%

of prostate cancer. Furthermore, these CHK2 variants exhibited a diminished effect on

restricting prostate cancer cell growth. We observed that knockdown of CHK2 led to an

increase in PCa cell survival in response to IR. This suggests that the deregulation of

CHK2 in PCa compromises the DDR and can confer resistance to radiation. In a previous

study, we showed that CHK2 knockdown hypersensitized PCa cells to castrate levels of

androgen and increased AR transcriptional activity on both androgen-activated and

androgen-repressed genes [4]. As part of a feedback loop, AR transcriptionally represses

CHK2 levels. Thus, these data along with our previously published results suggest a

model where CHK2 antagonizes AR through direct binding and inhibition of transcription

of AR targets, including DDR genes (Figure 9). The K373E mutation of CHK2 or loss of

CHK2 expression in PCa leads to increased AR transcriptional activity and survival in

response to DNA damage, all leading to a more aggressive cancer. Collectively, the work

provides a foundation for the continued study of CHK2–AR interactions and functional

consequences to benefit PCa therapies.

MATERIALS AND METHODS

Cell culture

LNCaP and C4-2 cells (a gift from Dr. L. W. K. Chung) were grown in DMEM:F12 (Invitrogen) with 5% Non-Heat Inactivated serum (Gemini) and 1% Insulin-Transferrin-Selenium-Ethanolamine (ITS) (ThermoFisher). CWR22Rv1 (Rv1) (gift from Drs. Steven Balk) and 293T cells (gift from Dr. Tim Bender) were grown in DMEM (Invitrogen) with 10% Heat-Inactivated serum. For growth experiments, phenol-red free DMEM:F12 media with 5% Charcoal-Stripped Serum (CSS) (Gemini) was used. Commercial DNA fingerprinting kits (DDC Medical) verified cell lines. The following STR markers were tested: CSF1PO, TPOX, TH01, Amelogenin, vWA, D16S539, D7S820, D13S317 and D5S818. Allelic score data revealed a pattern related to the scores reported by the ATCC, and consistent with their presumptive identity.

Reagents

Transfection: Fugene 6 (Promega); TransIT-2020 (Mirus Bio).Inhibitors: Enzalutamide (Selleck Chemicals), BML-277 (Santa Cruz Biotech).Antibodies: CHK2 (2G1D5), pCHK2 T68, ERK1/2 (137F5), Actin, Flag-Tag, V5-Tag, HA-Tag, γH2AX (Cell Signaling); AR, pAR S308 (in-house); pAR S81 (Millipore); Cy3-labeled donkey anti-rabbit (Jackson ImmunoResearch). Western blotting performed as previously described [4].

Far Western Blot

To measure direct protein interactions, the protocol was adapted from Prickett *et al* [52] and Wu *et al* [53]. 293T cells were transfected with 1) Flag-wtAR, 2) HA-wtAR, 3) Flag-ERK2, 4) V5-wtCHK2, or 5) empty vector control. Cells were treated with vehicle, enzalutamide, or BML-277, one hour before ionizing radiation (IR) exposure. Whole cell

extracts were made using Triton-X lysis buffer, sonicated, and immunopurified using anti-

Flag, anti-HA, or anti-V5 beads (Sigma) for 2hr at 4°C. Protein bound to beads was

washed three times with Triton-X lysis buffer, eluted with 35µl 2X sample buffer, and

boiled for 5 min. Proteins were resolved by SDS-PAGE and transferred to PVDF

membrane. Proteins on the membrane were denatured and renatured in buffers with

varying guanidine–HCl concentrations. Membranes were blocked in 3% blocking buffer

(3% bovine serum albumin in Tris-buffered saline/Tween 20) for 1hr. Probes were diluted

in 3% blocking buffer and incubated overnight at 4°C. Membranes were washed three

times with PBS for 5min followed by fixation using 0.5% paraformaldehyde for 30 min at

room temperature. Membranes were then rinsed quickly twice with PBS and quenched

using 2% glycine in PBS for 10 min at room temperature. The membrane was blotted for

Flag, HA, V5, AR, CHK2, or ERK1/2 and analyzed using the LI-COR Odyssey system

and software.

Immunoprecipitation

CHK2 or AR protein was immunoprecipitated from 1mg cell lysate from LNCaP,

C42, and Rv1 cells cultured in the appropriate growth media or LNCaP cells transiently

transfected with Flag-wtAR/Flag-S81A/Flag-S308A plus V5-wtCHK2 or Flag-

wtCHK2/Flag-K373E/Flag-T387N plus HA-wtAR for 48hrs; treated with radiation.

Immunoprecipitations were performed with either agarose or magnetic beads, proteins

were separated by 7.5% SDS-PAGE; and immunoblotted with AR, pAR S81, pAR S308,

CHK2, pCHK2 T68, HA, or ERK1/2 antibodies.

CyQuant Growth Assays

Assay was performed as previously described [4]. Briefly, shCHK2-209, shCHK2-

588, wtCHK2, K373E, T387N or Vector control virus was added to fibronectin-coated

(1µg/ml) 96well plates. Constructs of CHK2 wild-type and variants were verified by

sequencing. Cells were plated in phenol-red free DMEM:F12 or DMEM media with 5%

CSS in the presence or absence of 0.05nM R1881. CyQuant reagent was added on Day

7 according to the manufacturer's protocol (ThermoFisher). Quantification was performed

using a BioTek Synergy 2 plate reader.

qPCR

RNA isolation and quantitative real-time PCR (qPCR) was performed as previously

described [54], [55]. RNA concentrations were determined using a NanoDrop 2000 UV-

Vis Spectrophotometer (Thermo Scientific). Primer sequences and annealing

temperature: DNAPKc FW (ATGAGTACAAGCCCTGAG); DNAPKc RV

(ATATCAGAGCGTGAGAGC) (Tm=60deg). RAD54B FW

(ATAACAGAGATAATTGCAGTGG); RAD54B RV (GATCTAATGTTGCCAGTGTAG)

(Tm=60deg). PSMB6 FW (CAAACTGCACGGCCATGATA); PSMB6 RV

(GAGGCATTCACTCCAGACTGG) (Tm=60deg).

Clonogenic Survival Assay

LNCaP cells were transduced with lentiviral particles expressing vector or CHK2

shRNAs and treated with 0-6Gy of radiation 72hrs after transduction. Cells were

trypsinized, counted, and appropriate numbers were plated in triplicate with the

appropriate growth media for colony formation assays (100 cells/0Gy, 200 cells/2Gy,

1000 cells/4Gy, and 6000 cells/6Gy). After 10-14 days, colonies consisting of 50-70 cells

were counted using crystal violet. Plotted is the surviving fraction (number of colonies

counted/(number of cells seeded x PE) where PE = plating efficiency = number of colonies

counted/number of cells seeded) following radiation.

Comet Assay

All Comet Assay steps were performed in the dark. Cells were washed twice with

PBS , scraped and suspended in PBS. Cells were combined with molten LMAgarose

(Trevigen, 4250-050-02) and placed into comet suitable sides. Samples were left at 4°C

for 15 minutes order to create flat surface. Slides were immerse in lysis solution (Trevigen,

4250-050-01) for 40 minutes at 4°C and then in alkaline solution for 30min at room

temperature. Slides were electrophoresed in 200mM NaOH, 1mM EDTA in water; pH>13

at 21Volts (300mA) for 30 minutes at 4°C. After the electrophoresis, slides were gently

drained, washed twice in dH2O for 10min and immersed in 70% ethanol for 5min.

Samples were left to dry overnight at RT. Samples were stained with SYBR Green at 4°C

for 5 minutes and left to dry completely overnight. For quantification, images were

acquired using a fluorescence microscope (Olympus BX51, High-mag) equipped with a

20×, 0.5 NA objective and a camera (DP70). Images were acquired with DPController

software. Images were analyzed by ImageJ software and graphs generated using Prism

(GraphPad Software). All imaging was performed at ~24°C.

Immunofluorescence (IF)

LNCaP cells were transduced with lentivirus expressing vector or CHK2 shRNAs

on 1µg/ml fibronectin-coated coverslips and treated with radiation 48hrs after

transduction. Cells were allowed to recover from IR exposure for 0, 15, and 45mins.

Coverslips were washed 3X with PBS, permeabilized with 0.2% Triton-X for 10mins,

blocked with 2% FBS/BSA/donkey serum in PBS for 2hrs at room temperature, and

incubated with γH2AX antibodies overnight at 4°C. Coverslips were mounted with

Vectashield containing DAPI (ThermoFisher), and images were acquired with a LSM 880

confocal microscope (Carl Zeiss). γH2AX signals were measured using ImageJ software.

Scientific Rigor

Each experiment was performed independently a minimum of three times and

each experiment had technical replicates for measuring the endpoint. An independent

experiment is defined as an experiment performed on a different day with a different

passage number. The number of independent experiments is reported in each figure

legend. All data are shown, no outliers were removed. Statistical analysis was performed

using GraphPad Prism 8.2.1 and the test used is reported in each figure legend.

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COMPETING INTERESTS

The authors declare no competing financial interests

REFERENCES

[1] N. Rhind and P. Russell, "Chk1 and Cds1: linchpins of the DNA damage and replication checkpoint pathways," *J. Cell. Sci.*, vol. 113 (Pt 22), pp. 3889–3896, Nov. 2000.

[2] W. R. Polkinghorn *et al.*, "Androgen receptor signaling regulates DNA repair in prostate cancers," *Cancer Discov*, vol. 3, no. 11, pp. 1245–1253, Nov. 2013.

[3] J. F. Goodwin *et al.*, "A hormone-DNA repair circuit governs the response to genotoxic insult," *Cancer Discov*, vol. 3, no. 11, pp. 1254–1271, Nov. 2013.

[4] H. Q. Ta *et al.*, "Checkpoint Kinase 2 Negatively Regulates Androgen Sensitivity and Prostate Cancer Cell Growth," *Cancer Res.*, vol. 75, no. 23, pp. 5093–5105, Dec. 2015.

[5] S. Matsuoka, M. Huang, and S. J. Elledge, "Linkage of ATM to cell cycle regulation by the Chk2 protein kinase," *Science*, vol. 282, no. 5395, pp. 1893–1897, Dec. 1998.

[6] S. T. Kim, D. S. Lim, C. E. Canman, and M. B. Kastan, "Substrate specificities and identification of putative substrates of ATM kinase family members," *J. Biol. Chem.*, vol. 274, no. 53, pp. 37538–37543, Dec. 1999.

[7] J. Ahn, M. Urist, and C. Prives, "The Chk2 protein kinase," *DNA Repair (Amst.)*, vol. 3, no. 8–9, pp. 1039–1047, Sep. 2004.

[8] J. Li *et al.*, "Structural and functional versatility of the FHA domain in DNA-damage signaling by the tumor suppressor kinase Chk2," *Mol. Cell*, vol. 9, no. 5, pp. 1045–1054, May 2002.

[9] C. García-Limones *et al.*, "CHK2 stability is regulated by the E3 ubiquitin ligase SIAH2," *Oncogene*, vol. 35, no. 33, pp. 4289–4301, 18 2016.

[10] L. Tsvetkov, X. Xu, J. Li, and D. F. Stern, "Polo-like kinase 1 and Chk2 interact and co-localize to centrosomes and the midbody," *J. Biol. Chem.*, vol. 278, no. 10, pp. 8468–8475, Mar. 2003.

[11] S. Yang, C. Kuo, J. E. Bisi, and M. K. Kim, "PML-dependent apoptosis after DNA damage is regulated by the checkpoint kinase hCds1/Chk2," *Nat. Cell Biol.*, vol. 4, no. 11, pp. 865–870, Nov. 2002.

[12] C. Stevens, L. Smith, and N. B. La Thangue, "Chk2 activates E2F-1 in response to DNA damage," *Nat. Cell Biol.*, vol. 5, no. 5, pp. 401–409, May 2003.

[13] A. Hirao *et al.*, "DNA damage-induced activation of p53 by the checkpoint kinase Chk2," *Science*, vol. 287, no. 5459, pp. 1824–1827, Mar. 2000.

[14] J. Bartek and J. Lukas, "Chk1 and Chk2 kinases in checkpoint control and cancer," *Cancer Cell*, vol. 3, no. 5, pp. 421–429, May 2003.

[15] C. Y. Peng, P. R. Graves, R. S. Thoma, Z. Wu, A. S. Shaw, and H. Piwnica-Worms, "Mitotic and G2 checkpoint control: regulation of 14-3-3 protein binding by phosphorylation of Cdc25C on serine-216," *Science*, vol. 277, no. 5331, pp. 1501–1505, Sep. 1997.

[16] B. Dai *et al.*, "Functional and molecular interactions between ERK and CHK2 in diffuse large B-cell lymphoma," *Nat Commun*, vol. 2, p. 402, 2011.

[17] "National Comprehensive Cancer Network. Prostate Cancer http://www.nccn.org/professionals/physician_gls/pdf/prostate.pdf."

[18] S. M. Dehm, L. J. Schmidt, H. V. Heemers, R. L. Vessella, and D. J. Tindall, "Splicing of a novel androgen receptor exon generates a constitutively active androgen receptor that mediates prostate cancer therapy resistance," *Cancer Res*, vol. 68, pp. 5469–77, 2008.

[19] S. Chen, Y. Xu, X. Yuan, G. J. Bubley, and S. P. Balk, "Androgen receptor phosphorylation and stabilization in prostate cancer by cyclin-dependent kinase 1," *Proc Natl Acad Sci U S A*, 2006.

[20] V. Gordon *et al.*, "CDK9 regulates AR promoter selectivity and cell growth through serine 81 phosphorylation," *Mol Endocrinol*, vol. 24, pp. 2267–80, 2010.

[21] S. Chen, S. Gulla, C. Cai, and S. P. Balk, "Androgen receptor serine 81 phosphorylation mediates chromatin binding and transcriptional activation," *J. Biol. Chem.*, vol. 287, no. 11, pp. 8571–8583, Mar. 2012.

[22] D. Gioeli *et al.*, "Androgen receptor phosphorylation. Regulation and identification of the phosphorylation sites," *J Biol Chem*, vol. 277, pp. 29304–14, 2002.

[23] H. Zong *et al.*, "Cyclin D3/CDK11p58 complex is involved in the repression of androgen receptor," *Mol Cell Biol*, vol. 27, pp. 7125–42, 2007.

[24] Y. Koryakina, K. E. Knudsen, and D. Gioeli, "Cell-cycle-dependent regulation of androgen receptor function," *Endocr. Relat. Cancer*, vol. 22, no. 2, pp. 249–264, Apr. 2015.

[25] M. Higashiguchi *et al.*, "Clarifying the biological significance of the CHK2 K373E somatic mutation discovered in The Cancer Genome Atlas database," *FEBS Lett.*, Oct. 2016.

[26] M. Wasielewski *et al.*, "Deleterious CHEK2 1100delC and L303X mutants identified among 38 human breast cancer cell lines," *Breast Cancer Res. Treat.*, vol. 113, no. 2, pp. 285–291, Jan. 2009.

[27] K. Jividen, K. Z. Kedzierska, C.-S. Yang, K. Szlachta, A. Ratan, and B. M. Paschal, "Genomic analysis of DNA repair genes and androgen signaling in prostate cancer," *BMC Cancer*, vol. 18, no. 1, p. 960, Oct. 2018.

[28] A. R. Collins, "The comet assay for DNA damage and repair: principles, applications, and limitations," *Mol. Biotechnol.*, vol. 26, no. 3, pp. 249–261, Mar. 2004.

[29] J. Vignard, G. Mirey, and B. Salles, "Ionizing-radiation induced DNA double-strand breaks: a direct and indirect lighting up," *Radiother Oncol*, vol. 108, no. 3, pp. 362–369, Sep. 2013.

[30] W. M. Bonner *et al.*, "γH2AX and cancer," *Nature Reviews Cancer*, vol. 8, no. 12, pp. 957–967, Dec. 2008.

[31] M. I. Affentranger and W. Burkart, "Assessment of radiation-induced DNA strand breaks and their repair in unlabeled cells," *Cytometry*, vol. 13, no. 1, pp. 31–38, 1992.

[32] I. Singh *et al.*, "High mobility group protein-mediated transcription requires DNA damage marker γ-H2AX," *Cell Res.*, vol. 25, no. 7, pp. 837–850, Jul. 2015.

[33] H. Bunch *et al.*, "Transcriptional elongation requires DNA break-induced signalling," *Nature Communications*, vol. 6, p. 10191, Dec. 2015.

[34] J.-H. Ji *et al.*, "De novo phosphorylation of H2AX by WSTF regulates transcription-coupled homologous recombination repair," *Nucleic Acids Res.*, vol. 47, no. 12, pp. 6299–6314, Jul. 2019.

[35] M. C. Haffner *et al.*, "Androgen-induced TOP2B-mediated double-strand breaks
and prostate cancer gene rearrangements," *Nat. Genet.*, vol. 42, no. 8, pp. 668–
675, Aug. 2010.
[36] P. Chatterjee *et al.*, "Supraphysiological androgens suppress prostate cancer
growth through androgen receptor-mediated DNA damage," *J. Clin. Invest.*, vol.
130, Jul. 2019.
[37] J. Mateo *et al.*, "DNA-Repair Defects and Olaparib in Metastatic Prostate Cancer,"
N. Engl. J. Med., vol. 373, no. 18, pp. 1697–1708, Oct. 2015.
[38] L. Li *et al.*, "Targeting poly(ADP-ribose) polymerase and the c-Myb-regulated DNA
damage response pathway in castration-resistant prostate cancer," *Sci Signal*, vol.
7, no. 326, p. ra47, May 2014.
[39] Y. Yin *et al.*, "Chk1 inhibition potentiates the therapeutic efficacy of PARP inhibitor
BMN673 in gastric cancer," *Am J Cancer Res*, vol. 7, no. 3, pp. 473–483, 2017.
[40] M. J. Schiewer *et al.*, "Dual roles of PARP-1 promote cancer growth and
progression," *Cancer Discov*, vol. 2, no. 12, pp. 1134–1149, Dec. 2012.
[41] G. L. Mayeur, W. J. Kung, A. Martinez, C. Izumiya, D. J. Chen, and H. J. Kung, "Ku
is a novel transcriptional recycling coactivator of the androgen receptor in prostate
cancer cells," *J Biol Chem*, vol. 280, pp. 10827–33, 2005.
[42] S. Yeh *et al.*, "Increase of androgen-induced cell death and androgen receptor
transactivation by BRCA1 in prostate cancer cells," *Proc. Natl. Acad. Sci. U.S.A.*,
vol. 97, no. 21, pp. 11256–11261, Oct. 2000.
[43] L. Wang *et al.*, "Human checkpoint protein hRad9 functions as a negative
coregulator to repress androgen receptor transactivation in prostate cancer cells,"
Mol. Cell. Biol., vol. 24, no. 5, pp. 2202–2213, Mar. 2004.
[44] C. Wang *et al.*, "MDC1 functionally identified as an androgen receptor co-activator
participates in suppression of prostate cancer," *Nucleic Acids Res.*, vol. 43, no. 10,
pp. 4893–4908, May 2015.
[45] Y. Yin *et al.*, "Androgen Receptor Variants Mediate DNA Repair after Prostate
Cancer Irradiation," *Cancer Res.*, vol. 77, no. 18, pp. 4745–4754, 15 2017.
[46] L. Zannini, D. Delia, and G. Buscemi, "CHK2 kinase in the DNA damage response
and beyond," *J Mol Cell Biol*, vol. 6, no. 6, pp. 442–457, Dec. 2014.
[47] H.-H. Choi *et al.*, "CHK2 kinase promotes pre-mRNA splicing via phosphorylating
CDK11(p110)," *Oncogene*, vol. 33, no. 1, pp. 108–115, Jan. 2014.
[48] T. Choudhuri, S. C. Verma, K. Lan, M. Murakami, and E. S. Robertson, "The
ATM/ATR signaling effector Chk2 is targeted by Epstein-Barr virus nuclear antigen
3C to release the G2/M cell cycle block," *J. Virol.*, vol. 81, no. 12, pp. 6718–6730,
Jun. 2007.
[49] M. Smida *et al.*, "MEK inhibitors block growth of lung tumours with mutations in
ataxia-telangiectasia mutated," *Nat Commun*, vol. 7, p. 13701, 06 2016.
[50] E. O. Berge, V. Staalesen, A. H. Straume, J. R. Lillehaug, and P. E. Lønning,
"Chk2 splice variants express a dominant-negative effect on the wild-type Chk2
kinase activity," *Biochim. Biophys. Acta*, vol. 1803, no. 3, pp. 386–395, Mar. 2010.
[51] K. J. Jensen, C. B. Moyer, and K. A. Janes, "Network Architecture Predisposes an
Enzyme to Either Pharmacologic or Genetic Targeting," *Cell Syst*, vol. 2, no. 2, pp.
112–121, Feb. 2016.

[52] T. D. Prickett *et al.*, "TAB4 stimulates TAK1-TAB1 phosphorylation and binds
polyubiquitin to direct signaling to NF-kappaB," *J. Biol. Chem.*, vol. 283, no. 28, pp.
19245–19254, Jul. 2008.
[53] Y. Wu, Q. Li, and X.-Z. Chen, "Detecting protein-protein interactions by Far western
blotting," *Nat Protoc*, vol. 2, no. 12, pp. 3278–3284, 2007.
[54] V. Gordon *et al.*, "CDK9 regulates AR promoter selectivity and cell growth through
serine 81 phosphorylation," *Molecular Endocrinology (Baltimore, Md.)*, vol. 24, no.
12, pp. 2267–2280, Dec. 2010.
[55] H. Whitworth *et al.*, "Identification of Kinases Regulating Prostate Cancer Cell
Growth Using an RNAi Phenotypic Screen," *PLoS ONE*, vol. 7, no. 6, Jun. 2012.
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FIGURE LEGEND

Figure 1. CHK2 directly binds AR. 293T cells were transfected with Vector, Flag-wtAR,

Flag-wtCHK2, Flag-ERK2, HA-wtAR, or V5-wtCHK2 using Fugene 6. 48hrs following

transfection, Flag, HA, and V5 were immunoprecipitated, and far western blotting was

performed. Membranes were blotted with the following antibodies: Flag, HA, V5, AR,

CHK2, and ERK2. Blots were visualized using the Odyssey CLx. (A) Probe = V5-wild-

type CHK2; Targets = Flag-wtAR and Flag-ERK2. Representative blots are shown, n=3.

(B) Probe = HA-wtAR; Targets = Flag-wtCHK2. Representative blots are shown, n=3.

Figure 2. Radiation transiently increases CHK2-AR association. CHK2 immune

complexes were generated one hour following radiation (6Gy) from 1mg cell extract from

(A) LNCaP and (B) Rv1 cells grown in serum-supplemented media, separated by 7.5%

SDS-PAGE, and immunoblotted with AR, CHK2, and ERK1/2 antibodies. Plotted is the

AR or AR-V7 signal normalized to total CHK2, and compared to untreated cells (Rv1).

Representative blots are shown for (A) LNCaP (n=4, p<0.003) and (B) Rv1 cells (n=3,

p<0.02). (C,D) LNCaP and C4-2 cells were seeded in serum-supplemented growth media

and allowed to adhere for 48hrs. Cells were exposed to 6Gy IR and CHK2 immune

complexes were immunoprecipitated using a magnetic bead system 0-24hrs after

radiation from 1mg cell extracts, separated by 7.5% SDS-PAGE, and blotted with AR,

CHK2, pCHK2 T68, and ERK1/2 antibodies. (C) Representative blots are shown, n=3.

(D) Plotted is the AR signal normalized to total CHK2 and compared to untreated cells,

p<0.0001. Error bars, SEM. Band signals were quantitated on Odyssey LICOR imaging

system. Statistical analysis was performed using ANOVA and Tukey test.

Figure 3. AR phosphorylation and CHK kinase activity regulates CHK2-AR association. (A) CHK2-AR interactions requires AR phosphorylation on serines 81 and 308. LNCaP cells were transduced with lentiviral particles expressing wtAR, S81A, or S308 for 48hrs. Cells were irradiated with 6Gy, and CHK2 was immunoprecipitated one hour after IR. Representative blots are shown. Plotted is the AR signal normalized to total CHK2 and compared to untreated cells, n=3, p<0.009. Error bars, SEM. Blots were quantitated on Odyssey LICOR imaging system. Statistical analysis was performed using ANOVA and Tukey test. (B) Expression of CHK2 variants with reduced kinase activity inhibits the radiation-induced increase in CHK2-AR interactions. LNCaP cells were transfected with HA-wtAR, HA-S81A, or HA-S308 in combination with Flag-wtCHK2 for 48hrs using TransIT-2020 (Mirus). Cells were irradiated with 6Gy, and Flag was immunoprecipitated using a magnetic bead system one hour after IR. Representative blots are shown. Plotted is the HA-AR signal normalized to total Flag-CHK2 and compared to untreated cells. Error bars, SEM. Blots were quantitated on Odyssey LICOR imaging system. Statistical analysis was performed using ANOVA and Tukey test, n=3, p<0.02.

Figure 4. Radiation increases direct CHK2-AR binding. (A) Radiation increases direct binding of AR and CHK2. Probe = V5-wtCHK2 + IR; Targets = Flag-wtAR and Flag-ERK2 -/+ IR. Representative blots are shown, n=3, p=0.004. (B) Radiation of both CHK2 and AR is required for the increase in direct association. Probe = V5-wtCHK2 - IR; Targets = Flag-wtAR and Flag-ERK2 -/+ IR. Representative blots are shown, n=3. Quantitation was

performed on Odyssey LICOR imaging system. Error bars represent standard error of the

mean (SEM). Statistical analysis was performed using ANOVA and Tukey test.

Figure 5. AR and CHK2 activity required for direct CHK2-AR binding. (A)

Enzalutamide significantly impairs the association of CHK2 with AR. 293T cells were

transfected with Vector, Flag-wtAR, Flag-ERK2, or V5-wtCHK2 using Fugene 6. 48hrs

following transfection, cells were irradiated with 6Gy, and Flag and V5 were

immunoprecipitated one hour following radiation. Far western blotting was performed.

Membrane was blotted with the following antibodies: V5, AR, and ERK2. Representative

blots are shown. Plotted is the V5-CHK2 signal normalized to total wtAR or ERK2 and

compared to untreated cells, n=3, p<0.02. Error bars, SEM. (B) Inhibition of CHK2 with

BML-277 blocks the increase in CHK2-AR interactions. 293T cells were transfected with

Vector, Flag-wtAR, Flag-ERK2, or V5-wtCHK2 using Fugene 6. 48hrs following

transfection, cells were pre-treated with vehicle or 10μM BML-277 for 1hr, irradiated with

6Gy, and Flag and V5 were immunoprecipitated one hour following radiation. Far western

blotting was performed. Membrane was blotted with the following antibodies: V5, AR, and

ERK2. Representative blots are shown. Plotted is the V5-wtCHK2 signal normalized to

total AR or ERK2 and compared to untreated cells, n=3. Error bars, SEM. No statistical

difference was observed between the groups.

Figure 6. Wild-type CHK2 negatively regulates prostate cancer cell growth. (A)

LNCaP, (B) C4-2, and (C) Rv-1 cells were transduced with lentiviral particles expressing

vector, shCHK2-exon 12, or shCHK2-3'UTR in combination with wtCHK2, K373E, or

T387N in the presence or absence of 0.05nM R1881. CyQuant assay was performed 7

days after transduction. Cell growth was compared with untreated vector control and the

values were averaged across biological replicates. Error bars, SEM, n=3. Statistical

analysis was performed using ANOVA and Tukey test, p<0.01. Representative blots of

CHK2 expression are shown.

Figure 7. CHK2 knockdown increases the transcription of DDR genes in the

presence and absence of radiation. Transcript levels of DDR genes in LNCaP cells

transduced with CHK2 shRNAs and pLKO vector control and grown in CSS

supplemented with 1nM DHT were measured by qPCR. 48hrs following transduction,

cells were exposed to 2Gy ionizing radiation and RNA was isolated 6 hours later.

Transcript levels were normalized to the housekeeping gene, PSMB6, and compared to

pLKO. Values were averaged across biological replicates +/- standard error of the mean,

n=3. Shown are the histograms for (A) DNAPKc and (B) Rad54B in LNCaP cells.

Statistical analysis was performed using one-way ANOVA and Tukey's test. * p<0.02.

Figure 8. CHK2-depleted cells show increased survival and DNA damage following

radiation. (A) Knockdown of CHK2 desensitizes cells to IR. LNCaP cells were transduced

with lentiviral particles expressing pLKO or CHK2 shRNAs for 48hrs, treated with 0-6Gy

IR, and seeded at the appropriate cell number for colony survival assays. Results were

normalized to untreated pLKO control and fitted to a standard linear quadratic model.

Error bars, SEM. Statistical analysis was performed using the Student's t-test, n=4-8,

p<0.01. (B) Representative images of phospho-γH2AX, CHK2, and AR immunostaining

quantified in (C) . (C) phospho-γH2AX is elevated in cells depleted of CHK2. LNCaP cells

were transduced with lentiviral particles expressing empty vector or CHK2 shRNAs on

fibronectin-coated coverslips in the appropriate growth media. Cells were irradiated with

5Gy after 48hrs. Coverslips were processed for IF at 0, 15, and 45min following IR. Plotted

is the γH2AX signal, which equals the mean grey value intensity x number of foci per

nucleus. Statistical analysis was performed using ANOVA and Tukey test, $p < 0.0001$.

Figure 9. Model of CHK2-AR. We hypothesize the following model. In response to IR,

CHK2 activation antagonizes AR through direct binding and inhibition of transcription of

AR targets. CHK2 mutation, or loss of expression, that occurs in PCa leads to sustained

AR transcriptional activity, an increase in DDR gene transcripts, and survival in response

to DNA damage.

Supplemental Figure 1. AR S81 and S308 phosphorylation are not altered with

radiation. LNCaP and C4-2 cells were seeded in serum-supplemented growth media for

48hrs, exposed to 6Gy IR, and AR was immunoprecipitated using a magnetic bead

system 1hr after radiation from 1mg cell extracts. Proteins were separated by 7.5% SDS-

PAGE, and blotted with AR, pAR S81, pAR S308, CHK2, and ERK1/2. Representative

blots are shown. Plotted is the pAR signal normalized to total AR and compared to

untreated cells, n=3, no statistical difference between the groups by ANOVA. Blots were

quantitated on Odyssey LICOR imaging system.

Supplemental Figure 2. CHK2 Knockdown does not alter DNA breaks. LNCaP (A)

and Rv1 (B) cells were seeded in whole media for 48 hours, irradiated at the indicated

doses at the specified times and processed for comet assays. Show is the percent DNA

in the comet tail, comet tail length, and tail moment (% DNA x tail length). n=3 for LNCaP

and n=2 for Rv1. At the same irradiation conditions there was no statistical difference

between vector control and CHK2 knockdown by ANOVA and Tukey's multiple

comparisons test.

Supplemental Figure 3. Automated quantitation of foci. Confocal images are captured

on a Zeiss LSM 880 at 40x oil using Zeiss Zen digital imaging software and processed

into individual TIFF files for each fluorescence channel using ImageJ. An outline of nuclei

(mask) from DAPI channel is created and applied to all channels. Macro-enabled image

processing to measure multiple fluorescence parameters with background subtraction

using the following parameters: area, IntDen, RawIntDen, Min and Max, fluorescence,

background, foci count, CorDen, CorMean. gH2AX signal is the product of foci number

per nuclei and mean grey value (IntDen/area).

Supplemental Figure 4. CHK2 Knockdown does not alter hormone induced

phospho-γH2AX foci. LNCaP and Rv1 cells were transduced with lentiviral particles

expressing empty vector or CHK2 shRNA on fibronectin-coated coverslips in whole media

for 48hrs. Media was changed to CSS overnight and cells were treated with hormone for

6 hours. Plotted is the number of phospho-γH2AX foci per cell. n=3 for LNCaP and n=2

for Rv1. At the same dose of hormone there was no statistical difference between vector

control and CHK2 knockdown by ANOVA and Tukey's multiple comparisons test.

A.

B.

Figure 1

Figure 2

Figure 3

A

B

Figure 4

A

Probe: V5-wtCHK2 + IR & Vehicle

B

Probe: V5-wtCHK2 + IR & 10μM BML-227

Figure 5

Figure 6

A.

DNAPKc

B.

Rad54B

Figure 7

A.

LNCaP

Surviving Fraction

0   2   4   6
IR (Gy)

pLKO
CHK2 KD

*

B.

| | control | | 15' | | 45' | |
| | pLKO | CHK2 KD | pLKO | CHK2 KD | pLKO | CHK2 KD |

gH2AX

CHK2

AR

C.

LNCaP

γH2AX signal [AU]

15000

12000

9000

6000

3000

CHK2 KD   -   +   -   +   -   +

Time (min)   -   15   45

Figure 8

wtCHK2

mutCHK2

Figure 9

LNCaP: AR, CHK2, ERK1/2

C4-2: AR, CHK2, ERK1/2

Lysate

AR IP: pAR S81, AR

AR IP: pAR S308, AR

IR (6Gy)

pAR S81

Fold Change

2.5
2.0
1.5
1.0
0.5
0.0

− + − + IR (6Gy)

LNCaP   C4-2

pAR S308

Fold Change

2.5
2.0
1.5
1.0
0.5
0.0

− + − + IR (6Gy)

LNCaP   C4-2

Supplemental Figure 1

Supplemental Figure 2

1) **Create a mask from DAPI channel**

2) **Apply DAPI mask onto the gH2AX channel**

3) **Background subtraction**

4) **Maxima points (foci)**   **Example of output**

Supplemental Figure 3

A

B

Supplemental Figure 4