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Role of N-terminal domains of p400 ATPase in the ATM interaction and DNA damage response

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Abstract

Efficient repair of damaged DNA and preservation of genomic integrity is integral in the maintenance of proper cellular function and prevention of unrestricted cell proliferation. One critical threat to the stability of the genome is the double strand break (DSB), arguably one of the most cytotoxic lesions to DNA. Interference with the DSB repair mechanism can lead to dysregulation of cellular systems and the prospective development of malignancies. Two critical proteins in DSB repair are the Ataxia Telangiectasia Mutated (ATM) kinase, a serine/threonine kinase from the Phosphatidylinositol 3-Kinase-related Kinase (PIKK) family, and p400, an ATPase chromatin remodeler. ATM is one of the first responders to DSBs and is responsible for the phosphorylation of a multitude of protein substrates including the histone variant H2AX. Beyond its phosphorylation ability, ATM has been proposed as a potential shuttle for other repair machinery, aiding in the early and efficient recruitment of proteins to the DNA damage foci. One such proposed protein is p400. The exact role of p400 in DSB repair is unknown but previous studies show that there is a decrease in repair efficiency in its absence. A prospective interaction is supported by previous studies in which p400 and p400 N-terminal derivatives co-immunoprecipitate with ATM *in vivo* in HEK293T cells.

This study aimed to confirm the interaction of ATM and p400 N-terminal derivatives *in vitro* and explore the functional implications of the association *in vivo* in U2OS cells. It was not possible to isolate full-length p400 derivatives *in vitro* and thus no conclusive results were obtained. Functional assays revealed the ability of one p400 fragment, F1, to inhibit DNA repair and cell proliferation after DNA double-strand break induction with bleomycin. Ectopic expression of the other two p400 N-terminal fragments, F2 and F3, induced an inhibition of cell proliferation under standard growth conditions. Although no conclusive results were acquired, a trend emerged suggesting that N-terminal fragment F1 is able to interfere with ATM protein-protein interactions resulting in a decrease in the efficiency of the DNA damage response and repair. These results implicate F1 as a potential target for further research in both DNA repair and cancer therapy.

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Abbreviations

°C	degrees Celsius
-ve	negative
A	ampere
Ac	acetylation
Amp	ampicillin
APS	ammonium persulphate
AT	Ataxia Telangiectasia
ATM	ataxia telangiectasia mutated
ATP	adenosine triphosphate
ATR	ataxia telangiectasia mutated and Rad3-related protein
BCA	bicinchoninic acid
BME	β-mercaptoethanol
bp	base pair
BSA	bovine serum albumin
c-Abl	Abelson murine leukemia viral oncogene homolog 1
cDNA	complementary DNA
CIP	calf intestinal phosphatase
CMV	cytomegalovirus
Co-IP	co-immunoprecipitation
DAPI	4', 6-diamidino-2-phenylindole
ddH ₂ O	double distilled water
DMEM	Dulbecco's Modified Eagle Medium
DMSO	dimethylsulfoxide
DNA	Deoxyribose nucleic acid
DNA-PKcs	DNA-dependent protein kinase catalytic subunit
dNTPs	Deoxyribonucleic triphosphate
DSB	Double strand break
DTT	Dithiothreitol
<i>E. coli</i>	<i>Escherichia coli</i>
EDTA	ethylene diamine tetra-acetic acid
EtBr	ethidium bromide
EtOH	ethanol
FAT	FRAP-ATM-TRRAP
FAT-C	FAT domain located at the protein's C-terminus
FBS	fetal bovine serum
g	gram
g	relative centrifugal force (force x gravity)
GSH	glutathione
GST	glutathione S-transferase
h	hours

H2Av	Drosophila H2A.Z and H2A.X homologue
H2AX	histone variant of H2A
γ H2AX	histone variant H2A.X phosphorylated at serine 139
HA	hemagglutinin
HAT	histone acetyl transferase
HCl	hydrochloric acid
HEK293T	human embryonic kidney cell line
HD	high definition
HF	high fidelity
HP1	heterochromatin binding protein 1
HR	homologous recombination
HRP	horseradish peroxidase
HSA	helicase and SANT associated
IF	immunofluorescence
IP	immunoprecipitation
ITPG	isopropyl β -D-1-thiogalactopyranoside
K	lysine
kb	kilobase
kDa	kilodalton
L	liter
LB	Luria-Bertani bacteriological media
M2 agarose	α -FLAG antibody immobilized on agarose beads
mA	milliampere
Mb	megabase
MCS	multiple cloning site
mg	milligram
min	minute
mL	milliliter
mM	millimol
mRNA	messenger ribonucleic acid
MRN	Mre11-Rad3-Nsb1
Mre11	meiotic recombination 11
MW	molecular weight
NBS	Nijmegen breakage syndrome
ng	nanogram
NHEJ	non-homologous end joining
NLS	nuclear localization sequence
nm	nanometer
NP-40	tergitol-type nonyl phnoxypolyethoxyethanol 40 (Igapal CA-630)
OD	optical density
PAGE	polyacrylamide gel electrophoresis
P3	generation 3 of baculovirus
PBS	phosphate buffered saline

PCR	polymerase chain reaction
PEG	polyethylene glycol
pen/strep	penicillin-streptomycin solution
PFA	paraformaldehyde
PHYRE2	protein homology/analogy recognition engine V 2.0
PI3K	phosphatidylinositol 3-kinase
PIKK	phosphatidylinositol 3-kinase-like protein kinase
pmol	picomol
PMSF	phenylmethanesulfonyl fluoride solution
PVDF	polyvinylidene fluoride transfer membrane
qPCR	quantitative real-time PCR
RE	restriction endonuclease
RNA	ribose nucleic acid
RNase	ribonuclease
RT	reverse transcription/reverse transcriptase
RT-qPCR	reverse transcription quantitative real-time PCR
S	serine
s	second
SANT	SWI3-ADA2-N-CoR-TFIIB
SDS	sodium dodecyl sulphate
SDS-PAGE	sodium dodecyl sulphate polyacrylamide gel electrophoresis
Sf9	clonal isolate of <i>Spodoptera frugiperda</i> Sf21 cells
siRNA	small interfering RNA
SWI2/SNF2	switch 2/sucrose non-fermentable 2
TAT	transactivator of transcription
TBE	tris boric acid EDTA
TBS/T	tris-buffered saline with tween-20
TE	tris EDTA buffer
TEMED	N, N, N', N'-tetramethylethylenediamine
TIP48	transactivation-domain interacting protein of 48 kDa
TIP49	transactivation-domain interacting protein of 49 kDa
TIP60	HIV-1 TAT interacting protein of 60 kDa
Tris	2-amino-2-hydroxymethyl-1,3-propanediol
TRRAP	transformation/transcription domain-associated protein
µg	microgram
µL	microliter
UV	ultraviolet light
V	volts
v/v	volume per volume
w/v	weight per volume
WT	wild type

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