RC VI.

Challenges in radiation protection research and their radiobiological bases

Katalin Lumniczky National Public Health Centre, Budapest The topic of the refresher course is focused on cellular and molecular mechanisms of non-targeted effects of ionizing radiation and how these effects impact direct irradiation effects and modify an individual's response to ionizing radiation.

Challenges in radiation protection research and their radiobiological bases

Katalin Lumniczky National Public Health Centre Department of Radiobiology and Radiohygiene

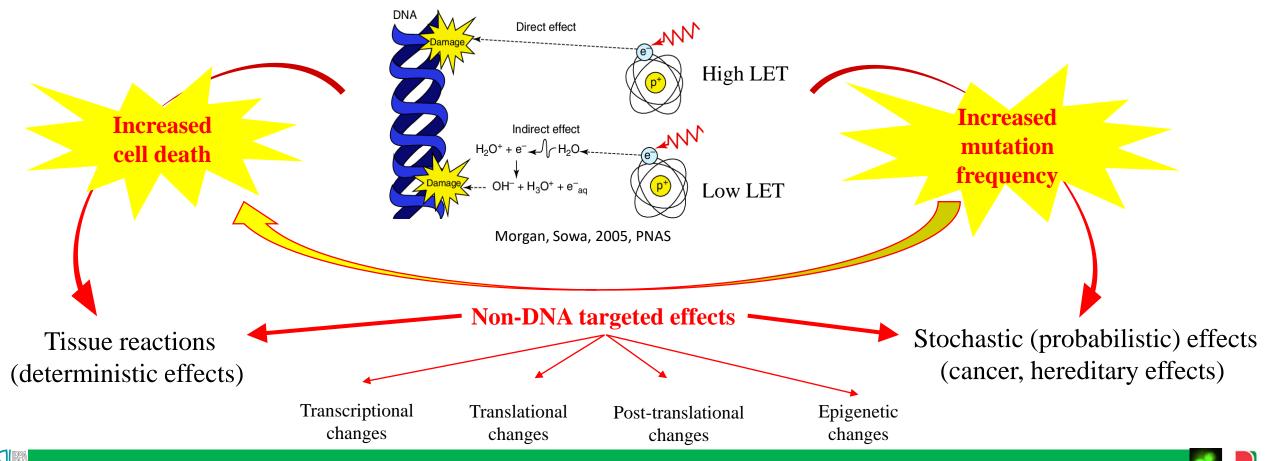


The biological effects of ionizing radiation

Targeted effects:

(Cellular damage due to direct absorbsion of ionizing radiation energy within the cells)

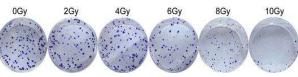
DNA targeted effects



Cell death

Mitotic cell death

- Cells loose their clonogenic potential – failed mitosis
- Slow process
- Cells temporarily maintain some metabolic activity
- Most frequent after IRQuantification:Colony forming assay

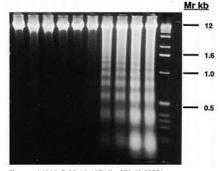


Liang et al 2018, doi.org/10.2147/CMAR.S176536

<u>Apoptosis</u>

- Programmed cell death
- Quick process
- Characteristic for certain cell types after IR
 Quantification:

<u>Apoptosis detection assays</u> (DNA fragmentation assays, Annexin, Caspase activation, etc.)



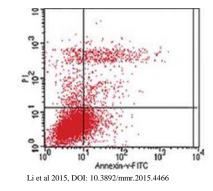
Shao et al 1998, DOI: 10.1074/jbc.272.52.32739

<u>Necrosis</u>

- ✤ Cell disintegration
- Mainly after high doses
- Quick process
- Characteristic after high IR doses

Quantification:

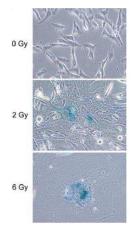
Eg. Annexin assay



Senescence

- Permanent cell cycle arrest
- Slow development
- Metabolic and secretory activity maintained
- Characteristic: increased secretory capacity of cells (SASP = senescenceassociated secretory phenotype)

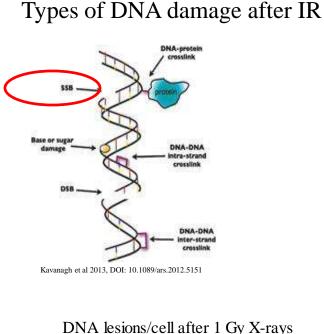
Quantification: Eg. β -gal assay



Jinno-Oue et al 2010, DOI: 10.1016/j.ijrobp.2009.08.054

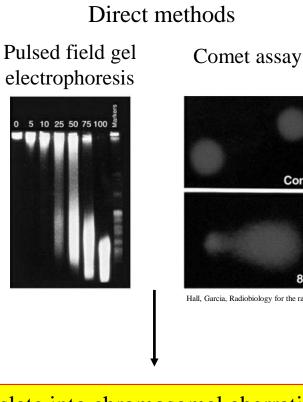


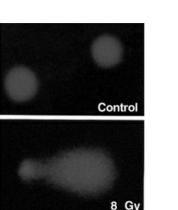
DNA damage



	11 10/5
Double-strand breaks (DSBs)	40
Single-strand breaks (SSBs)	1000
Base damage	>2000
DNA-DNA crosslinks	30

(measuring DNA double-strand breaks and repair kinetics)





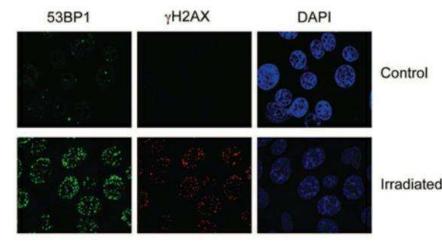
Hall, Garcia, Radiobiology for the radiologist, 8th Edition

Translate into chromosomal aberrations

Indirect methods

Detecting signaling and repair proteins that localize to sites of DNA strand breaks and form foci

(H2AX, 53BP1, ATM, RAD51, BRCA1)



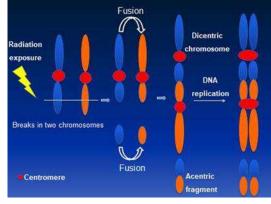
Hall, Garcia, Radiobiology for the radiologist, 8th Edition



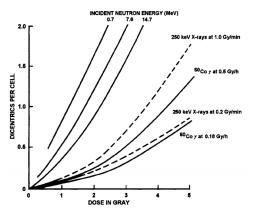


Chromosomal aberrations typical for ionizing radiation exposure

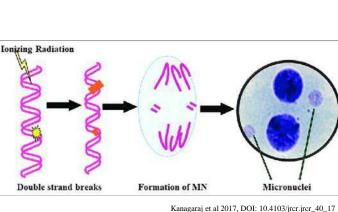
Dicentric chromosomes



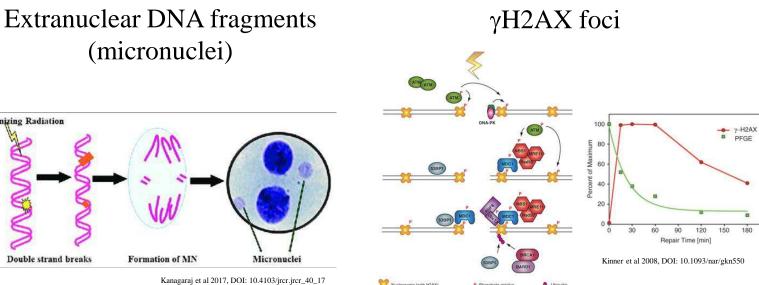
Balajee et al 2018, DOI: 10.21926/obm.genet.1804042

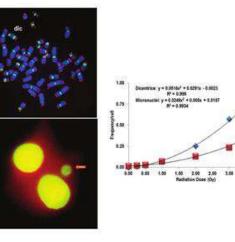


Choppin et al 2002, doi:10.1016/b978-075067463-8/50018-2

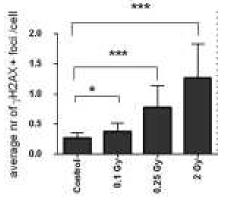


(micronuclei)





Zeegers et al 2017, DOI: 10.4103/2041-9414.198911

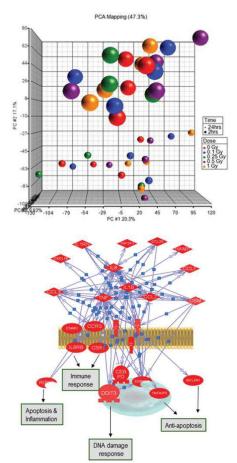


Szatmári et al 2017, DOI: 10.3389/fimmu.2017.00347

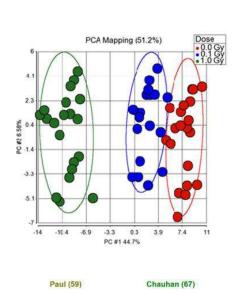


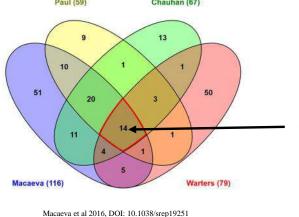
Non-DNA targeted effects

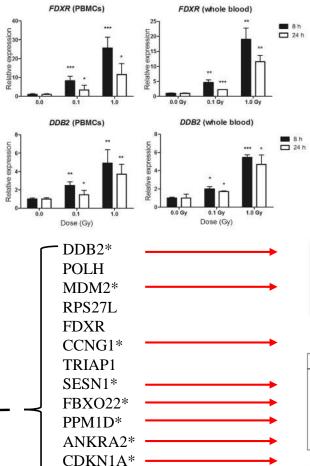
Transcriptional changes In the blood



Zeegers et al 2017, DOI: 10.4103/2041-9414.198911







TRIM22* BBC3

Transcriptional changes In the skin

-log(pValue)

- 1. Cell cycle_ESR1 regulation of G1/S transition
- 2. Cell cycle_Regulation of G1/S transition (part 1)
- 3. Translation Regulation of translation initiation
- 4. Cell cycle Role of SCF complex in cell cycle regulation
- 5. Development Angiopoietin Tie2 signaling
- 6. Immune response_IL-7 signaling in T lymphocytes
- 7. Development_Role of Activin A in cell differentiation and proliferation
- 6. Immune response_IL-7 signaling in 8 lymphocytes
- 9. Development Thrombopoietin-regulated cell processes
- 10. Development_TGF-beta receptor signaling
- 11. Signal transduction_PKA signaling
- 12. Development_Thrombopoetin signaling via JAK-STAT pathway

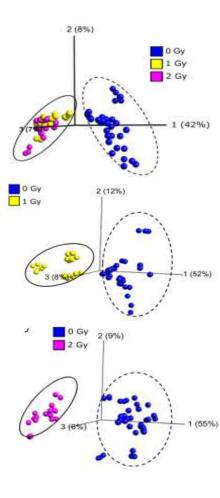
Immune response	Metabolic processes DNA damage: Regulation of G1/S checkpoints	WNT signalling Mitotic phase checkpoints Nek regulation in cell cycle Cell adhesion Apoptosis– Granzyme A signallin		
Dose 100 cGy SCF complex regulation of cell cycle Regulation of G1/S transition Cytoskeleton remodelling	DNA-damage:Regulation of G2/M checkpoints DNA-damage:Regulation of G1/S checkpoints Apoptosis	Glutathione metabolism Mitotic phase checkpoints Mitosis phase processes WNT signaling Nek regulation in cell cycle		
3 hours	8 hours TIME	> 24 hours		





Non-DNA targeted effects

Changes in the proteome (quantitative protein changes)



		Fold change*					Fold change*		
Accession no.	Protein name (Gene symbol)	1Gy	2 Gy	adjusted p value ^b	Accession no.	Protein name (Gene symbol)	1 Gy	2 Gy	adjusted p value ^b
Upregulated pro	teins				Down-regulated	1 proteins	in press.	1	
Q9H2G4	Testis-specific Y-encoded-like protein 2 (TSPYL2)	14.97 ± 5.50	15.26±5.69	3.81E-12 ^c	P69905	Hemoglobin subunit alpha (HBA1)	10.91 ± 3.30	12.60±2.94	4.44E-10 ^c
P22570	NADPH:adrenodoxin oxidoreductase, michchondrial (FDXR)	2.85±0.23	3.47±0.33	6.70E-11°	P68871	Hemoglobin subunit beta (HBB)	9.64±0.14	10.63±1.31	4.92E+10 ^c
H0YNJ6	GMP reductase (GMPR2)	2.23 ± 0.16	2.59 ± 0.17	1.94E-09*	O00479	High mobility group nucleosome-binding domain-containing	2.25±0.14	2.16±0.32	8.23E-08 ^c
P12814	Alpha-actinin-1 (ACTN1)	2.03 ± 0.13	2.56±0.14	1.01E-09*		protein 4 (HMGN4)			
Q07812	Apoptosis regulator BAX (BAX)	2.32 ± 0.28	2.37±0.17	8.96E-09*	E7EX17	Eukaryotic translation initiation factor 4B (EIF4B)	2.00±0.19	1.89±0.20	1.74E-08 ^c
Q92466	DNA damage-binding protein 2 (DDB2)	2.04±0.20	2.21±0.18	1.12E-08 ^c	Q9Y2W1	Thyroid hormone receptor-associated protein 3 (THRAP3)	1.92 ± 0.21	1.83 ± 0.14	3.83E+11*
Q8WWP7	GTPase IMAP family member 1 (GIMAP1)	1.89±0.23	2.02 ± 0.33	1.39E+08 ^c	P62263	405 ribosomal protein S14 (RPS14)	1.80 ± 0.29	1.82 ± 0.23	8.72E+08 ^c
Q6UXH1	Cysteine-rich with EGF-like domain protein 2 (CRELD2)	1.62 ± 0.10	2.01 ± 0.26	1.73E-08 ^c	Q9NYF8	Bcl-2-associated transcription factor 1 (BCLAF1)	1.56 ± 0.10	1.82 ± 0.18	7.39E+095
Q9NRX4	14 kDaphosphohistidine phosphatase (PHPT1)	1.77 ± 0.19	1.93±0.22	2.73E+09*	O15400	Syntaxin-7 (STX7)	1.76 ± 0.23	1.65±0.16	3.34E+08°
P06127	T-cell surface glycoprotein CD5 (CD5)	1.75±0.12	1.82±0.23	1.43E-08 ^c	D6RBZ0	Heterogeneous nuclear ribonucleoprotein A/B (HNRNPAB)	1.61±0.12	1.62 ± 0.05	1.94E+11°
P04083	Annexin A1 (ANXA1)	1.20 ± 0.06	1.73±0.15	2.44E-08*	P38159	RNA-binding motif protein, X chromosome (RBMX)	1.56 ± 0.14	1.57 ± 0.09	6.49E+09 ^c
Q01831	DNA repair protein complementing XP-C cells (XPC)	1.29±0.10	1.58±0.12	2.19E-07*	P35611	Alpha-adducin (ADD1)	1.48 ± 0.11	1.46 ± 0.05	9.65E+08 ^c
P21291	Cysteine and glycine-rich protein 1 (CSRP1)	1.49±0.10	1.52 ± 0.14	4.73E-07*	Q96PK6	RNA-binding protein 14 (RBM14)	1.36 ± 0.07	1.43 ± 0.06	4.91E+10 ^c
55175151	cAMP-dependent protein kinase catalytic subunit alpha	101530-512000241	-25865656555	1445575100	075400	Pre-mRNA-processing factor 40 homolog A (PRPF40A)	1.37 ± 0.07	1.42 ± 0.07	9.52E-09*
P17612	(PRKACA)	1.28 ± 0.09	1.52 ± 0.02	2.28E+095	Q00839	Heterogeneous nuclear ribonucleoprotein U (HNRNPU)	1.28 ± 0.05	1.40 ± 0.08	4.29E-09*
A0A087WZM2	Ribonuclease T2 (RNASET2)	1.26 ± 0.05	1.48 ± 0.10	2.98E+09*	X6R4W8	BUB3-interacting and GLEBS motif-containing protein	1.25±0.10	1.39±0.13	1.57E-08 ^c
P08311	Cathepsin G (CTSG)	1.64 ± 0.20	1.44 ± 0.13	2.71E-08 ^d		ZNF207 (ZNF207)			
Q9UHD8	Septin-9 (SEPT9)	1.22 ± 0.06	1.36 ± 0.07	4.09E-08 ^c	Q12874	Splicing factor 3 A subunit 3 (SF3A3)	1.22 ± 0.04	1.38±0.09	1.27E-08 ^c
Q96HC4	PDZ and LIM domain protein 5 (PDLIM5)	1.21 ± 0.09	1.34 ± 0.08	1.73E-08*	Q13435	Splicing factor 3B subunit 2 (SF3B2)	1.24 ± 0.08	1.32 ± 0.08	3.35E-08 ^c
P19367	Hexokinase-1 (HK1)	1.09 ± 0.05	1.34 ± 0.09	2.02E+08 ^c	Q9NR30	Nucleolar RNA helicase 2 (DDX21)	1.17 ± 0.03	1.29 ± 0.04	1.01E-08 ^c
P08133	Annexin A6 (ANXA6)	1.15 ± 0.06	1.30 ± 0.05	4.20E+08c			Lee et al 2018	, DOI: 10.1038/s4	1598-018-3174
P21283	V-type proton ATPase subunit C1 (ATP6V1C1)	1.26 ± 0.09	1.29 ± 0.07	1.74E-07*				,	
P48426	Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha (PIP4K2A)	1.30±0.06	1.25±0.05	1.04E-074					
P20073	Annexin A7 (ANXA7)	1.15 ± 0.06	1.24 ± 0.07	1.12E-07*					
P46777	60S ribosomal protein L5 (RPL5)	1.09±0.13	1.23±0.18	1.46E-06*					
075083	WD repeat-containing protein 1 (WDR1)	1.14 ± 0.05	1.21 ± 0.07	1.98E-08 ^c					
Q9Y490	Talin-1 (TLN1)	1.20 ± 0.05	1.20 ± 0.06	5.18E+08 ^c					
A0A024R4M0	40S ribosomal protein S9 (RPS9)	1.30±0.11	1.19±0.11	3.00E-08 ^d	-				

 1.22 ± 0.05

1.10±0.07 1.24E-07^d

Protein tyrosine phosphatase, receptor type, C, isoform CRA_d

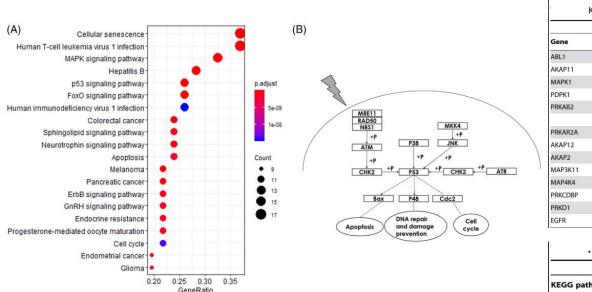
A0A0A0MT22

(PTPRC)



Post-translational modifications – protein phosphorylation

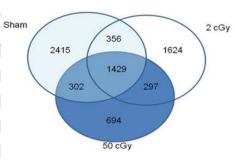
Non-DNA targeted effects



Kinases and regulators affected by radiation.

Gene	Peptide	T-test: 2 cGy	T-test: 50 cGy	Change2 cGy	Change 50 cGy
ABL1	K.GQGESDPLDHEPAVS*PLLPR.K	0.0113	0.0008	2.6	2.9
AKAP11	R.SVS*PTFLNPSDENLK.T	0.1771	0.0046	2.7	2.0
MAPK1	R.VADPDHDHTGFLTEY*VATR.W	0.0009	0.0031	2.8	2.5
PDPK1	R.ANS*FVGTAQYVSPELLTEK.S	0.0043	0.0132	3.5	3.2
PRKAB2	R.DLSSS*PPGPYGQEMYAFR.S	0.0009	0.0106	3.6	2.7
		G-Test: 2 cGy	G-Test: 50 cGy	Spectra: 0:2 cGy	Spectra: 0:50 cGy
PRKAR2A	VADAKGDS*ES*EEDEDLEVPVPSR	16.76	11.45	38:11	38:11
AKAP12	VLSKPPEGVVSEVEMLSS*QER	0.52	7.35	0:1	0:7
AKAP2	TNGHS*PSQPR	6.73	4.94	11: 2	11: 2
MAP3K11	NVFEVGPGDS*PTFPR	5.13	0.23	5:0	5:3
MAP4K4	RDS*PLQGSGQQNSQAGQR	0.78	4.37	8:5	8:1
PRKCDBP	APEPLGPADQSELGPEQLEAEVGES*S*DEEPVESR	0	37.86	0:0	0:35
PRKD1	RLS*NVSLTGVSTIR	1.28	4.13	5:2	5:0
EGFR	ELVEPLT*PSGEAPNQALLR	5.13	4.13	5:0	5:0

Phosphopeptides



KEGG pathways affected by radiation.

KEGG pathway	2 cGy		50 cGy				
	Count	Proteins	Count	Proteins			
Insulin signaling pathway	8	MAPK1, PDPK1, IRS2, EIF4EBP1, PRKAR2A, TSC1, PRKAB2, TSC2	6	PDPK1, IRS2, PRKAR2A, EIF4EBP1, TSC1, PRKAB2			
Pathways in cancer	7	EGFR, MAPK1, CCDC6, HDAC1, RALBP1, JUN, ABL1	5	EGFR, HDAC1, PML, LOC652671, ABL1			
MAPK signaling pathway	6	EGFR, MAPK1, JUN, RRAS, STMN1, MAP3K11	6	EGFR, MAP4K4, NF1, RRAS, NFATC4, STMN1			
mTOR signaling pathway	6	EIF4B, MAPK1, PDPK1, EIF4EBP1, TSC1, TSC2	4	EIF4B, PDPK1, EIF4EBP1, TSC1			
Tight junction	6	EPB41L2, RAB3B, TJP1, MAGI1, RRAS, TJAP1	4	EPB41L2, MAGI1, RRAS, TJP2			
Adherens junction	6	EGFR, MAPK1, TJP1, BAIAP2, LMO7, VCL	3	EGFR, LMO7, CTNND1			
Endocytosis	5	EGFR, DAB2, RABEP1, SH3KBP1, IQSEC1	4	EGFR, USP8, SH3KBP1, IQSEC1			
Spliceosome	1	SF3B2	6	SFRS4, SFRS9, SNW1, SFRS1, PRPF38B, SF3B2			

Yang et al 2010, DOI: 10.1371/journal.pone.0014152

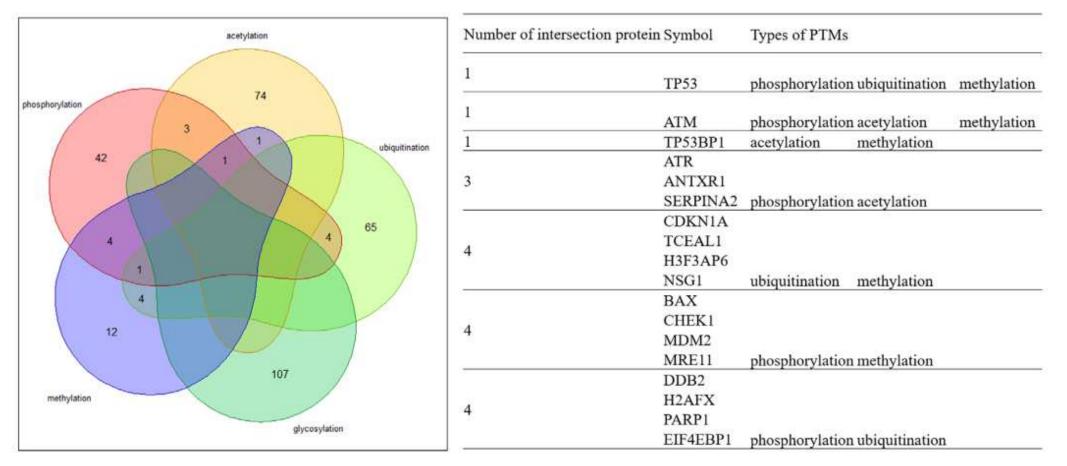
Liu et al 2019, DOI: 10.1002/cbf.3467





Non-DNA targeted effects

Post-translational modifications



Liu et al 2019, DOI: 10.1002/cbf.3467

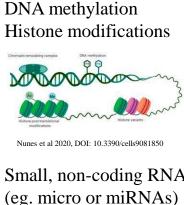


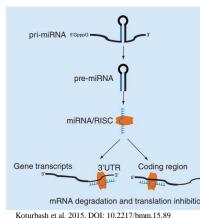


Non-DNA targeted effects

Epigenetic changes miRNA changes

Epigenetics: heritable changes in gene activity, transcript architecture (eg. splice variants), without changes in the DNA sequence





Serum or plasma miRNAs as IR biomarkers in human samples.

miRNAs	Material	Species	Predictors	References				
miR-199a-5p†	Serum	Human	Radiotherapy prognosis	Baek et al. (2020)	EGFR Receptor Family	- FIII	\langle	м
miR-218-5p†	Serum	Human	-	Chen et al. (2021)				Cytop
miR-29a-3p], miR-150-5p]	Plasma	Human	IR-induced organ injury	Dinh et al. (2016)	C	a miR-30e	OH O	OH ROS .
miR-92a-1-5p], miR-25-5p], miR-1290†	Serum	Human	Radiotherapy prognosis	Fan et al. (2020)	↓ ↓ miR-21	niR-106b	ILou	B CON CONCERNMENT
miR-34a†	Serum	Human	Dose estimation	Halimi et al. (2016)	RAS PI3K miR-144 miR-222	miR-214 miR-205	D	imaged DNA
miR-26b-5p↓	Serum	Human	Radiotherapy prognosis	Han et al. (2020)	miR-498 miR-96-5	miR-20a	niR-18a-5p niR-30a — ATFI	ATM ATR
Combination of 16 miRNAs(e.g. miR-100-5p, miR-106b-5p, miR-145-5p)	Serum	Human	IR-induced organ injury	Hawkins et al. (2015		P53 P53	miR-375	
miR-143↓	Serum	Human	Radiotherapy prognosis	Hiyoshi et al. (2017)	MEK AKT miR- miR-		P53 P53	CDC25A ←
miR-12811, miR-6732-3p1	Serum	Human	Radiosensitivity	Li et al. (2020a)	lead and search	b miR-19a	miR-200c	
miR-6731-5p†, miR-208b-3p†, miR-2116-3p↓, miR-574-3p↓etc.	Exosomes in plasma	Human	Radiotherapy prognosis	Li et al. (2020b)	→ → mTOR	P53 P21 H	- miR-106b	Cyclin
miR-130a†, miR-25†, miR-191*†	Serum	Human, mouse	Radiotherapy prognosis	Lv et al. (2020)	ERK MTOR		hsa-miR-874-5	5
Combination of miR-425-5p, miR-21-5p, miR-106b-5p, miR-590-5p, miR-674- 3p, miR-885-3p	Plasma	Human	Dose estimation	Summerer et al. (2013)		BCL-2 BAX		Checkpoint Activation
miR-142-3p, miR-186-5p, miR-195-5p, miR-374b-5p and miR-574-3p	Plasma	Human	Radiotherapy prognosis	Summerer et al. (2015)	Y	miR-190 OH ROS	Repair RAD51	– miR-34a
Combination of 11 miRNAs(e.g. miR-10b-5p, miR-125b-5p, miR-126-3p)	Serum	Human	Radiosensitivity	Sun et al. (2018)				
miR-208a [†] , miR-200a-3p [⊥] , miR-126-3p [⊥] , miR-29b-3p [⊥]	Serum	Human		Tang et al. (2016)	+	+	Ļ	+
Combination of miR-425-5p, miR-185-5p	Serum	Human	IR-induced organ injury	Tomasik et al. (2021	Proliferation	Apoptosis Compl	eted Cell Cycle	Cell Cycle Arrest
Combination of miR-155, miR-221	Serum	Human	IR-induced organ injury	Xu et al. (2014)		Chen	et al. 2021, DOI:10.100	07/s11356-021-1250
miR-3451	Serum	Human	Radiotherapy prognosis	Yu et al. (2016)				
miR-5041	Serum	Human	Radiotherapy prognosis	Zhao et al. (2015)				

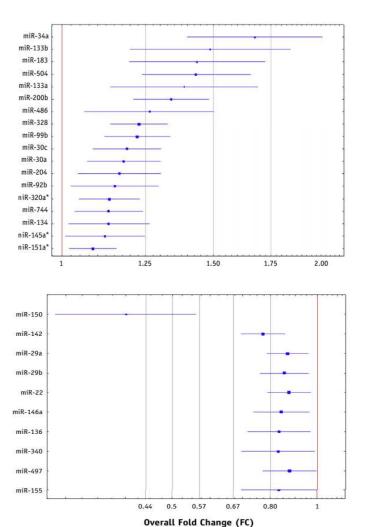
Jia et al. 2022, DOI: 10.3389/fcell.2022.861451

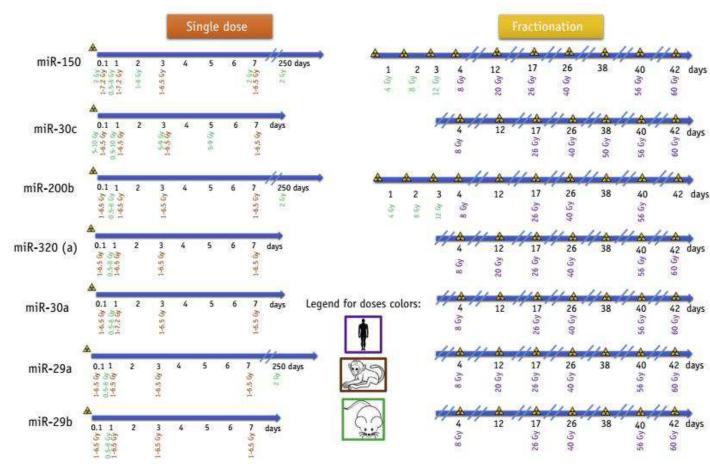




Non-DNA targeted effects

Epigenetic changes – miRNA changes





Malachowska et al. 2019, DOI:10.1016/j.ijrobp.2019.10.028

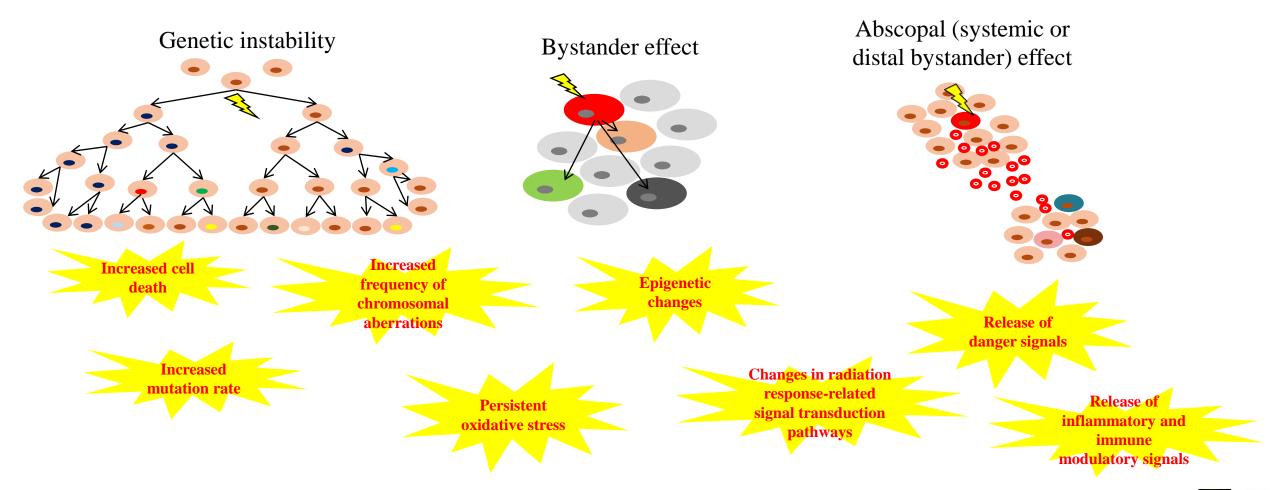




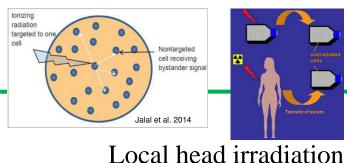
The biological effects of ionizing radiation

Non-targeted effects:

(Cellular damage in cells not directly hit by ionizing radiation)







Bystander effects

Experimental in vivo evidence

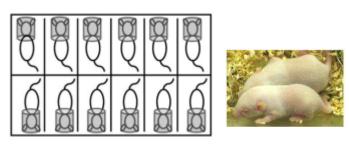
Irradiation of the lower part of the body

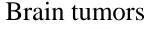
Control Whole body exposed Head Exposure Scatter exposure

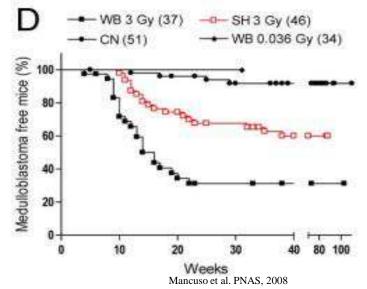
Distant changes in the spleen DSBs

BALB/c 1.2 1.2 1.2 0.8 0.2 CT BH 6 hours BALB/c 1872/1000 982/1000 824/1000 774/1000 BH 4 days

Koturbash et al. IJROBP, 2008

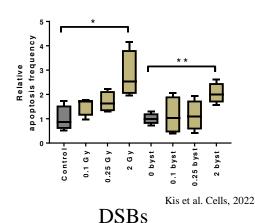


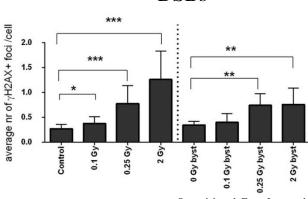




Mice treated systemically with extracellular vesicles originating from irradiated mice

Apoptosis

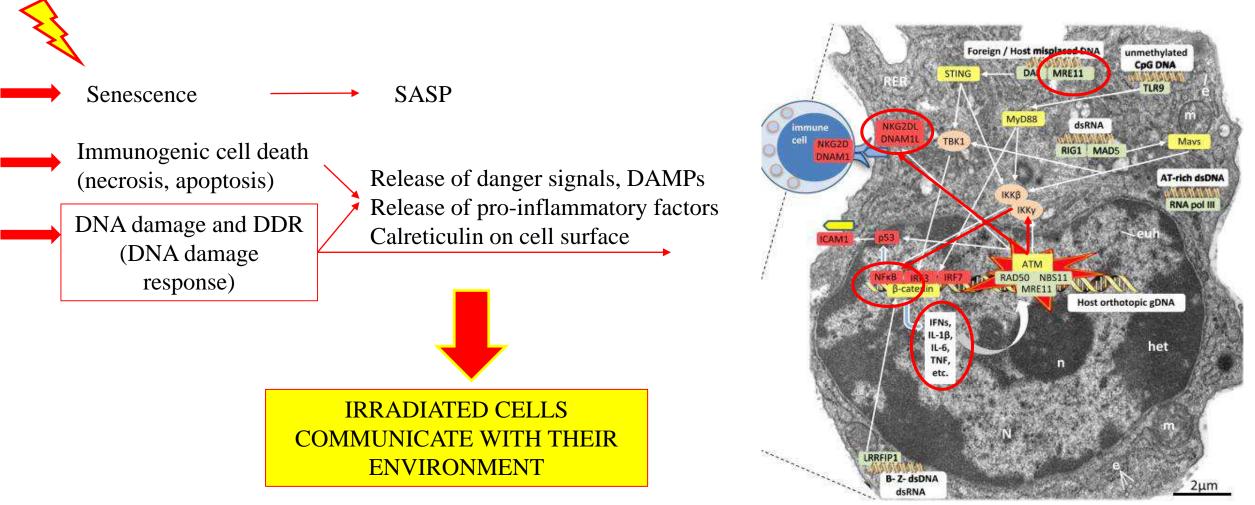




Szatmári et al. Front Immunol, 2017

Bystander effects

Hypothetical mechanism

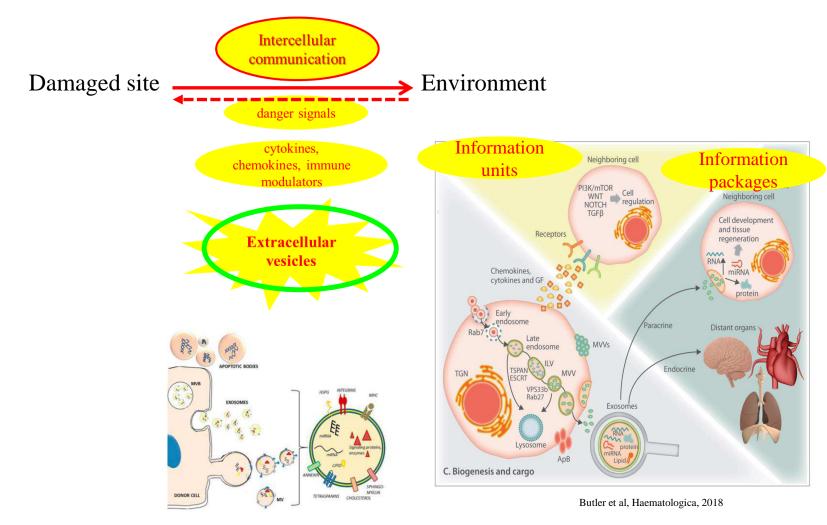


Pateras et al. Pharmacol & Therapeutics 2015



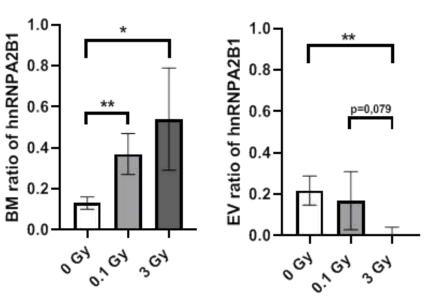


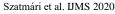
Bystander effects



hnRNPA2B1

- A major RNA-binding protein involved in miRNA transport into the EVs
- It is involved in DNA damage response and in altered telomere maintenance

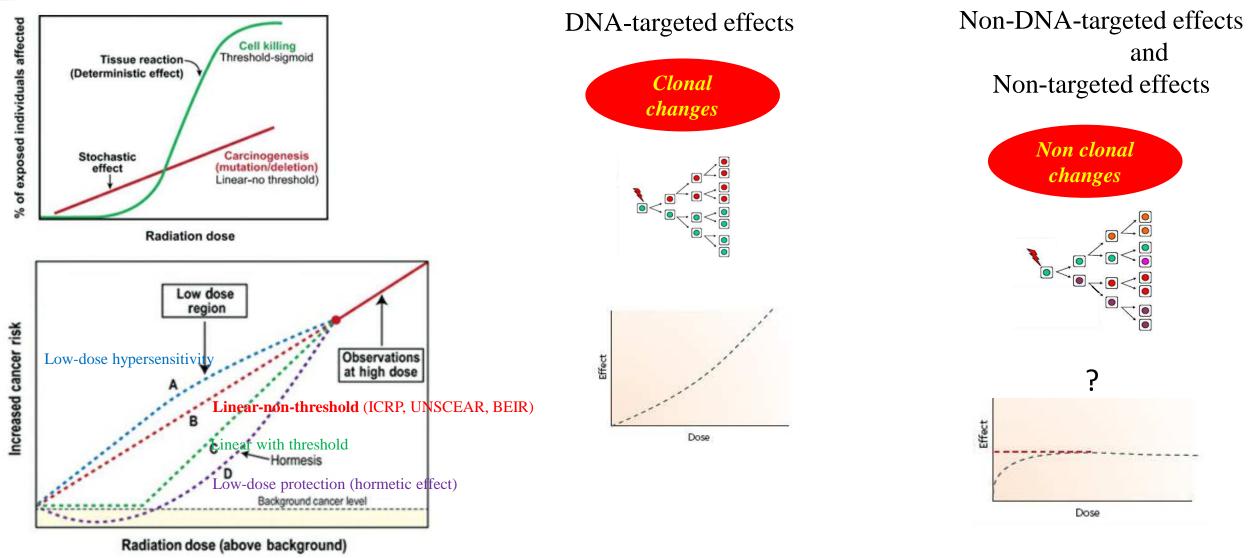








Dose-response relationships



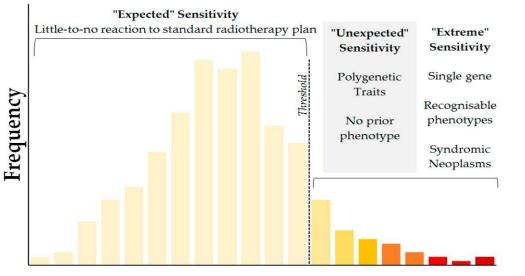
 $Hall,\,Garcia-Radiobiology\,for\,the\,Radiobiologist,\,8th\,Edition$



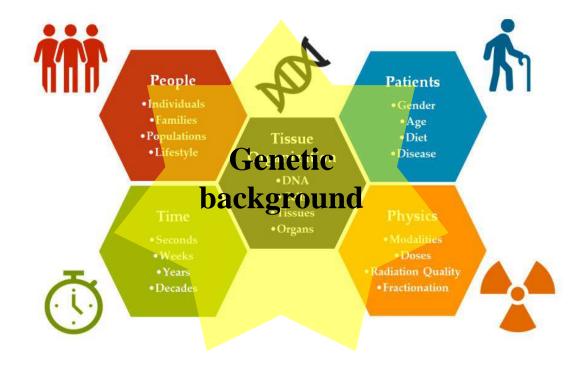
Biological modifiers of radiation effects

Individual radiosensitivity and susceptibility:

(Individual tolerance to ionizing radiation induced toxic effects within the healthy tissues and the probability to develop cancer after exposure to a given dose of radiation)



Increasing Sensitivity to Acute/Late Radiotoxicity \rightarrow



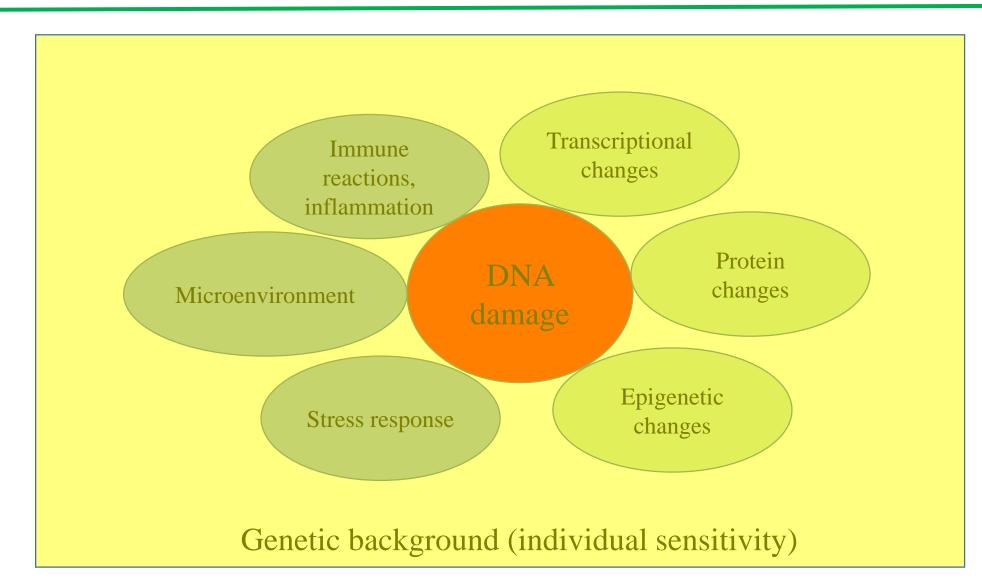
Polygenic!

Habash et al. Cancers 2017



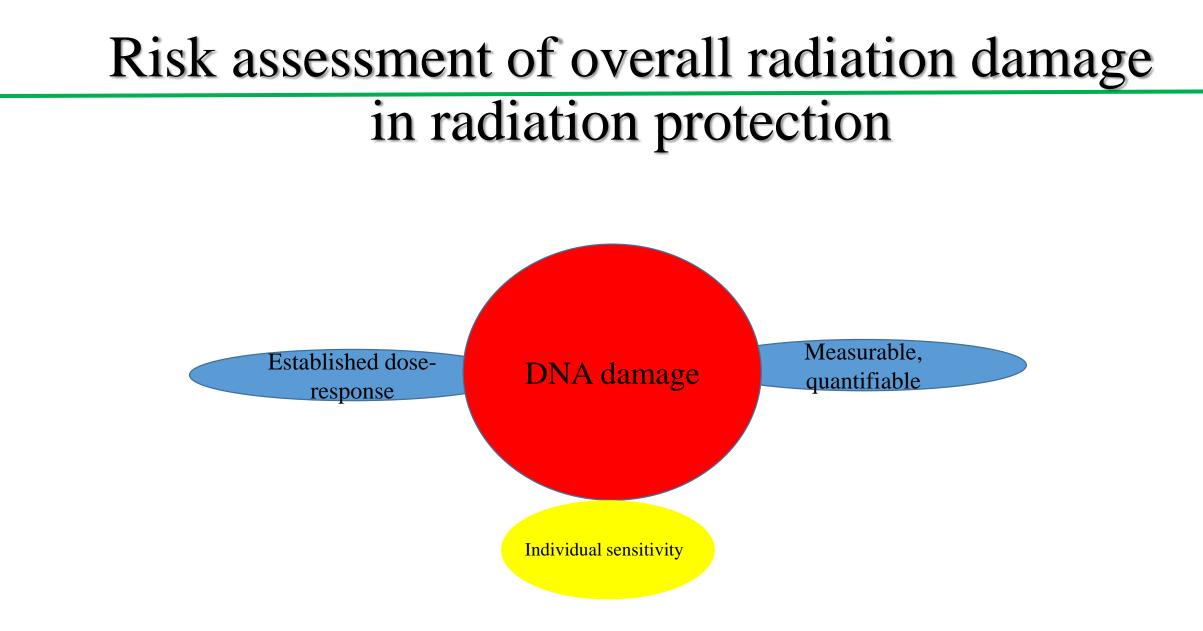


Overall radiation damage













Thank you for your attention!









